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US-09-001-984C-106
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Sequence 35, Appl	US-09-206-942-35	4,	915	•	118.5	
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Sequence 106, Application US/09001984C

Patent No. 6245331

General Discretion (245331

General Discretion)

APPLICANT: Laal, Suman

APPLICANT: Zolla-Pazzer, Susan

APPLICANT: Zolla-Pazzer, Susan

APPLICANT: Belisle, John T

TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE

FILE REFERENCE: NYU-011

CURRENT APPLICATION NUMBER: US/09/001,984C

CURRENT APPLICATION NUMBER: 1996-12-31

FRIOR APPLICATION NUMBER: 60/034,003

PRIOR PILING DATE: 1996-12-31

NUMBER OF SEQ ID NOS: 106

SOFTWARE: Patentin Ver. 2.1

LENGTH: 741
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100.0%; Score 3810;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 740; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Mycobacterium tuberculosis
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us-09-688-672a-2.rai

Db 242 LIDPESQUGTTDRAGUKDVILESAITTIMDFEDSVAAVDAADKUGYRNWLGINKGDLAA 301 302 AVDKGGTAFLRVLANRDRNYTAPGGGOFTLPGRSIMFVRNVGHLMTNDAIVDTDGSEVFEG 360 302 AVDKGGTAFLRVLANRDRNYTAPGGGOFTLPGRSIMFVRNVGHLMTNDAIVDTDGSEVFEG 361 303 AVDKGGTAFLRVLANRDRNYTAPGGGOFTLPGRSIMFVRNVGHLMTNDAIVDTDGSEVFEG 361 304 DADLFTGLIAHGLKAADVAGPLINSRTGSIYIVKPKCHGPAEVAFTCELFSRVEDVLG 420 421 IMAGOFWARTGIMDESRRTTVNLKACIKAADRAVEINTGFLDRTGDETHTSNEAGPRVRKG 481 422 LADONTWKIGIMDESRRTTVNLKACIKAADRAVEINTGFLDRTGDETHTSNEAGPRVRKG 481 424 LADONTWKIGIMDESRRTTVNLKACIKAADRAVEINTGFLDRTGDETHTSNEAGPRVRKG 481 425 LADONTWKIGIMDESRRTTVNLKACIKAADRAVEINTGFLDRTGDETHTSNEAGPRVRKG 481 426 LADONTWKIGIMDESRRTTVNLKACIKAADRAVEINTGFLDRTGDETHTSNEAGPRVRKG 481 427 LADONTWKIGIMDESRRTTVNLKACIKAADRAVEINTGFLDRTGDETHTSNEAGPRVRKG 481 428 TWKSOPWILAYEDHNVDAGFSGRAADRAVEINTGFLDRTGDETHTSNEAGPRVRKG 481 439 TWKSOPWILAYEDHNVDAGLAAGFSGRAADRAVEINTELMADNVETKIAOPRAGASTAW 541 480 TWKSOPWILAYEDHNVDAGLAAGFSGRAADRAMTELMADNVETKIAOPRAGASTAW 541 481 VPSFTAATLHALHYHQVDVAAVQGGLAGKRRATIEQLLTIPLAKELMAPDEIREEVDNN 601 542 VPSFTAATLHALHYHQVDVAAVQGGLAGKRRATIEQLLTIPLAKELMAPDEIREEVDNN 601 601 CQSILGYVVRWVDQGVGSKVPDIHDVALMEDRATLRISSQLLANWLRHGVITSADVRAS 661 602 CQSILGYVVRWVDGGVGSKVPDIHDVALMEDRATLRISSQLLANWLRHGVITSADVRAS 661 603 LGRMAPLVDRQNAGDVAYRPMARNPEDRATLRISSGLLANWLRHGVITSADVRAS 661 604 LERMAPLVDRQNAGDVAYRPMARNPEDRATLLISGAQOPNGYTEPILHRRRREF 721	SULT 3 SULT 3 -0-252-991A SQUENCE 225 SQUENCE 225 SACHORCE 225 SACHORCE 225 SACHORCE 225 SACHORCE 225 CURREAL INFO FILE REFERE CURRENT FIL PRIOR APPLI PRIOR FLILIN PRIOR APPLI PRIOR FLILIN PRIOR APPLI PRIOR FLILIN	SEQ 1D NO 2224 INORDER OF S214
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80 MLIDDYHRNN-SGTIDQEAYEDFLKEIGYLVEEPEAAEIRTQNVDTEISSTAGPQLVVPI 138
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                                                                                                                                                                   60.1%; Score 2289; DB 2;
61.3%; Pred. No. 4.1e-213;
ive 90; Mismatches 184;
      (718) 884-6600
                                                 4
   TELEPHONE: (718) 884-66C
TELEFAX: 718/601-1099
TELEX: 620428
INPORMATION FOR SEQ ID NO: 2
SEQUENCE CHRARACTERISTICS:
LENGTH: 739 amino acids
TYPE: amino acids
                                                                                                                                                                                                  Conservative
                                                                                                      TOPOLOGY: linear;
MOLECULE TYPE: protein
US-08-836-943-2
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US-09-328-352-7603
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                 300 AAVDKDGTAFLRVLNRDRNYTAPGGGOFTLPGRSLMFVRNVGHLMTNDALVDTDGSEVFE
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COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION NUMBER: US/08/836,943
FILING DATE: 08-MAX-1997
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Myers, Jonathan
REGISTRATION NUMBER: 26,963
REFERENCE/DOCKET NUMBER: 20357
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08836943
Patent No. 5965391
GENERAL INFORMATION:
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APPLICANT: Eikmanns, Bernhard
APPLICANT: Sahm, Hermann
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US-08-836-943-2
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Length 739; Indels 540

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SLERMAPLVDRONAGDVAYRPMAPNFDDSIAFLAAQELILSGAQOPNGYTBPILHRRRR
                                              SLERMAVVVDKQNAGDEAYRDNAFNYDASLAFQAAKDLIFEGTKSPSGYTEPILHARRRE
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Patent No. 6562958
GENERAL INFORMATION:
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al Similarity
167; Conserv
                                                                                       SEQ ID NO 5503
LENGTH: 3892
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APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUDANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7603
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97; Mismatches 185;
                                                                                                   , ORGANISM: Acinetobacter baumannii
US-09-328-352-7603
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432; Conservative
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BANDAMINI FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BANDAMINI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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21.6%; Pred. No. 0.0043;
tive 78; Mismatches 300; Indels 228;
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US-09-328-352-5503
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RESULT

RESULT 6 US-09-328-352-5503 ; Sequence 5503, Application US/09328352 us-09-688-672a-2.rai

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SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/237,919
3498 AAANQ-FLDTLARHRARRGLTS--
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US-008-237-919-2
Sequence 2, Application US/08237919
; Patent No. 5610281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-D0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B080;
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-341
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CITY: Boston
STATE: MA
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Matches 134;
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3213 SSRIT--EFEQRERAISGGRGIDVVLNALSGDFVDASARLLREGGR-FVEMGKTDIRIDL 3269
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   Sequence 3, Application US/09428517
Fatent No. 6251636
Fatent No. 6251636
GENERAL INFORMATION.
APPLICANT: Betlach, Mary C.
APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: McDanial, Robert
APPLICANT: Tang, Li
TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 30062-20029.00
CURRENT APPLICATION NUMBER: US/09/428,517
CURRENT PILING DATE: 1999-10-28
EARLIER APPLICATION NUMBER: 60/120,254
EARLIER FILING DATE: 1999-02-16
EARLIER FILING DATE: 1998-10-29
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
FEMALE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence: Recombinant; OTHER INFORMATION: Oleandolide PKS
US-09-428-517-3
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3.5%; Score 135; DB 3; Length 3816;
Best Local Similarity 21.3%; Pred. No. 0.01;
Matches 190; Conservative 112; Mismatches 297; Indels 29
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GENERAL INFORMATION:
APPLICANT: Brenner, Michael B
APPLICANT: Cepek, Karyn L
TITLE OF INVENTION: Methods and Compositions for
TITLE OF INVENTION: Methods and Compositions for TITLE OF INVENTIONS METHOD TO THE TO 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3603 HRPSARAGTATAAPATGPEAFARELAAAPDPRRALRDLVRGHVALVLGHSGPBAIDAEQA 3662
---VSLGWGLWHEASGLTGGLADIDRDRMS--RAGI 3549
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No. 0.004; tive 66; Mismatches 210; Indels 2
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600 Atlantic Avenue
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PRIOR FILING DATE: 1995-05-03
BRIOR APPLICATION NUMBER: US 08/732,429
PRIOR FILING DATE: 1996-11-01
NUMBER OF SEQ ID NOS: 9
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                                                                                          Best Local Similarity 22.0
Matches 134; Conservative
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                          , MOLECULE TYPE: protein US-08-732-429-2
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amino acid
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US-09-798-267-2
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 --KDVILESAITTIMDFEDSVAAV 278
                                                                                                        279 DAADKVLGYRNWLGLN--KGDLAAAVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMF 336
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                                                                                                                                                                                                                                                                                            DEERRITVNLKACIKAAADRVVFINTGFLDRIGDEIHTSMEAGPMVRKGTMKSQPWILAY 491
                                                                                                                                                                                                                                                                                                                                                                                 ----VEAGLOIPAILGILG-----GILAL--LILILLLLLFLRRRAVVKEPLLP-PEDD 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methods and Compositions for Modulating Heterotypic E-cadherin Interactions with T {\rm Lymphocytes}
                                                                                                                                                                   337 VRNVGHLMTNDAIVDTD-GSEVFEGIMDALFTGLIAIHGLKASDV--NGPLINSRTGSIY
                                                                                                                                                                                                                                                                                                                                                                                                                    -----QVDVAAVQQGLAGK----RRATIEQLLTIPLAKELAWAPDEI
                                                                                                                                      ------RIWILEINPOTGAISTRAELDREDFEHVKN--STÝTA------
                                                                 OPERATING SYSTEM: PC_DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/732,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Wolf, Greenfield & Sacks P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
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                                             LLINHGLHIEILIDPESQVGTTDRAGV-
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APPLICATION NUMBER: 08/237,919
FILING DATE: 3 MAY 1994
ATTORNEY/AGENT INFORMATION:
NAME: PLUMEY, Elizabeth R
REGISTRATION NUMBER: 36,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08732429
Patent No. 6300080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
AMBUTTER: IBM PC COMPATIBLE
PC-DOS/MS.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEPAX: 617-720-2441
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                594 REEVDNNCQS
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STATE: MA
COUNTRY:
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APPLICANT: Brenner, Michael
APPLICANT: Gepek, Karyn
TITLE OF INVENTION: Methods and Compositions for Modulating Heterotypic E-cadherin
TITLE OF INVENTION: Interactions with T Lymphocytes
FILES REPRENOTE: L0560/7008RPB
CURRENT APPLICATION NUMBER: US/09/798,267
CURRENT APPLICATION NUMBER: US 08/237,919
PRIOR FILLING DATE: 1994-065-03
PRIOR FILLING DATE: 1994-065-03
PRIOR PAPLICATION NUMBER: PCT/US 95/05518
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                                                                                                                                                                                                                                                   142 YGTDVIPETDGAEKGPTYNKV--RGD-----KVIAYARKFLDDSVPLSSGSFGDATGFT 193
                                                                                                                                                                                                                                                                                                                   354 TATAVITVIDINDNPPIENPTTYKGOVPENEANVVITTLKVIDADAPNTPAWEAVYTILN 413
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                                                                                                                           91 LPEPDDFTI-----TTSGVDAEITTTAGPQLVVPVLNARFALNAANARWGSLYDAL
                                                                  Gaps
                                                                  Indels 200;
3.4%; Score 128; DB 4; Length 878; 22.0%; Pred. No. 0.004; ive 66; Mismatches 210; Indels 2.
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Patent No. 6406870
GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Methods and Compositions for Modulating Heterotypic
TITLE OF INVENTION: E-cadherin Interactions with T Lymphocytes
TITLE OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks P.C.
STREET: 600 Atlantic Avenue
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                                                                                                                                                                                                             Length 878;
                                                                                                                                                                                                         3.4%; Score 128; DB 4; I
22.0%; Pred. No. 0.004;
tive 66; Mismatches 210;
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; PRIOR FILING DATE; 1996-11-01; NUMBER OF SEQ ID NOS: 9; SOFTWARE: Patentin version 3.0; SEQ ID NO 3; LENGTH: 878; TYPE: PRT ORGANISM: HOMO SAPIENS
US-09-798-267-3
                                                                                                                                                                                                         Query Match
Best Local Similarity 22.0%
Matches 134; Conservative
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Patent No. 6406870

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Methods and Compositions for Modulating Heterotypic E-cadherin
TITLE OF INVENTION: Interactions with T Lymphocytes
FILE REFERENCE:
CURRENT APPLICATION NUMBER:
US/09/798,267

CURRENT APPLICATION NUMBER:
US/08/237,919

PRIOR PILING DATE:
1994-05-03

PRIOR APPLICATION NUMBER:
US/08/237,919

PRIOR APPLICATION NUMBER:
US/08/237,919

PRIOR APPLICATION NUMBER:
US/08/237,919

PRIOR APPLICATION NUMBER:
US/08/237,919
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                                                                                                                                                             Query Match
3.4%; Score 128; DB 4; Length 878;
Best Local Similarity 22.0%; Pred. No. 0.004;
Matches 134; Conservative 66; Mismatches 210; Indels 200;
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                                                                                            ; ORGANISM: Homo sapiens
US-09-798-267-2
SOFTWARE: PASEO ID NO 2
LENGTH: 878
TYPE: PRT
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US-09-798-267-3
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22.0%; Pred. No. 0.004;
iive 66; Mismatches 210; Indels 200;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRINT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05518
FILING DATE: herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  394 IVKPK-----MHG----PAEVAFTCEL-FSRV--
                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/237,919
FILING DATE: 3 May 1994
ATTORNEY AGENT INFORMATION:
NAME: Plumer, Elizabeth R
REGISTRATION NUMBER: 36,637
REPRENCE/DOCKET NUMBER: B0801/7023
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 678 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 22.0
Matches 134; Conservative
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304 GNFIDENLKA 813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----QHLIRQALAD--ARLT----- 10582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10700 VGGTNAHVVLBEAPAVBESPAVBPPAGGGVVPWPVSAKTSAALDAQIGQLAAYABDRTDV 10759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 VLNARFALNAANARWGSLYDAL-YGTDV---IPETDGAEKGPTYNKVRGDKVIAYARK-- 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 FLDDSVPLSSGSFG----DATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLINHGLHI------EILIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDA 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A---DKVLGYRNWLGLNKGDLAAAVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFV 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----RNVGHLMTNDAIVDTDGSEV--FEGIMDALFTG--LIAIHGLKASDVNGPL 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INSRIGSIYIVKPKWHGPAEVAFTCELFSRVEDVLGLPQNTMKIGIMDEERRTTVNLKAC 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --HALHYHQV 557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.4%; Score 128; DB 3; Length 11877;
20.7%; Pred. No. 0.34;
tive 85; Mismatches 319; Indels 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 11877;
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                                                                                                                                                                          APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
APPLICANT: Zhao, L.
TILLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600.438US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVGKGMWTMTELMADMVETKIAQPRAGASTA-W-VPSPTAATL-
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                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          445 IKAAADRVVFINTGFLDRTGDEIHT---
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Sequence 6, Application US/09105537A
Patent No. 6265202
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 11877
TYPE: PRT
ORGANISM: Streptomyces venezuelae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 20.7
Matches 172; Conservative
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Dp	1645G	GIDPTSLQGQQVGVFAGTNGPHYEPLLRNTAEDLEGYVGTGNAAS 1689	
δγ	194 VQD	VQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEILIDPESQVGTTDR 253	
Db	: 1690 IMS	I	
ογ	254 AGV	254 AGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAAAVDK 304	
Db	1737 GG-	VIVMSTPTTFVBFSRQRGLAEDGRSKAFAASADG-FGPAEGVGMLLVERLSDARR 1792	
ò	305 DGT	AFLRYLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDALVDTDGSE 356	
Db	1793 NGH	1793 NGHRVLAVVRGSAVNQDGASNGLTAÞNGPSQQRVIRRALADARLTTADVD 1842	
δ	357 VFE	GIMDALFTGTIALHGLKASDVNGPLINSRTGS 391	
• q 0	1843	843VVEAHGTGTRLGDPIEAQALIATYG-QGRDTEQPLRLGSLKSNIGHTQAAAGVSGI 1897	
٥'n	392 IYI	IYIVKPKAHGPAEVAFTCELFSRVEDVLGLPQNTMKIGIMDEBRRTTVNLKACIKAAA 449	
Db	1898 IKM	IKANYQAMRHGVLPKTLHVDRPSDQIDWSAGTVELLTBAMDWPRKQEGGLR 1947	
٥'n	450 DRV	VFINTGFLDRTGDEIHTSMEAGPMVRKGTMKSQPMILAYEDHNVDAGLAAG 503	
qq	1948 -RA	-RAAVSSFGISGTNAHIVLEBAPVDEDAPADEPSVGGVVPWLVSAKTPAA 1996	
٥٨	504 FSG	FSGRAQVGKGMWTWTELMADMVETKIAQPRAGASTAWVPSPTAATLHALHYHQVDVA 560	
qq	1997 LD-	LDAQIGRLAAFASQGRTDAADPGAVARVLAGGRAQFEHRAVALGTGQDDLA 2047	
λŏ	561	AVQQGLAGKRRATI	
qq	2048 AAL	2048 AALAAPEGIVRGVAGVGRVAFVFPGQGTQWAGMGAELLDVSKEFAAAMAE 2098	
Oy.	600 NCO	NCQSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRHGVITS 654	
QQ	2099 -CE	-CEAALAPYVDWSLEAVVRQAPGAPTLERVDVVQP-VTFAVMVSLAKVWQHHGVTPQ 2153	
ογ	655 ADV	ADVRASLERMAPLVDRQNAGDVAYRPMAPNFDDSIAFLAAQELILS 700	
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Search completed: November 21, 2003, 16:11:36 Job time : 18.6054 secs

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November 21, 2003, 15:50:31 ; Search time 44.8027 Seconds (without alignments) 2621.664 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1107863 seqs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                      Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Cuery Date Length DB ID Description and Local Description and Local Description and Local Date DB ID Description Description and Local Date DB ID Description Description DB ID Description DB ID Description DB ID Description DB ID Description DESCRIPTI							
Score Match Length DB ID 3810 100.0 741 22 AAB05665 3810 100.0 172 22 AAB010900 3804 99.8 739 16 AAB00117 2289 60.1 739 16 AAB77501 2275 59.7 739 22 AAB79539 2253 59.1 712 22 AAB79540 9915 26.0 119.0 22 AAB795453 741.5 19.5 830 22 AAB795453			,de			SUMMARIES	
100.0 741 22 AABOS665 100.0 1172 22 AAU01900 99.8 2502 21 AAB00117 60.1 739 16 AAR77501 60.1 739 22 AAB79534 59.7 739 22 AAB79539 59.1 712 22 AAB79539 25.1 712 22 AAB79540 19.5 830 22 ABG18357	Result No.	Score	Query	Length	DB		Description
100.0 1172 22 AAU01900 99.8 2502 21 AAB00117 60.1 739 16 AAR77501 60.1 739 22 AAG73334 59.7 739 22 AAB79539 25.1 712 22 AAB79540 26.0 1190 22 AAG78547 19.5 830 22 AAG785453	1	3810	100.0	:	22	AAE05665	Mycobacterium tube
99.8 2502 21 AAB00117 60.1 739 16 AAR77501 60.1 739 22 AAG92234 59.7 739 22 AAB79539 59.1 712 22 AAB79540 56.0 1190 22 AAB7854 19.5 830 22 ABG18357	2	3810	100.0		22	AAU01900	M. tuberculosis Th
60.1 739 16 AAR77501 60.1 739 22 AARG93234 59.7 739 22 AAB79539 59.1 712 22 AAB79540 19.5 830 22 AGG1857	٣	3804	8.66		21	AAB00117	M. tuberculosis po
60.1 739 22 AAG93234 59.7 739 22 AAB79539 59.1 712 22 AAB79540 26.0 1190 22 ABG1857 19.5 830 22 ABG28453	4	2289	60.1		19	AAR77501	Malate synthase.
59.7 739 22 AAB79539 59.1 712 22 AAB79540 26.0 1190 22 ABG18357 19.5 830 22 ABG28453	Ŋ	2289	60.1		22	AAG93234	C dlutamicum prote
59.1 712 22 AAB79540 26.0 1190 22 ABG18357 19.5 830 22 ABG28453	9	2275	59.7		22	AAB79539	Corvnebacterium dl
26.0 1190 22 ABG18357 19.5 830 22 ABG25453	7	2253	59.1		22	AAB79540	Corvnebacterium gl
19.5 830 22 ABG25453	00	991.5	26.0		22	ABG18357	Novel human diagno
	σ	741.5	19.5		22	ABG25453	Novel human diagno

	numan dia	dia	Novel human diagno	ORFX prot	i malate s	scheri	cicus 8	sccus	erculosis a	human diac	uman dia	nce of hum	uman E-cadl	E-cadherin	nezuelae pik	H	eptide #419	ein #4020 enc	an brain ex	uman bone marrow	le #4010	uman titin	RGS11	d sec	S. venezuelae macr	. venezuelae	Narbonolide syntha	5	Haemophilus paraga	Q.	\neg	Ramoplanin biosynt	U	· KD	a	S. venezuelae narb
, C	0 1	33	335	ABP0300	AAR37585	570	270	480	0588	916	500	AAR55060	348	147	718	153	999	202	744	AAM69843	532	339	178	363	719	7720	720	7166	53	8842	719	7	192	1864	~	ABG71664
	77	22	22	23	13	24	21	23	23	22	22	15	16	23	21	22	22	22	22	22	22	22	24	21	21	21	21	24	13	50	21	23	15	21	21	24
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Š	r (85.	33.	N	•	89	3	•	3	•	28.	128	CA	CA	$^{\circ}$	27.	27.	27.	27.	27.	27.	27.	27.	26.		26.	26.	26.	25.	O	$^{\circ}$	124	124	123	123	123
(2 :	11	12	13								21																	38		40		42	43	4.4	45

ALIGNMENTS

Mycobacterial disease, infection, 88-kDa protein, tuberculosis, TB, early antigen; human immunodeficiency virus, HIV; secreted protein. Mycobacterium tuberculosis 88 kDa secreted protein. Zolla-Pazner S, Belisle JT; (UYNY-) UNIV NEW YORK MEDICAL CENT. (COLS) UNIV COLORADO STATE. AAE05665 standard; peptide; 741 AA 97US-0001984. 97US-0034003 Mycobacterium tuberculosis (first entry) WPI; 2001-424324/45. 31-DEC-1997; 02-JAN-1997; 24-SEP-2001 US6245331-B1 12-JUN-2001. AAE05665; Laal S,

Detecting a mycobacterial disease (tuberculosis) in individuals comprise assaying a biological sample for the presence of

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                                                       The present invention relates to a method for early detection of active mycobacterial disease or infection comprises assaying a biological fluid sample for the presence of early antibodies specific for an 88-kDa Mycobacterium tuberculosis (Mt) protein or immune complexes consisting of an 88-kDa Mytobactusis protein antigen complexed with an antibody specific for the antigen. The method is useful for the early and rapid detection of mycobacterial disease, particularly tuberculosis, in individuals at heightened risk of developing tuberculosis. This individuals include human immunodeficiency virus (HtV)-infected subjects or other immunocompromised individuals. The method is a rapid and the present sequence is a Mt 88 kDa secreted protein early antigen, used in the exemplification of the invention.
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anti-Mycobacterium tuberculosis antibodies or M. antigen-antibody complex
                                   Claim 14; Column 121; 96pp; English.
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The sequence represents Mycobacterium fusion protein antigen TbF14 consisting of a His tag for purification, antigen MtB81 and antigen Mc2. Compositions comprising at least 2 hererologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially humans) against infection by Mycobacteria. The compositions contain at least 2 heterologous antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease frequently affecting patients with acquired immunodeficiency disease, ADS.
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/label= Histidine_tag
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the fusion protein"
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                                                                                                                                                             LIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAA
                                                                                                                                                                                                                                                    AQIDKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPV
                         AQIDKWHRRRVIEPIDMDAYRQFLTBIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPV
                                                    LNARFALNAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVP
                                                                                                                LSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEI
                                                                                                                                                                                        AVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEG
                                                                                                                                                                                                             AVDKDGTAFLRVLNRDRNYTAPGGGFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEG
                                                                                                                                                                                                                                       IMDALFTGLIAIHGLKASDVNGPLINSRTGSIYIVKPKMHGPAEVAFTCELFSRVEDVLG
                                                                                                                                                                                                                                                                                                         LPQNTMKIGIMDEERRITVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPWVRKG
                                                                                                                                                                                                                                                                                                                                                                             VPSPTAATLHALHYHQVDVAAVQQGLAGKRRATIEQLLITIPLAKELAWAPDEIREEVDNN
                                                                                                                                            LIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAA
                                                                                                                                                                                                                                                                                    LPQNTMKIGIMDEERRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMVRKG
                                                                                                LSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEI
                                                                                                                                                                                                                                                                                                                                TMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTWTELMADMVETKIAQPRAGASTAW
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                                                                                                                                                                                                                                                                                                                                                                                                                           CQSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRHGVITSADVRAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis; antigen; Mtb-91; Mtb-67.2; APC; antigen presenting cell; serodiagnosis; detection; human immunodeficiency virus; HIV; acquired immune deficiency syndrome; AIDS.
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08-FEB-2001

AAB00117;

RESULT 3

useful for

portion of M. tuberculosis antigens Mtb-81 and Mtb-67.2, use diagnosis, treatment and monitoring therapy of tuberculosis

Claim 1; Fig la-f; 91pp; English.

Polypeptides comprising an immunogenic portion of Mycobacterium tuberculosis antigens Mtb-81 or Mtb-67.2 or variants that differ by substitutions, additions, insertions and/or deletions but which still react with antigen specific antisers or T-cells are described. Also described are polymucleotides encoding the polypeptides. The polypeptides, expression vectors expressing the polypeptides or comprising an antisense polymucleotide, or an antigen presenting cell comprising a sequence encoding the polypeptides are useful for determining the presence or absence of M. tuberculosis in whole blood, serum, sputum, plasma, saliva, cerebrospinal fluid or urine in a patient infected with human immunodeficiency virus (HIV).

2502 AA;

Sequence

.5 hte= "Encoded by TAA stop codon"	2 te= "Encoded	160 note= "Encoded by TAA stop codon"	1 te= "Encoded by TGA stop codon"	.154 .note= "Encoded by TAA stop codon"	18/ note= "Encoded by TAA stop codon" 100	LBS "Encoded by TGA stop codon"	1211 /note= "Encoded by TGA stop codon"	1253 note= "Encoded by TGA stop codon" 1412	L344 Vnote= "Encoded by TAA stop codon" 1940	1348 Note= "Encoded by TAA stop codon" 136	_note= "Encoded by TAA stop codon"	Incte "Encoded by TAA stop codon"	ote= "Encoded by TGA stop codon"	inote= "Encoded by TGA stop codon"	te "Encoded by TGA stop codon"	te= "Encoded by TGA stop codon"	ods." Tote= "Encoded by TGA stop codon" 673); ote= "Encoded by TAA stop codon"	.883. //octe= "Encoded by TAA stop codon"	re= "E	912438 abel= Mtb-81 polypeptide	sy ote= "Encoded by TAG stop codon"	10 5)te= "Encoded by TGA stop codon"	ote= "Encoded by TAA stop codon"	71 ote= "Encoded by TGA stop codon"	/8 ote= "Encoded by TGA stop codon"	55 ote= "Encoded by TAA stop codon"			00WO-US07196.	8-0272975.	·	Lodes MJ, Houghton RL;	1.	m tuberculosis polypeptide comprisi	-
FT Misc-difference 1039 FT /no	Misc-difference 1	sc-difference 1	Misc-difference 1	Misc-difference	Misc-difference	Miscadiference	Misc-difference	Misc-difference	Misc-difference	FT Misc-difference 15 FT Misc-difference 138	M: 22 - 22 - 22 - 22 - 22 - 22 - 22 - 22	Misc. A. Frovence	Misc-difference	Miso-difference	Misc-difference	Misc-difference	Misc-directence	Misc-difference	Misc-difference	Misc-difference 16	Protein 16	Misc-difference	Misc-difference	MISCAULTERING 7	Misc-difference 2	Misc-difference	Misc-difference/	PN WO200055194-A2.	PD 21-SEP-2000.	17-MAR-2000; 20	XX PR 18-MAR-1999; 99US	XX PA (CORI-) CORIXA CORP XX	Hendrickson RC,	AA WPI; 2000-638180/6 DR N-PSDB; AAAS3971.	Novel Mycob	•

/note= "Encoded by TAA stop codon" Misc-difference 1035

2358 2418 2058 2118 2178 2238 1818 1878 1938 1998 0 540 099 180 300 420 480 600 720 240 360 120 9 61 AQIDKWHRRRVIEPIDMDAYRQFLTBIGYLLPEPDDFTITTSGVDABITTTAGPQLVVPV LIDPESQVGTTDRAGVKDVILESALTTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAA IMDALFTGLIAIHGLKASDVNGPLINSRTGSIYIVKPKWHGPAEVAFTCELFSRVEDVLG 2119 LPQNIMKIGIMDEERRITVNLKACIKAAADRVVFINTGFLDRIGDEIHISWEAGBWVRKG VPSPTAATLHALHYHQVDVAAVQQGLAGKRRATIEQLLTIPLAKELAWAPDEIREEVDNN LERMAPIVDRONAGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTEPILHRRREF 1699 IDRVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQ LIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAA 301 AVDKDGTAFLRVLNRDRNYTAPGGGOFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEG LPQNTMKIGIMDEERRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMVRKG TMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAGASTAW CQSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRHGVITSADVRAS TDRVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQ 121 LNARFALNAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVP LSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEI Gaps . 0 Score 3804; DB 21; Length 2502; Pred. No. 9.3e-315; 1; Mismatches 1; Indels 0; Query Match
Best Local Similarity 99.7%;
Matches 738; Conservative 181 241 1939 361 481 2179 541 2299 661 2359 421 601 8 6 8 8 6 6 6 B g 8 g ò 임 $\dot{\delta}$ q ò 쉱 à g 8 B 8 ò ò

KARAAEKPAPSDRAGDDAAR 740

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                                                                                                                                                                                                                                                                                                                                    NCQSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRHGVITSADVRA 659
                                                                                                                                                                                                                                                                                                                                                       615 NCQSILGYVVRWVEHGVGCSKVPDIHDIDLMEDRATLRISSQMLANWIRHDVVSKEQVLE 674
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                        IMDALFTGLIAIHGLKASDVNGPLINSRTGSIYIVKPKMHGPAEVAFTCELFSRVEDVLG
                                                                                                  IMDAVLTIVCAIPGIAPON---KMRNSRKGSIYIVKPKQHGPEEVAFINELFGRVEDLLD
                                                                                                                                    LPONTMKIGIMDEERRITIVNLKACIKAAADRVVFINTGFLDRIGDEIHTSMEAGPMVRKG
                                                                                                                                                                                                                          TMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAGASTAW
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la M, Ozaki A;
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senoh A, Ikeda M,
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2000JP-0159162.
2000JP-0280988.
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03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR77501 is encoded by an approx. 3 kb BfrI-Pvul fragment contg. the aceB gene from Cornyeform glutamicum (see AAT05501). Nucleotides 1 to 574 can be isolated and used to regulate the expression of a proterin-encoding structural gene placed downstream of it, after incorporation into a vector and transfer into a Cornyeform bacterium. Induction of protein expression occurs even when the culture medium contains carbon sources other than acetate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TDRVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 TERVDAGGMQVAKVLXDFVTEAVLPRVGVDAEKFWSGFAAIARDLTPRNRELLARRDELQ
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                                                                                                                                                                                                              aceB gene; malate synthase; Cornyeform bacterium; regulatory region;
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KARAAEKPAPSDRAGDDAAR 2438
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N-PSDB; AAT05501.
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Best Local Simi
Matches 444;
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2419
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium. Coryneform bacterium coryneform bacterium coryneform sequence of a gene derived from coryneform bacterium. Coryneform sactorials producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
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61.3%; Pred. No. 3.1e-186;
ive 90; Mismatches 184;
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Corynebacterium glutamicum; carbon metabolism and energy production; SMP protein; sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleoside; lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; diagnosis; Corynebacterium diphtheriae; evolutionary study.
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or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated Corynebacterium glutamicum nucleic acid encoding a metabolism and oxidative phosphorylation protein for production modulation of production of fine chemicals e.g. amino acids, carbohydrates or enzymes
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                                                                           Corynebacterium glutamicum SMP protein sequence SEQ ID NO:594
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         AAB79539 standard; Protein; 739
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99DE-1032973.
99DE-1033005.
99DE-1040765.
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99DE-1031431.
99DE-1031433.
99DE-1031434.
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99DE-1032230.
99US-0143208.
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                                                                                                                                                                                             Corynebacterium glutamicum
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N-PSDB; AAF71656.
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08-JUL-1999
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AAB79539
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FKAK

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standard; Protein; 712

AAB79540

AAB79540 ID AAB7

RESULT

AAB79540;

(first entry)

30-APR-2001

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AAB79243 to AAB 79633 which are involved in carbon metabolism and energy production. The C. glutamicum SMP gene can be used in vectors [II] for expression in host cells and production or modulation of production of fine chemicals, such as, an organic acid, a proteinogenic amino acid (preferred), a purine or pyrimidine base, or nomproteinogenic amino acid (preferred), a purine or pyrimidine base, acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a polyketide, or an enzyme. The presence of [I) or SMP proteins (III) encoded by them are used for diagnosing the presence or activity of corpusational diphtheriae in subject. (I), (III) or not cells containing them are used for diagnosing the presence or activity of containing them are used to map genomes of cognisms related to containing them are used to map genomes of organisms related to containing them are used to map genomes of organisms related to containing the presence or activity of in evolutionary studies, in determining SMP protein regions required for for function, in modulating SMP protein activity, in modulating the metabolism of sugars, and in modulating high-energy molecule production in a cell (i.e. ATP, NADPH).
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739 AA; Sequence

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                                                                       TDRVSVGNIRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQ
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Query Match 59.7%; Score 2275; DB 22; Best Local Similarity 61.0%; Pred. No. 4.9e-185; Matches 442; Conservative 90; Mismatches 186;
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Corynebacterium glutamicum; carbon metabolism and energy production; SMP protein; sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; diol; diagnosis; Corynebacterium diphtheriae; evolutionary study.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated Corynebacterium glutamicum nucleic acid encoding a metabolism and oxidative phosphorylation protein for production omodulation of production of fine chemicals e.g. amino acids, carbohydrates or enzymes -
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                                                              Corynebacterium glutamicum SMP protein sequence SEQ ID NO:596.
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99DE-1031413-

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99DE-1032237-

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99DE-1042076-
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                                                                                                                                                                                           Corynebacterium glutamicum
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N-PSDB; AAF71657.
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08-JUL-1999;
08-JUL-1999;
09-JUL-1999;
09-JUL-1999;
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14-JUL-1999;
14-JUL-1999;
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31-AUG-1999;
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metabolism and oxidative phosphorylation (SMP) proteins given in metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243 to AAB 79633 which are involved in carbon metabolism and energy production. The C. glutamicum SMP gene can be used in vectors (II) for expression in host cells and production or modulation of production of fine chemicals, such as, an organic acid, a proteinogenic or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty a caid, a caid, a cabbydydrate, an around compound, a vitemin, a coffactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins (III) encoded by them are used for diagnosing the presence or activity of corprabacterium diphtheriae in a subject. (I) (II). (III) or host cells containing them are used to map genomes of organisms related to containing them are used to map genomes of organisms related to in evolutionary studies, in determining SMP protein regions required for function, in modulating sMP protein activity, in modulating the metabolism of sugars, and in modulating high-energy molecule production in a cell (i.e. ATP, NADPH).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 RRVIEPIDMDAYRQFLTBIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPVLNARFALN 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 AANARWGSLYDALYGTNAIPETDGAEKGKEYNPVRGQKVIEWGREFLDSVVPLDGASHAD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAAAVDKDGTA 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 LRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQAQIDKWHR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189 ATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEILIDPESQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 VEKYNITDGKLAAHIGDSVYRLKANRESYRGFTGNFLDPEAILLETNGLHIELQIDPVHPI
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Best Local Similarity 61.2
Matches 438; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence , 712 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129
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Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
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                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID No 48716; 103pp; English.
                                                                Novel human diagnostic protein #18348.
               ABG18357 standard; Protein; 1190 AA.
                                                                                                                                                                                                                Tang YT;
                                                                                                                                                        30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                       31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                Liu C,
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195; Conserv
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                                                                                                                         WO200175067-A2
                                                                                                                                                                                                                                                                                 biodiversity
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                                               18-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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The invention relates to isolated polymuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, colymerase chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The color polymuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a cod supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical cod supplement. (II) and its binding partners are useful in medical assorbing to repensive for general activity. (II) and (II) are useful in medical disorders involving aberrant protein esquences have applications in the polypeptide and polymuclectide sequences have applications in diagnostics, for generic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABGOOOIO-ABGSO377 represent novel human of diagnostic amino acid sequences of data and products dependent on DNA and consideration but was obtained in electronic format directly from WIPO specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S6 RDELQAQIDKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTÄGPQ
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ilarity 53.1%; Pred. No. 3.6e-75;
Conservative 66; Mismatches 97; Indels 9;
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The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerse chain reaction (PCR) primers. Oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating
DDSVPLSSGSFGDATGFTVQDGQLVVALPD-KSTGLANPGQFAGYTGAAESPTSVLLINH 234
                                                             294
                                                                                                                              424
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                                                                                                                  KGDLAAAVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDALVDTDG
                                                                                                                                                                                                             GLHIEILIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; chromosome mapping; gene mapping; gene therapy; forensic; supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human diagnostic protein #25444
                                                                                                                                                                                                                                                                                                                                                                     ABG25453 standard; Protein; 830
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IETMLGI 545
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N-PSDB; AAS89640.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of date and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the published pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                      412 FSRV--EDVLGLPQNTMKIGIMDEERRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHT
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FSKMAGHDIIVLGTEYLKWGIMDEERRTSINLRSCIAQARNRVAFINTGFLDRTGDEMHS
                                                                                                                                                                                                                                                                                                                            SMEAGPMVRKGTMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKI
                                                                                                                                                                                                                                                                                                                                              458 VMEAGPMLRKNQMKSTPWIKAYERNNVLSGLFCGLRGKAQIGKGMWAMPDLMADMYSQKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                      585 ELAWAPDEIREEVDNNCQSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
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О
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Best Local Similarity 60.3%; Pred. No. 4.5e-54;
Matches 146; Conservative 34; Mismatches 53; Indels 9;
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food supplement; medical imaging; diagnostic; genetic disorder
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23-AUG-2000; 2000US-0649167.
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N-PSDB; AAS82545.
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                                                                                                                                                                         Seguence
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Human; chromosome mapping; gene mapping; gene therapy; forensic;
                                                                                                                             biodiversity
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            Drmanac RT,
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                                                 The interaction (PCR) primars, oligomers, and for chromosome and purpeptide (II) sequences (I) brimers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of data and products dependent on DNA and amino acid sequences of the invention.

**Content of the produce of the tris patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the top when the printed specification, but was obtained in electronic format directly from WIPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 RRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPVLNARFALN 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNPGPVKDKAAYKSFLRELGYLVPOPERVTVETTGIDSEITSQAGPQLVVPAMNARYALN 258
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food supplement, medical imaging, diagnostic, genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                               Length 504;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGFTVQDGQLVVALPD-KSTGLANPGQFAGYTGAAESPTSVLLIN 233
                                                                                                                                                                                                                                                                                                                                                                                   Score 594.5; DB 22; Lucus-
Pred, No. 7.6e-42;
                                         invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                           40; Mismatches
             Claim 20; SEQ ID No 48717; 103pp; English
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50.9%;
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2000US-0649167.
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Best Local Similarity 50.99
Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                   504 AA;
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23-AUG-2000;
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The invention relates to isolated polynucleotide (1) and polypeptide (11) sequences. (1) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome polymerase chain reaction (PCR) primers, oligomers, and for chromosome conjunction and probability and in recombinant production of (11). The polynucleotides are also used in diagnostics as expressed sequence tags for for identifying expressed genes. (1) is useful in gene therapy techniques to restore normal activity of (11) or to treat disease states involving (11). (11) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (11) and its binding partners are useful in medical inaging of sites expressing (11). (1) and (11) are useful in medical inspectors in the polypeptide and polymicleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and call sequences. Absd00010-Absd30377 represent novel human amino acid sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 LRIARVLYDFVNNEALPGIDIDPDSFWAGVDKAVADLTPQNQALLNARDELQAQIDKWHR
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                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                    Claim 20; SEQ ID No 48715; 103pp; English.
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Tang
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                                                                      WPI; 2001-639362/73.
Liu C,
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(first entry)

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Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; ostecarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertansion; hypothyrodism; cholsterol ester storage disease; immune deficiency, immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis; myasthenia gravis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
                                              Human ORFX protein sequence SEQ ID NO:5996,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, SEQ ID 5996; 1037pp; English
                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000; 2000US-206132P.
29-AUG-2000; 2000US-228716P.
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                                                                                                                                                                                                                                                          WO200192523-A2.
                                                                                                                                                                                                                             Homo sapiens.
                 24-JUN-2002
                                                                                                                                                                                                                                                                                           06-DEC-2001
 The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (FCR) primars, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The chromosome polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical insolutes involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in disponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. Abg00010-Abg30377 represent novel human construction, but was obtained in electronic format directly from WIPO and the print of the financial common and the printed in electronic format directly from WIPO
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food supplement; medical imaging; diagnostic; genetic disorder.
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nes 37;
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larity 55.9%; Pred. No. 3.4e
Conservative 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; SEQ ID No 48714; 103pp; English.
                                                                                                                                                                                                                                          Tang YT;
                                                                                                                                                            31-MAR-2000; 2000US-0540217, 23-AUG-2000; 2000US-0649167.
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N-PSDB; AAS82542.
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Matches 81; Conserv
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The present the specification). ABN15762 to ABN27252 encode the human ORFX in the specification). ABN15762 to ABN27252 encode the human ORFX or proteins given in ABN00101 to 0.0 ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating or preventing a pathology associated with an ORFX polymucleotide syndrome associated with ORFX-associated disorder. ORFX polymucleotide squances can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, disorders mellitus, systemic storage diseases, various immune deficiencies and disorders, inffectious diseases, autoimmune thyroiditis, ampathenia gravis, graft-versus-host disease and autoimmune inflammatory eve disease. ORFX proteins are also ö 9 61 N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage. 2 TERVQGGSLQVAKVLYDFVVEEAVPGAGVDAETFWAGADKVITELAPKNRDLLAKRDDLQ 1 TDRVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQ present invention describes substantially purified human proteins .. 0 Indels 11.0%; Score 420; DB 23; 59.7%; Pred. No. 7.9e-28; ive 24; Mismatches 28; at ftp.wipo.int/pub/published_pct_sequences. 77; Conservative Similarity 130 AA; Sequence Query Match Best Local (Matches à g

342

129 AANARWGSLYDALYGTDVIPETDGA 153

403

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ABP03007 standard; Protein; 130 AA.

283 LRIDANFKRFVDEEVLPGTGLDAAFWRNFDEIVHDLAPENRQLLAERDRIQALDEWHR

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264 AITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAAAVDKDGTAFLR-VLNRDRNYTAP 322
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N-PSDB; AAL52112.
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           144 TDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVPLSSGSFGDATGFTVQDGQLVVAL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 PDKSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEILIDPESQVGTTDRAGVKDVILES 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 IQQQQDIDN-GTLPDFISETASIRDADWKIRGIPADLEDRRVEITGPVERKWVINALNAN 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----THFTPORNKLLAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     promoter sequence joined to the coding sequence of the E.coli aceb gene at a unique Sall site. This sequence was then joined by the 3' sequence of exon 5 of sheep growth hormone gene. Minor sequence modification around the initiation codon of the bacrerial aceb gene was made by site-directed mutagenesis. The construct was transferred to transgenic mice and the mice were analysed for expression of malate synthase. The value for expression (nmoles product formed/mg See AAAQ43177-Q43183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene expression cassette for high level expression of bacterial and/or plant genes - comprises inducible promoter and 3'-non-coding sequence of growth hormone exon 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89;
                                                                                                                                                                                                          Growth Hormone; metallothionein Ia; inducible promoter;
bacterial gene expression; malate synthase; glyoxylate cycle;
transgenic animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.0%; Score 189.5; DB 13; Length 22.7%; Pred. No. 3.1e-07; ive 67; Mismatches 253; Indels
                                                                                                                                                                                         E.coli malate synthase expressed from MTAceB2 construct
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                                                                                                                                                                                                                                                                                                                                                                                   Ward
                                                                                                                AAR37585 standard; Protein; 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Fig 6; 8pp; English.
                                                                                                                                                                                                                                                                                                                     92WO-AU00164.
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(first entry)
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                                        LNARFALNA 129
                                                             LNARFALNA 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                533 AA;
                                                                                                                                                                                                                                                       Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAQ43182.
                                                                                                                                                                                                                                                                                                                     13-APR-1992;
                                                                                                                                                                                                                                                                           WO9218635-A1
                                                                                                                                                                                                                                                                                                                                         16-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                   Brownlee AG,
                                                                                                                                                          25-MAR-2003
29-JUL-1993
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Best Local Simi
Matches 120;
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                    62
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-----VIDGQINLRDAVNGTISYTNE 149
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                                                                                                                                                                                                                                                                                                 380 VNGPLINSRTGSIYIVKPKWAHGPAEVAFTCELFSRVEDVLGLPQNTMKIGIMDEERRTTV 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---HNVDA----GLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAGASTAWVPSPTA 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention comprises a method of preparing L-amino acids. The method involves fermenting microorganisms of Enterobacteriaceae family that produce the desired L-amino acid, in which the aceB (malate synthase A) agene is eliminated. The method is useful for preparing L-amino acids (e.g. L-threonine). The L-amino acids produced by the method of the invention are useful in human medicine and in the pharmaceuticals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enzyme, L-amino acid preparation, malate synthase A; aceB; L-threonine, human medicine, pharmaceutical industry, foodstuffs, animal nutrition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       372 A------DIAMAVFNDILGSRKNQLEVMREQDAPITADQLLAPCDGERTEEGMRAN
                                                                                                       323 GGGOFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEGIMDALFT-GLIAIHGLKA--SD
                                                                                                                                                                                                                                                                                                                                                                                              206 GSGP-----YFYLPKTQSWQEAAWWSEVFSYAEDRFNLPRGTIKATLLIETLPAVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257 OMDEILHALRDHIVGLNCGRWDYIFSYİKTLKNYPDRVLPDROAVTMDKPFLNAYSRLLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        317 KTCHKRGAFAMGGMAAFIPSKDEEHNNQ-VLNKVKAD----KSLEANNGHDGTWIAHPGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATLHALHYHQVDVA-AVQQGLAGKRATIEQL--LTIPLAKELAWAP---DEIREEVDNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      440 NLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMV---RKGTMKSQPWLLAYED---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       422 IRVAVQYIEAWI-SGNGCVPI----YGLMEDAATAEISRTSIWQWIHH 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    601 CQSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRH
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111 VKVFMADFEDSLAP------DW-
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2001US-306867P.
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                                                                                                                                                                                                                                144 IDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVPLSSGSFGDATGFTVQDGQLVVAL 203
                                                                                                                                                                                                                                                                                                                                 204 PDKSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEILIDPESQVGTTDRAGVKDVILES 263
                                                                                                                                                                                                                                                                                                                                                                          52 IQQQQDIDN-GTLPDFISETASIRDADWKIRGIPADLEDRRVEITGPVERKMVINALNAN 110
                                                                                                                                                                                                                                                                                                                                                                                                                                   264 AITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAAAVDKDGTAFLR-VLNRDRNYTAP 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       323 GGGQFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEGIMDALFT-GLIAIHGLKA--SD 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        380 VNGPLINSRIGSIYIVKPKWHGPAEVAFICELFSRVEDVLGLPONIMKIGIMDEERRITV 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.7 QMDEILHÄLRÖHIVGLNCGRWDYIFSYİKTLKNYPDRVLPDRQAVTMDKPFLNAYSRLLI 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 494 ---HNVDA----GLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAGASTAWVPSPTA 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 317 KTCHKRGAFAMGGMAAFIPSKDEEHNNQ-VINKVKAD----KSLEANNGHDGTWIAHPGL 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     547 ATLHALHYHQVDVA-AVQQGLAGKRRATIEQL--LTIPLAKELAWAP---DEIREEVDNN 600
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                                                                                                                                                                                                                                                                              51
industry, the foodstuffs industry and in animal nutrition. The present amino acid sequence represents the Escherichia coli aceB protein.
                                                                                                                         Query Match 5.0%; Score 189.5; DB 24; Length 533; Best Local Similarity 22.7%; Pred. No. 3.1e-07; Matches 120; Conservative 67; Mismatches 253; Indels 89; Gaps.
                                                                                                                                                                                                                                                                 601 COSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRH 649
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Sequence 10434, A Sequence 10434, A Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 4, Appl Sequence 6, Appl Sequence 6, Appl Sequence 28, Appl Sequence 28, Appl Sequence 15, Appl Sequence 15, Appl

Sequence

Sequence Sequence

Sequence

Sequence 33, Appl Sequence 33, Appl Sequence 33, Appl Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli

Sequence 6, Appli Sequence 37319, A Sequence 32438, A Sequence 2, Appli

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AQIDKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPV
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; Sequence 2, Application US/09272975
; Sequence 2, Application US/09272975
; bublication No. US20030027774A1
; GENERAL INFORMATION:
; APPLICANT: Hendrickson, Ronald C.
APPLICANT: Lodes, Michael J.
; APPLICANT: Hodes, Michael J.
; TITLE OF INVENTION: TUBERCULOSIS ANTIGENS AND METHODS;
TITLE OF INVENTION: OF USE THEREFOR
; FILE REFERENCE: 210121.474
; CURRENT APPLICATION NUMBER: US/09/272,975
; CURRENT APPLICATION NUMBER: US/09/272,975
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2.
1 US-09-988-384B-6
US-09-864-761-37319
US-109-759-1868-32438
US-10-09-861-289-33
US-09-986-3846-33
US-09-986-3846-33
US-09-986-3846-33
US-09-986-3846-33
US-09-986-384-39
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US-10-186-384-39
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US-09-986-1884B-37
US-09-986-1884B-37
US-09-986-1884B-37
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US-09-986-1884B-37
US-09-986-1889-37
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 740; Conservative 0; Mismatches
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US-09-272-975-2
   LENGTH: 748
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Sequence 58, Appl
Sequence 6988, Ap
Sequence 9582, Ap
Sequence 958, Appl
Sequence 45, Appl
Sequence 539, Appl
Sequence 2, Appl
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1 TDRVSVGNLRIARVLYDFVN.......KARAAEKPAPSDRAGDDAAR 740
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/ cgn2_6/ptodata//pubpaa/USO0_NEW_PUB.ppp:*
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                      GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-09-272-975-38
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US-09-905-983-48
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US-10-165-049-2
US-09-861-289-6
US-09-861-289-6
US-09-860-846-6
US-09-860-946-6
US-09-860-946-6
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US-09-860-946-6
US-09-860-946-6
US-09-860-946-6
                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                              666188 segs, 182559486 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext
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length: 2000000000
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Perfect :
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GENERAL INFORMATION:
APPLICANT: NAKAGAMA, SATOSHI
APPLICANT: MAZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: TATEISHI, MIKIRO
APPLICANT: TATEISHI, MAKIRO
APPLICANT: TATEISHI, MAKIRO
APPLICANT: TEREDA, MASATO
APPLICANT: SENOH, AKINITRO
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APPLICANT: SENOH, AKINITRO
APPLICANT: OZAKI, AKIO
APPLICANTON NOWER: US 99/377484
PRIOR APPLICATION NUMBER: UP 00/189162
PRIOR APPLICATION NUMBER: JP 00/189162
PRIOR APPLICATION NUMBER: JP 00/280988
SENIR APPLICATION NUMBER: JP 00/280988
SENIR APPLICATION NUMBER: JP 00/280988
SENIR APPLICATION NUMBER: JP 00/280988
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; Publication No. US20030027774A1
; GENERAL INFORMATION:
; APPLICANT: Hondrickson, Ronald C.
APPLICANT: Hondrickson, Ronald C.
; APPLICANT: Hondrickson, Raymond L.
; TITLE OF INVENTION: TUBERCULOSIS ANTIGENS AND METHODS
; TITLE OF INVENTION: OF USE THEREFOR
; FILE REFERENCE: 2.10.12.474
; CURRENT FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 63
; SEQ ID NO SEQ ID NOS: 63
; LENGTH: 753
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ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches.
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US-09-272-975-58
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Best Local Similarity
Matches 740; Conserv
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US-09-272-975-58
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TYPE: PRT
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MASAHIRA

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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-30
PRIOR FILING DATE: 2011-08-02
NUMBER: JP 2001-272697
PRIOR FILING DATE: 2101-08-02
NUMBER OF SEQ ID NOS: 15109
LENGTH: 530
                                                                                                                                                                  , ORGANISM: Streptomyces avermitilis US-10-156-761-9582
                                                                                                                                                       TYPE: PRT
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                                                                                       Gaps
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                                                                                     Indels
                                                        Query Match 60.1%; Score 2289; DB 10;
Best Local Similarity 61.3%; Pred. No. 4.3e-205;
Matches 444; Conservative 90; Mismatches 184;
    ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6988
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                                                                                            -LIDPES 246
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                                                                                                                                 33 GRIVAAPGERRPELIKERRRQAIRLAAGSALDFPLATAGVRADASWRVAAPAPGLTDRRV
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                                                124;
  Length 530;
                                                Indels
                                                                                          197 GOLVVALPDKSTGLANPGOFAGYTGAAESPTSVLLINHGLHIEI---
4.8%; Score 184; DB 15;
21.9%; Pred. No. 4e-08;
ive 74; Mismatches 245;
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HORIKAWA, HIROSHI
SHIBA, TADAVOSHI
SAKAKI, YOSHIYUKI
HATTORI, MASAHIRA
                        Similarity 21.9
24; Conservative
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                        Best Local Simi
Matches 124;
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WS-10-156-761-9582.

Sequence 9582, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, UUN
APPLICANT: SHIRAWA, HIROSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SARAKI, YOSHIYUKI

us-09-688-672a-2.rapb

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3663 FRDIGFDSLTAVELRNRLNAETGLRLPGTLVFDYPN----PSALADHLLELLAP-
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                                                                                                                                                                                                                                                                     Query Match 3.8%; Score 145.5; DB 15; Length 541; Best Local Similarity 20.1%; Pred. No. 0.00017; Matches 101; Conservative 67; Mismatches 210; Indels 125;
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APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: Tang, Li.
TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 30062-20029,00
CURRENT PELLING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: US/09/428,517
PRIOR APPLICATION NUMBER: US/09/428,517
PRIOR APPLICATION NUMBER: 60/120,254
PRIOR FILING DATE: 1999-02-16
TITLE OF INVENTION: NOVEL POLYNUCLECTIDES
FILE REPERBRENE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-02
SEQ ID NO 5338
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ORGANISM: Streptomyces avermitilis
US-10-156-761-9538
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Publication No. US20030027287A1
GENERAL INFORMATION:
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                                                                                                                                                                                 LENGTH: 541
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US-09-808-880-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DE-----SMEACIKAAADRVVFINTGFLDRTGDEIHT---SMEAGPMVRKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   481 TMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMW----TMTELMADMVETKIAQPRAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :| :: || | :: || AAANQ-FIDTLARHRARRGLTS-----VSLGWGLWHEASGLTGGLADIDRDRMS--RAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 PG----TDIDPD-SFWAGVDKVVADLIPQNQALLNARDELQAQIDKWHRRRVIEPID---
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                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: Recombinant OTHER INFORMATION: Oleandolide PKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.5%; Score 135; DB 11; Length 3816;
llarity 21.3%; Pred. No. 0.04;
Conservative 112; Mismatches 297; Indels 294
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PRIOR APPLICATION NUMBER: 60/106,100
PRIOR FILING DATE: 1998-10-29
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 3
LENGTH: 3816
TYPE: PRT
CREATURE: PRT
CREATURE: PRT
FEATURE:
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Best Local Similarity
Matches 190; Conserv
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OY 595 BEVDNNCQSILGYVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLR 648 Db 4676 PPRDAWERVLCBAFREVLGVAEVGADDDFFALGGDSIGSIQLVGRVR 4722	OY 649 HGVITSADVRASLERMAPLVDRQNAGDVAYRPWAPNFDDSIAFLAAQELIL 699	Qy 700 SGAQQPNGYIEPILHRRREFKARAABKPAPSDRA 734	Db 4777 GGAAEGYNQSVLLRVPAQADEA 4798		; Publication No. US20030129601A1 ; GENERAL INFORMATION: . a abstrawn: Offic S T	APPLICANT: COLES, 20. TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR THE DIAGNOSIS, PROPHYLAXIS OR MATCHES OF INVENTION: TRENTMENT OF MAYORAGETS FOR	; TITLE OF INVESTION 1 REASONABLE OF MICCORCIERIOSES ; TILE REFERENCE: 03495.0218 ; CURRENT APPLICATION NUMBER: US/10/080,170	ILING DATE: 2002-0 LICATION NUMBER: 60 ING DATE: 2001-02-2	; NUMBER OF SEQ ID NOS: 652 ; SOFTWARE: Patentin Ver. 2.1 ; SPO ID NO 639	339 624	, ORGANISM: Mycobacterium tuberculosis US-10-080-170-539	Query Match 3.4%; Score 130; DB 16; Length 1624; Rest Local Similarity 20.9%; Pred. No. 0.029;	Goda Similaricy 20.9%; Fred. Mo. es 135; Conservative 87; Mismato	153 ÅEKG-PTYNKVRGDKVIAYARKFLDDSVPLSSGSFGDATGFTVQDGQLVVALPDKST 20	Db 916 ADKGTATFSDIANDVAKSYG-FWLGDAF-ASGGSVGYDHXAMGITAR	961GANEAVKRHFREIGIDTQTQDFTVVGIGDMSGDVFGNG 99	GY 260 -ILESALTTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAAAVDKDGTAFL 310	Db 999 MLLSKHIRLIAAFDHRHIFLDPADAVSWAERRRMFELPRSSWS 1043	Gy 311 RVLNRDRNYTAPGGGFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEGI 361	DYDRSLISEGGGVYSREQKAIPLSAQVRAVLGIDGSVDGGAAEMAPPNLIRAILRAP	362 MDALFTGLIAIHGLKASDVNGPLINSRTGSIYIVKPKWHGPAEVAFTCELFSRVEDVLGL 42	1101 VDLLFNGGIGTYDRANDPVRV	422 PONTWKIGIMDEERRITTVNLKACIKAAARVVVFINIGFLDRIGDEIHT	Db 1134 NANOYRAKVIGEGGNLGVTALGRVEFDLSGGRINTDALDNSAGVDCSDHEVNI 1186 Ov 470 GMFACDM/DRCTHWRSODMILAVEDHNUDAGLAAGRSGAOVGKGWWTMTRIMADMVET 527	1187 KILIDSLVSAGTVKADERTQLLESMTDEVAQLVLADN	KIAQPRAGASTAWVPSPTAA	DD 1224 EDQNDLMGTSRANAASLLPVHAMQIKYLVAERGVNRELEALPSEKEIARRSEAGI 1278	QY 577 LLTIP-LAKELAWAPDEIREEVDNNCQSILGYVVRWVDQCVGCSKVPDIHDVALMEDRAT 635
673 AGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTEPILHRRREFKARAA 725 	RESULT 7 US-10-329-079-45	Sequence 45, Application US/10329079 Publication No. US20030198981A1 EBENEAL INFORMATION:	PPLICANT: FARNET, Chris DPLICANT: AZACPUJOS, Emmanuel DPLICANT: CASAPON 1165-040	APPLICANT: STAFFA, ALIFEGO TITLE DO PROTEINS INVOLVED IN THE BIOSYNTHESIS OF LIPOPEPTIDES FILE REFERENCE: 3002-110S CURRENT APPLICATION NUMBER: US/10/329,079	URRENT FILING DATE: 2002-12-24 MDRER OF SEQ ID NOS: 66 CENTRAL VOS: 67	SSOTUMARE: Patentin Version 3.0 SEQ ID NO 45 LENGTH: 5245	TYPE: PRT SAGANISM: Streptomyces refuineus -10-329-079-45	3.5%; Score 132.5; DB 12; Length 5245;	; Conservative 85; Mismatches 260; Indels 291; Gaps	70 RVIEFIDMAXRQPELEGYLLP	119 PVINARFALNAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVR-GDKVIAYARKFLDD 177	:	178 SVPLSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAB 224	PLDAE	225 SPISVLLINHGLHIBILIDDESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDA 280	YRNWIGLINKGDLAAAVDKDGTAFLRVLNRDRNYTAPGGGOFTLPGRSL-M		336 FVRNVGHLMTNDAIVDTDGSEVFEGIMDALFTGLIAIHGLKASDVNGP 383	4353 LVRSAARYRGAAGTVLLHGSPAFDLTVTLFTFLVAGGCIVVADLDAAEGDAPNRPDLLK 4412	384HGPAEVAFTCE 410	VTPSHLAFLDGIASWAAPAADLVVGGEQLTGARLARLRAAHPGMRVYNDYGPTEATVSCA	LFSRVEDVLGLPQNTMKIGIMDEERRTTVNLKACIKAAADRVVFIN	DFV-LEPGDELPADAVPIGRPLAGHRLFVLDERLRPVPAGVPGELYIAGVGVA	457 TGFLDRIGDEIHTSMEAGPMVRKGTMKSQPWILAYEDHNVDAGLAAGF 504	505 SGRAOVGKGMMTMTELMADMVETKIAOPRAGASTAWVPSFTAATLHAL		553 HYHQVDVAAVQQGLAGKRRATIEQLLTIPLAKELAWAPDEIR 594	4619EFDPAALREGLAARLPRYMVPAAIVRLDALPLAPGGKLDHRALPEPPAPAPHDRR 4675

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APPLICANT: Cepek, Karyn

TITLE OF INVENTION: Methods and Compositions for Modulating Heterotypic E-cadherin
TITLE OF INVENTION: Interactions with T Lymphocytes
TITLE OF INVENTION: Interactions with T Lymphocytes
FILE SPERENCE: L00560/70010ERP
CURRENT APPLICATION NUMBER: US/10/165,049
CURRENT APPLICATION NUMBER: US/80 08/237,919
PRIOR APPLICATION NUMBER: PS/05-03
PRIOR FILING DATE: 1994-05-03
PRIOR FILING DATE: 1995-05-03
PRIOR FILING DATE: 1995-05-03
PRIOR FILING DATE: 1996-01-01
PRIOR FILING DATE: 1996-01-01
PRIOR FILING DATE: 1996-01-03
PRIOR FILING DATE: 1996-01-03
PRIOR FILING DATE: 1996-01-03
PRIOR FILING DATE: 1996-01-03
PRIOR FILING DATE: 2001-03-01
SOFTWARE PARENT PRIOR NUMBER: USSN 09/798,267
PRIOR FILING DATE: 2001-03-01
SOFTWARE PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT P
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        744 TRDNVYYYDEEGGGEEDQDFDLSQLHRGLDARPEVTRNDVAPTLMSVPRYLPRPANPDEI 803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 YGTDVIPETDGAEKGPTYNKV--RGD-----KVIAYARKFLDDSVPLSSGSFGDATGFT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            354 TATAVITVIDINDNPPIFNPTTYKGOVPENEANVVITTLKVTDADAPNTPAWEAVYTILN 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    414 DDGGQFVVTTNPVNNDGILKTAKGLDFBAKQQYILHVAVTNVVPFEVSLTTSTATVTVDV 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  337 VRNVGHLMTNDAIVDTD-GSEVFEGIMDALFTGLIAIHGLKASDV--NGPLINSRTGSIY 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      560 -----LIIATDNGSPVATG-----TGTLL---LILSDVNDNAPIPEPRTIFFC 599
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22.0%; Pred. No. 0.016;
iive 66; Mismatches 210;
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                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/10165049
Publication No. US20020192724A1
GENERAL INFORMATION:
APPLICANT: Bremner, Michael
APPLICANT: Cepek, Karyn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (800)..(808)
OTHER INFORMATION: HAV tripeptide
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LOCATION: (2225). (2295)
OTHER INFORMATION: transmembrane
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Best Local Similarity 22.0
Matches 134; Conservative
                                                                            594 REEVDNNCQS 603
                                                                                                                                804 GNFIDENLKA
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Sequence 48, Application US/09905983

Batent No. US20020045591A1

GENERAL INFORMATION:

APPLICANT: Geneze, Benjamin

APPLICANT: Ben-Ze'ev, Avri

APPLICANT: Ben-Ze'ev, Avri

APPLICANT: Ben-Ze'ev, Avri

APPLICANT: Ben-Ze'ev, Avri

APPLICANT: Ben-Ze'ev, Avri

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----LIIATDNGSPVATG-----TGTLL---LILSDVNDNAPIPEPRTIFFC 599
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22.0%; Pred. No. 0.016;
ive 66; Mismatches 210; Indels 200;
                                                                                                                                                                                                                                                                                                     DAIFG------VGHIWRR---IRAANLPIALSDRITLDTRR 1411
                                                                                                                                                                                                                        ELILSGAQOPNGYTEPILHRRRREFKARAAEKP-APSDRAGDDAAR 740
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1279 GLTSPELATLMAHVKLGLKEEV--
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Best Local Similarity 22.0
Matches 134; Conservative
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ORGANISM: Homo sapiens
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US-09-905-983-48
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Page 7

Db 560	492 EDHNVDAGLAAGFSGRAQVGKGMWTWTELMADMVETKIAQPRAGASTAWVPSTRAA	QY 548 TLHALHYHQVDVAAVQQGLAGKRRATIEQLLTIPLAKELAWAPDEI 593 Db 744 TRDNVYYYDEGGGEEDQDFDLSQLHRGLDARPEVTRNDVAPTLMSVPRYLPRPANPDEI 803 QY 594 REBVDNNCQS 603 Db 804 GNFIDENLKA 813	RESULT 12 US-09-661-289-6 Sequence 6, Application US/09861289 Fatent No. US20020110897A1 GENERAL INFORMATION: APPLICANT: Sherman, D.H. APPLICANT: Liu, H. APPLICANT: Ane, Y. ITILE OF INVENTION: DNA encoding methymycin and pikromycin FILE REFERENCE: 600-438U31 CURRENT PRILING DATE: 2001-05-18 CURRENT PELICATION NUMBER: 09/105,537 FRIOR FILING DATE: 1998-06-26 NUMBER OF SEQ ID NOS: 43 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 6 LENGTH: 11877 TYPE: PRT CRANISM: Streptomyces venezuelae US-09-861-289-6	Ouery Match Best Local Similarity 20.7%; Pred, No. 1.2; Matches 172; Conservative 85; Mismatches 319; Indels 256; Gaps 40; Qy 9 LRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQAQIDKWHR 68 Db 10193 LRAGGVL
Db 600 BRNPKPQVINIHDADLPPNTSPFTAELTHGRVPNWTIQYNDPTQESIILKFKMALEVG 657. Qy 432 DEBRRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPWVRGTWKSQPWILAY 491		Qy 594 REEVDNNCQS 603 bb 804 GNFIDENLKA 813 RESULT 11 US-10-165-049-3 ; Sequence 3, Application US/10165049 ; Publication No. US20020192724A1	GENERAL INFORMATION: APPLICANT: Brenner, Michael APPLICANT: Brenner, Michael APPLICANT: Brenner, Michael APPLICANT: Cepek, Karyn ITILE OF INVENTION: Interactions with T Lymphocytes TITLE OF INVENTION: Interactions with T Lymphocytes FILE REFERENCE: L00560/70010REP CURRENT FILING DATE: 2002-06-07. PRIOR PELICATION NUMBER: US/N 08/237,919 PRIOR PELICATION NUMBER: US/N 08/337,919 PRIOR FILING DATE: 1995-05-03 PRIOR FILING DATE: 1995-05-03 PRIOR FILING DATE: 1996-11-01 PRIOR FILING DATE: 1996-10-03-01 NUMBER OF SEQ ID NOS: 9 SOTWARE: Patentin Version 3.0 LENGTH: 878 TYPE: PRI CORGANISM: Homo sapiens	Duety Matc Quety Matc Best Local Matches 1 b 33 Y 19 Y 23 Y 27 Y 27 Y 27

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9 LRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQAQIDKWHR
                                                                                                                                                      ACSSSLVALHLALKGLRNGDCSTAL-VGGVAVL-
                          10349 FLDDAAGFDAAFFGISPREALAMDPQQRQLLEA
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Best Local Similarity 20.7
Matches 172; Conservative
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TYPE: PRT
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US-09-836-821-6
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SEQ ID NO 6
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                                                                                                            10582
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                ----RNVGHLMTNDAIVDTDGSEV--FEGIMDALFTG--LIAIHGLKASDVNGPL 384
                                                                                                                                                                         10583 ---SSDVDVVEGHGTGTRLGDPIEAQALLATYGQGRAPGQPLRLGTLKSNIGHTQAASGV
                                                                                                                                                                                                         -AGFSGRA
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                                                                                                                                                                                                                                                                                                                                                                                               -----REEVDNN------CQSILGYVVRWVDQGV--GCSKVPDIHDVALMEDRATL
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                                                                             INSRIGSIYIVKPKMHGPAEVAFTCELFSRVEDVLGLPQNIMKIGIMDEERRITVNLKAC
                                                                                                                                         445 IKAAADRVVFINTGFLDRTGDEIHT-----SMEAGPMVRKGTMKSQ-----
                                                                                                                                                                                                                                                                       -- HALHYHQV
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                                                                                                  3.4%; Score 128; DB 10; Length 11877; 20.7%; Pred. No. 1.2; ive 85; Mismatches 319; Indels 256;
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APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/860,846
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
                                                                                                                                                                                                                                                                     509 QVGKGMWTMTELMADMVETKIAQPRAGASTA-W-VPSPTAATL-
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
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Patent No. US20020164742A1
GENERAL INFORMATION:
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; ORGANISM: Streptomyces venezuelae
US-09-860-846-6
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Matches 172; Conservative
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US-09-860-846-6
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20.7%; Pred. No. 1.2;
tive 85; Mismatches 319; Indels 256;
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Publication No. US20030087405A1
GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Alao, Y.
TITLE OF INVENTION UNA encoding methymycin and pikromycin
FILE REFREENCE 600.438US1
CURRENT APPLICATION NUMBER: US/09/836,821
CURRENT PILING DATE: 2001-04-17
PRIOR FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
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PRIOR APPLICATION NUMBER: US 09/836,821
PRIOR FILING DATE: 2001-04-17
PRIOR PELING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 49
                                                                                        LENGTH: 11877
TYPE: PRT
OGANISM: Streptomyces venezuelae
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Query Match
3.4%; Score 128; DB 12; Length 11877;
Best Local Similarity 20.7%; Pred. No. 1.2;
Matches 172; Conservative 85; Mismatches 319; Indels 256;
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APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA Encoding Methymycin and Pikromycin
FILE REFERENCE: 600.5821031
CURRENT APPLICATION NUMBER: US/10/271,889
CURRENT FILING DATE: 2001-05-18
PRIOR PELING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 09/860,846
PRIOR APPLICATION NUMBER: US 09/860,846

Sequence 49, Application US/10271889 Publication No. US20030194784A1 GENERAL INFORMATION:

Search completed: November 21, 2003, 16:38:09 Job time : 32.8617 secs

us-09-688-672a-2.rpr

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

November 21, 2003, 15:57:31; Search time 15.4376 Seconds (without alignments) 4609.825 Million cell updates/sec

US-09-688-672A-2 3810 1 TDRVSVGNLRIARVLYDFVN......KARAAEKPAPSDRAGDDAAR 740 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

····	RESULT 1 F70722	
	probable C;Specie	>
-	C; Date: C; Access.	.7-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999 on: F70722
	R; Cole, ; Connor Rajandre	R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, : ; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Aslandream, M.A.; Rogers, J.; Rutter, S.; Seger, K.; Skelton, S.; Squares, S.
	A; Author A; Title: A; Referen	Aluthors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
	A; Status A; Molecu	Afaccession: F/0/22 AfStatus: preliminary; nucleic acid sequence not shown; translation not shown AfMolecule type: 1741 CONT.
	A; residudes: A; Cross-reff A; Experiment C; Genetics: A; Gene: glcl	A.Crossuces: 1711 COL) A.Crossuces: 1711 COL) A.Crossuces: 1711 COL) A.Experimental source: strain H37Rv C.Genetics: A.Gene: glcB
	Query Mai Best Loca Matches	Query Match Best Local Similarity 100.0%; Score 3810; DB 2; Length 741; Best Local Similarity 100.0%; Pred. No. 3.78-246; Matches 740; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	δλ	1 TDRVSVGNLRIARVLYDEVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQ 60
	qq	2 TDRVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQ 61
	δ	61 AQIDKWHRRRVIEPIDMDAYRQFLTBIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPV 120
	qq	62 AQIDKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPV 121
	δλ	121 INARPALNAANARWGSLYDALYGTDVIPETDGAEKGFTYNKVRGDKVIAYARKFLDDSVP 180
·	Q	122 INARFALNAANARWGSLYDALYGTDVIPBTDGAEKGPTYNKVRGDKVIAYARKFLDDSVP 181
	δ	181 LSSGSFGDATGFTVQDGQLVVALPDKSTGLANPCQFAGYTGAABSPTSVLLINHGLHIEI 240
	QQ	182 LSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEI 241
	δλ	241 LIDPESQVGTIDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGINKGDLAA 300
	Dp	242 LIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAA 301
	ò	301 AVDKDGTAFLRVINRDRNYTAPGGGGFTLPGRSIMFVRNVGHLMTNDAIVDTDGSEVFEG 360
	Ob	302 AVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDALVDTDGSEVFEG 361
	δò	361 IMDALFIGLIAIHGLKASDVNGPLINSRIGSIYIVKPKWHGPAEVAFICELFSRVEDVLG 420

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                                                                   TMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAGASTAW
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82.0%; Pred. No. 5.7e-200;
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M.J.; Br
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Cigrecies: Pseudomonas aeruginosa
Cigrecies: 15-89-2000 #sequence_revision 15-89-2000 #text_change 31-Dec-2000
CjAccesion: H8358m, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Er
RjStover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Er
adman, S.; Yuan, X.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Ittle: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Recession: H83586
A;Recession: H83586
A;Status: proliminary
A;Molecule Lype: DNA
A;Residues: 1-725 <5TO>
A;Cross-references: GB:AE004485; GB:AE004091; NID:g9946332; PIDN:AAG03871.1; GSPDB:GN001
C;Genetics:
A;Gene: glcB; PA0482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AQIDKWHRRRVIEPIDMDAYRQFLTBIGYLLPEPDDFTITTSGVDABITTTAGPQLVVPV
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                                                                                                                                                                                                    DVRASLBRMAPLVDRQNAGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTEPILHR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 INARFALNAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 LSSGSFGDATGFTVQDGQLVVALPDKS-TGLANPGQFAGYTGAAESPTSVLLINHGLHIE
                                     EVFEGIIDAVFIGLAAIHGLKTGEANGPLTNSRTGSIYIVKPKMHGPAEVAFTCELFSRV
                                                                                      EDVLGLPQNTMKIGIMDEERRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGP
                                                                                                                              EDVLGLPQGTLKVGIMDEERRTTLNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGP
                                                                                                                                                                           MVRKGTMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAG
EVFEGIMDALFIGLIAIHGLKASDVNGPLINSRIGSIYIVKPKMHGPAEVAFICELFSRV
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69.1%; Pred. No. 2.2e-163;
ive 77; Mismatches 139;
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Best Local Similarity
Matches 502; Conserv
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403

304

244

463

481 523

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malate synthase G (PA0482) [imported] - Agrobacterium tumefaciens (strain C58, Cereon) C; Species: Agrobacterium tumefaciens C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002 C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002 C; Accession : F97364 B; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 232-2328, 2001 A; Fitle: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97364 A; Accession: F97364                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRPNWTPEBIQRBLDNNAQGILGYVVRWVDQGVGCSKVPDINNIGLMEDRATLRISAQHM 661
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          VDPEIAVVAGPQLVVPVMNARYALNAANARWGSLYDALYGTDAISDADGAEKGRGYNPKR 184
                                                                                                                                                                                              224 ESPTSVLLINHGLHIEILIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADK 283
                                                                                                                                                                                                                                                                                                                                                                                      305 VLVYGNWLGLMRGDLTEAVSKGGNTFTRRINPDRYYTAPDGSALTLPGRSLMLVRNVGHL 364
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                                                                                                                                                                                                                                                                                                                      VLGYRNWLGLNKGDLAAAVDKDGTAFLRVLNRDRNYTAPGGGOFTLPGRSLMFVRNVGHL
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                                                                      GDKVIAYARKFLDDSVPLSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAA
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A,Gene: AGR C 78
A,Map position: circular chromosome
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462; Conserv
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AH2582

malate synthase G [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AH2582
E;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Wood, D.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
F,Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Ster, E.W.
F,Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Ster, E.W.
F,Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Ster, E.W.
F,Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Ster, E.W.
F,Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Ster, E.W.
F,Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Ster, E.W.
F,Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Ster, E.W.
F,Reference number: AB2577; MulD:21608550; PMID:11743193
F,Accession: AH2582
F,Accession: AH2682
F,Accession: A
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6 SDRLSVQSMPSEYKEAHVSRIDKFGLSIDDRLYAFLIDEVLPGTGLDSETFFEGFSAIVH 65
IQIDPSSPVGQTDAAGVKDVLMBAALTTIMDCEDSVAAVDADDKVVIYRNWLGLMKGDLA
                                                                                                       EEVSKGGSTFTRIMNPDRVYTRADGSELTLHGRSLLFVRNVGHLMTNDAILDKDGNEVPE
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                                                               AAVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDALVDTDGSEVFE
                                                                                                                                                                                           GIMDALFIGLIAIHGLKASDVNGPLI--NSRTGSIYIVKPKMHGPAEVAFTCELFSRVED
                                                                                                                                                                                                                                                                                                                   VLGLPQNTMKIGIMDEERRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMV
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a gene encoding malate synthase in Coryneba
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R.Reinscheld, D.J.; Elkmanns, B.J.; Sahm, H.
M.crobiology 140, 3099-3108, 1994
A.7Title: Malate Synthase from Corynebacterium glutamicum: sequence analysis of the A.Reference number: 140715; MUID:95111631; PMID:7812449
A.7Title: Malate Synthase from Corynebacterium glutamicum: sequence analysis of the A.Reference number: 140715; MUID:95111631; PMID:7812449
A.7Title: Malate Synthase from GB/EMBL/DDBJ
A.Residues: 1-739 ARES
A.Cross-references: EMBL:X78491; NID:9530011; PIDN:CAA55243.1; PID:9530012
R.Lee, M. Microbiol. Biotechnol. 4, 256-263, 1994
A.7Title: Molecular characterization of aceB, a gene encoding malate synthase in A.Reference number: 140836
A.Accession: 140836
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Residues: 1-739 ARES
A.Cross-references: GB:L27123; NID:9853573; PIDN:AAA68074.1; PID:9853574
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                                                                DKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPVLNA
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AF3299
malate synthase (EC 4.1.3.2) [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Dete: 01-Peb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002
C;Accession: AF229
R;DelVecChio, V.G; Kapatral, V.; Redkar, R.J; Patra, G.; Mujer, C.; Los, T.; Ivanova, J.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letese Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD252; PMID:11756688
A;Accession: AF2299
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-728 «KUR»
A;Residues: 1-728 «KUR»
A;Residues: Balo08917; PIDN:AAL51561.1; PID:g17982281; GSPDB:GN00190
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BME10380
A;Map position: I
C;Keywords: carbon-carbon lyase; coenzyme A; oxo-acid-lyase
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   ELSPKNRELLAKRDALQEKIDGWYRENG-APSDFDAYEAFLKEIGYLLPEGPGFKVETNN 124
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                                                   MVETKIAQPRAGASTAWVPSPTAATLHALHYHQVDVAAVQQGLAGKRATIEQLLTIPLA
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larity 61.8%; Pred. No. 1.2e-146;
Conservative 97; Mismatches 174; Indels 4
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RESULT 9
S51788

Malate synthase (EC 4.1.3.2) isoenzyme G - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 23-Aug-1995 #sequence_revision 13-Mar-1997 #text_change 01-Mar-2002
C;Accession: S51789; F65083
C;Accession: L; Pellicer, M.T.; Badia, J.; Aguilar, J.; Baldoma, L.
Bur. J. Biochem. 224, 541-548, 1994
A;Title: Molecular characterization of Escherichia coli malate synthase G. Differentiati
 A,Molecule type: DNA
A,Residues: 1-727 <STO>
A,Cross-references: GB:AP001514; GB:BA000004; NID:gl0174613; PIDN:BAB05852.1; GSPDB:GNOC
A,Experimental source: strain C-125
C;Genetics:
A,Gene: BH2133
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WHQKNK-GPIDFSAYHSFLEEIGYLEPIPEHVTITTENVDDEIAAQAGPQLVVPVNNARY
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(7)
                                                                                                   Score 2256.5; DB 2;
Pred. No. 1.5e-142;
; Mismatches 184;
                                                                                        59.2%; Scc...
60.7%; Pred
95; 1
                                                                                                Query Match
Best Local Similarity 60.7%
Matches 439; Conservative
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1883916

malacte synthase BH2133 [imported] - Bacillus halodurans (strain C-125)

malacte synthase BH2133 [imported] - Bacillus halodurans (strain C-125)

C;Species: Bacillus halodurans

C;Species: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001

C;Accession: E83316

By Tather Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans

A;Reference number: A83565; MUID:20512582; PMID:11058132

A;Status: preliminary
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                                                                                                                                  QIDPVHPIGKADKTGLKDIVLESAITTIMDFEDSVAAVDAEDKTLGYSNWFGLNTGELKE
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                                                                                                                                                                                                                               LNARFALNAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVP
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                                                                                       Gaps
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9
                                                                                     Indels
                               oxo-acid-lyase
                                                         Score 2289; DB 2;
Pred. No. 1.1e-144;
0; Mismatches 184;
                               coenzyme A;
                                                                                    90;
C,Genetics:
A,Gene: aceB
C,Keywords: carbon-carbon lyase;
                                                       60.1%;
larity 61.3%;
Conservative 9
                                                      Query Match
Best Local Similarity
Matches 444; Conserv
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RESULT 11
D91245
malate synthase A [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PKEYK-LRTDR-----TLP---TLIVRPRGWHL--EEKHVTIDGEPVSGSLFD-- 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          627 VALMEDRATLRISSQLLANWLRHGVITS----ADVRASLERMAPLVDRQNAGDVAYRPMA 682
                                                                                                                                                                      05-May-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X56672; NID:g2974; PIDN:CAA39994.1; PID:g2975 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 542;
                                                                                                                                                                                  C,Accession: S1774
R,Sandeman, R.A.; Hynes, M.J.; Fincham, J.R.S.; Connerton, I.F.
Mol. Gen. Genet. 228, 445-452, 1991
A;Title: Molecular organisation of the malate synthase genes of A;Reference number: S17773; MUID:91375430; PMID:1832736
                                                                                                                                                  C;Species: Neurospora crassa
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Superfamily: malate synthase
;Keywords: carbon-carbon lyase; coenzyme A; oxo-acid-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.4%; Score 205.5; DB 2; Best Local Similarity 24.4%; Pred. No. 6.6e-06; Matches 135; Conservative 64; Mismatches 205;
                                                                                                                                  synthase (EC 4.1.3.2) - Neurospora crassa
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                                                                                                                                                                                                                                                                                                  A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-542 < SAN>
719
                                LRE 719
                                                                                                                                                                                                                                                                                      A; Accession: S17774
A; Status: prelimina
RRE
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C; Superfamily: mc
C; Keywords: carbo
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                                                                                   A; Residues: 1-7.23 < RMDL: X74547; NID:g517246; PIDN:CAA52639.1; PID:g517247 R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc. A.; Roses, D.U.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997 A; Title: The complete genome sequence of Escherichia coli K-12, A; Reference number: A64720; MUID:97426617; PMID:9278503 A; Reference number: A64720; MUID:97426617; PMID:9278503 A; Reference number: A64720; MUID:97426617; PMID:9278503 A; Residues: preliminary; nucleic acid sequence not shown, translation not shown A; Residues: 1-723 < BLAT>
A; Cacossion: F65083 A; Blats
A; Cacossion: References: GB:AE000380; GB:U00096; NID:g1789344; PIDN:AAC76012.1; PID:g1789348; A; Experimental source: strain K-12, substrain MG1655 C; Genetics: A; Genes: glob
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Reference number: S51788; MUID:95010032; PMID:7925370
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A; Reference number: S51786
A; Accession: S51786
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-723 «MDL.
A; Cross-references: EMBL:
R; Blattner, F.R.; Plunket
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89;

Length 533; Indels

Score 190.5; DB 2; Pred. No. 6.4e-05; 67; Mismatches 241;

5.0%;

124 337 164 394 211 454

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A,Cross-references: GB:AE005174, NID:g12518944, PIDN:AAG59206.1, GSPDB:GN00145, UWGP:Z56
A;Experimental source: strain 0157:H7, substrain EDL933
A;Genterios:
A;Gente: aceB
C;Superfamily: malate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332 AFIPSKDEEHNNQ-VLNKVKAD----KSLEANNGHDGTWIAHPGLA------DTAM 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              272 INCGRWDYIFSYIKTLKNYPDRVLPDRQAVTMDKPFLNAYSRLLIKTCHKRGAFAMGGMA 331
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                                                                                                                                                                                                                                                                            159 YNKVRGDKVIAYARKFLDDSVPLSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAG
                                                                                                                                                                                                                                                                                                                 17 YGEQEKQILTABAVEFLTELV------THFTPQRNKLLAARIQQQQDIDN-GTLPD
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Best Local Similarity 22.8%
Matches 117; Conservative
          1-533 <STO>
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C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Date: 19-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: D91245
R;Hayashi, T; Makino, K; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C gasawara, M.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. B, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Residus: 1-533 <-HAX>
A;Residus: 1-533 <-HAX>
A;Residus: 1-533 <-HAX>
A;Residus: 1-533 <-HAX>
A;Cross-references: GB:Bh000007; PIDN:BAB38355.1; PID:g13364408; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs4932
C;Superfamily: malate synthase
                                                                                 K.; Han,
H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.0%; Score 190.5; DB 2; Best Local Similarity 22.8%; Pred. No. 6.4e-05; Matches 117; Conservative, 67; Mismatches 241;
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615 435

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Manuale synthase (EC 4.1.3.2) - Salmonella enterica subsp. enterica serovar Typhi (strain malate synthase (EC 4.1.3.2) - Salmonella enterica serovar Typhi (strain c) Species: Salmonella enterica subsp. enterica serovar Typhi (strain A,Note: this species has also been called Salmonella typhi (c) Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 (c) Accession: AD1011 Rsquence_revision 09-Nov-2001 #text_change 18-Nov-2002 (c) Accession: AD1011 A.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, N. S.; Moule, S.; O'Gaora, P. N.; Mature 413, 846-852, 2001 A.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K., A;Reference number: AB0502; MUID:21334947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIDN:CAD09189.1; PID:g16505193; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oxo-acid-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coenzyme A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Gene: STY4401
C,Superfamily: malate synthase
C,Keywords: carbon-carbon lyase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GB: AL513382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-533 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D.J.; Mayhew
K.; Apodaca,
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Length

2,

DB

Score 190;

5.0%;

Query Match

21; 203

89;

Indels

5.0%; Score 189.5; DB 1; 22.7%; Pred. No. 7.5e-05; iive 67; Mismatches 253;

Length 533;

144 IDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVPLSSGSFGDATGFTVQDGQLVVAL

TEGATTTDELAFTRPÝGEQEKQILTÁEAVEFLTELV---

263

---THFTPORNKLLAAR

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A;Experimental source: strain K-12, substrain MG1655 C;Genetics: A;Gene aceB A;Gene aceB A;Map position: 91 min C;Superfamily: malate synthase C;Keywords: carbon-carbon lyase; coenzyme A; glyoxylate bypass; oxo-acid-lyase
                                                                                                                         Query Match
Best Local Similarity 22.7<sup>3</sup>
Matches 120; Conservative
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                     27;
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                                                                                                                                                                                       IMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAAAVDKDGTAFLR-VLNRDRNYTAPGGGQ 326
                                                                                                                                                                                                                     115 MADFEDSLAP------DW---NK-----VIDGQINLRDAVNGTISYTNEAGKI 153
                                                                                                                                                                                                                                                                                                                             384 LINSRIGSIYIVKPRMHGPAEVAFTCELFSRVEDVLGLPQNTMKIGIMDEERRTTVNLKA 443
                                                                                                                                                                                                                                                                                                                                                    -----YFYLPKTQAWQBAAWWSBVFSYAEDRFNLPRGTIKATLLIETLPAVFQMDB 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------GLADTAMAVFNEVLGEHKNQLFITRDEDAPITAEQLLEPCEGERTEA 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       596 EVDNNCQSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRH----- 649
                                                                                        61
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                                                                                                                                                                                                                                                                                   TYNKVRGD----KVIAYARKFLDDSVPLSSGSFGDATGFTVQDGQLVVALPDKSTGLAN-
                                                                          FTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEGIMDALFT-GLIAIHGLKA--SDVNGP
                                                                                                                                                                                                                                                                                                                                                                                                                               261 ILHALRDHIVGLNCGRWDYIFSYİKTLKNHPDRVLPDRQVVTMDKPFLSAYSRLLIKTCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---TIPLAKELAWAP---DEIRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        417 GMRÅNIRVAVQYIEAWI-PGNGCVPI-----YGLMBDAATAEISRTSIWQWIHHEKTLSN
                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GXPVTKALFREMLAEEMRVIQDELGEHRYSSGRFDDAARLMEQITTSDDLIDFL 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KRGAFAMGGMAAFIPSKDVERNNQVLAKVKAD----KALEANNGHDGTWIAHP---
                                                                                                                                                                                                                                                                                                                                                                                              444 CIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMV---RKGTMKSQPWILAYED---
   23.2%; Pred. No. 6.9e-05; ive 67; Mismatches 249; Indels 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      552 LHYHQVDVAAVQQGLAGKRRATIEQLL-
Local Similarity 23.2
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AITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAAAVDKDGTAFLR-VLNRDRNYTAP 322 VKVFMADFEDSLAP------DW---NK-----VIDGQINLRDAVNGTISYTNE 149

111

52 IQQQQDIDN-GTLPDFISETASIRDADWKIRGIPADLEDRRVEITGPVERKMVINALNAN

04 PDKSTGLANPGOFAGYTGAAESPTSVLLINHGLHIEILIDPESQVGTTDRAGVKDVILES

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malate synthase A in Escherichia
RESULT 14
SYECMA
malate synthase (EC 4.1.3.2) A - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Species: 31-Mar-1990 #sequence revision 31-Mar-1990 #text_change 01-Mar-2002
                                                                                                                                                     Cydraces; Januar 1990 #Sequence_revision 31-war-1990 #text_or
Cydracesion: A32649; A30378; E65208; Q00592
R;Byrne, C.
Symmitted to the EMBL Data Library, July 1988
A;Reference number: 805692
A;Accession: A32649
A;Molecule type: DNA
A;Residues: 1-533 *ENR1>
R;Byrne, C.R.; Stokes, H.W.; Ward, K.A.
Nucleic Acids Res, 16, 10924, 1988
A;Title: Nucleotide sequence of the aceB gene encoding mala
A;Reference number: A30378; MUID:89083515; PMID:3060852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-533 <BYR2>
R;Blattner, F.R.; Plunkett III, G.; Bloch,
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Es
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GGGQFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEGIMDALFT-GLIAIHGLKA--SD 379
                                                                       150 AGKIYQLKPNPAVLICRVRGLHLPEKHVTWRG----BAIPGSLFDFALYFFHNYQALLAK 205
                                                                                                                                          VNGPLINSRIGSIYIVKPKMHGPAEVAFTCELFSRVEDVLGLPQNTMKIGIMDEERRTTV 439
                                                                                                                                                                                       257 QMDEILHALRDHIVGLNCGRWDYIFSYIKTLKNYPDRVLPDRQAVTMDKPFLNAYSRLLI 316
                                                                                                                                                                                                                                                                                                                                                                                                                               ---HNVDA----GLAAGFSGRAQVGKGMWTWTELMADMVETKIAQPRAGASTAWVPSPTA 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A------DIAMAVFNDILGSRKNQLEVMREQDAPITADQLLAPCDGERTEEGMRAN 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         547 ATLHALHYHQVDVA-AVQQGLAGKRRATIEQL--LTIPLAKELAWAP---DEIREEVDNN
                                                                                                                                                                                                                                                                                    440 NLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMV---RKGTMKSQPWILAYED---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KTCHKRGAFAMGGMAAFIPSKDEEHNNQ-VLNKVKAD----KSLEANNGHDGTWIAHPGL
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   323
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Cincession: H82287
Riteidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Acadardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Ermolaeva, M.D.; Vamathevan, J.; Ermolaeva, M.D.; Vanter, J.C.; Fraser, C.M.
I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A; Pitle: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A; Reference number: A82035; MUID:20406833; PMID:10952301
A; Status: preliminary
A; Status: Draliminary
A; Residues: 1-556 cHEIS
A; Cross-references: GB:AE004159; GB:AE003852; NID:g9655167; PIDN:AAF93899.1; GSPDB:GN001
A; Experimental source: serogroup 01; strain N16961; biotype El Tor
               01)
malate synthase A VC0734 [imported] - Vibrio cholerae (strain N16961 serogroup C,Species: Vibrio cholerae
C,Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
```

Length 556; Score 187; DB 2; Pred. No. 0.00012; 23.5%; A, Map position: 1 C; Superfamily: malate synthase Query Match Best Local Similarity

A/Status: preliminary; nucleic acid sequence not shown; translation not shown A/Status: DNA A/Acideule type: DNA A/Residues: 1-533 <BLAT>
A/Residues: 1-533 <BLAT>
A/Cross-references: GB:AE000474; GB:U00096; NID:g1790440; PIDN:AAC76984.1; PID:g1790444;

A)Reference number: A64720; MUID:97426617; PMID:9278503 A)Accession: E65208

A;Gene: VC0734

Genetics

S

V.; Riley, M.;

C.A.; Perna, N.T.; Burland,

Matches 116; Conservative 69; Mismatches 217; Indels 92; Gaps 23; Qy 249 GTTDRAGWEDILESALTTIMDFEDSVAAUDAADKUGYRNMLGUNKGDLAAAVDKDGTA 308											
### Add STEAD AGO AND A CONSERVATION 69 249 GTTDRAGVEDVILESAITTI 118 GPTDRAGVEDVILESAITTI 309 FLR-VLNRDRNYTAPGGG-Q 157 NLRDAILGSISYTNPDNGKED 157 NLRDAILGSISYTNPDNGKED 157 NLRDAILGSISYTNPDNGKED 158 FTGLIAIHGLKASDVNGPLI 159 FTGLIAIHGLKASDVNGPLI 150 MKIGINDERRRTTVNLKACI 150 MKIGINDERRRTTVNLKACI 151 NLRDAILDRAGGED- 152 MKIGINDERRRTTVNLKACI 153 MKIGINDERRRTTVNLKACI 154 NKSQPWILAYEDHNV 155 NGHDGTWVAHPGILA 156 NGKPFLNAYSRLLIYTCHKR 157 NGHDGTWVAHPGILA 158 NGHDGTWVAHPGILA 159 PDEIREVDNNCQSILGY 159 PDEIREVDNNCQSILGY 150 NGKREDNGGVVTNELFRDY 150 NGKREDNGGVVTNELFRDY 151 NGHGTWAGVVTNELFRDY 151 NGHGTHNGGVVTNELFRDY 152 NGHGTHNGGVVTNELFRDY 153 NGHGTHNGGVVTNELFRDY 151 NGHGTHNGGVVTNELFRDY 151 NGHGTHNGGVVTNELFRDY 151 NGHGTHNGGVVTNELFRDY 151 NGHGTHNGGVVTNELFRDY 151 NGHGTHNGGVVTNELFRDY 151 NGHGTHNGGVVTNELFRDY 151 NGHGTHNGGVVTNELFRDY 151 NGHGTHNGGVVTNELFRDY 151 NGHGTHNGGVVTNELFRDY 151 NGHGTHNGGVVTNELFRDY 151 NGHGTHNGGVVTNELFRDY 151 NGHGTHNGGVVTNELFRDY 151 NGHGTHNGGVVTNETHNGGVVTNATHNGGVVTNATHNGGVVTNATHNGGVVTNATHNGGVVTNATHNGGVVTNATHNGGVVTNATHNGGVVTNATHNGGVVTNATHNGGVVTNATHNGGVVTNA	23	308	365 216	425 265	482 325	533 381		647	698 536		
Matches	Conservative 69; Mismatches 217; Indels 92;	GTTDRAGVKDVILESAITTIMDFEDSVAAVDRADKVLGYRNWLGLNKGBLAAAVDKDGTA	FLR-VLNKDRNYTAPGGG-QFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEGIMD-AL	FTGLIAIHGLKASDVNGPLINSRTGSIYIVKPKMHGPAEVAFTCELFSRVEDVLGLFQNT 	MKIGIMDEERRITVNLKACIKAAADRVVFINIGFLDRIGDEIHTSMEAGPMVRKGTM	KSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMMTWTELMADMVETKIAQPR: ::	AGASTAMVPSPTAATLHALHYHQVDVA-AVQQGLAGKRRATIEQLLTIPL-AKELAWA	PDEIREEVDNNCQSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWL	RHGVITSADVRASLERMAPLVDRQNAGDVAYRPMAPNFDDSIAFLAAQELI :	LSGAQQ-PNGYTEP :: : LTTSQELPNFLTIP	
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Search completed: November 21, 2003, 16:09:50 Job time : 18.4376 secs

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November 21, 2003, 15:51:11; Search time 8.72562 Seconds (without alignments) 3988.226 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                          OM protein - protein search, using sw model
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BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

US-09-688-672A-2 3810 1 TDRVSVGNLRIARVLYDFVN......KARAABKPAPSDRAGDDAAR 740 Title: Perfect score: Sequence:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	-	-	Q9ae55 rhodococcus				pseudomona	rhizobiu	Q8uj85 agrobacteri	Q937w7 rhizobium l	Q92ta4 rhizobium m	Q8yir3 brucella me		P42450 corynebacte			Ω,	Q87z72 pseudomonas	escherichi	shigella f	P37330 escherichia		O	Φ	Q02216 candida tro			zea	Ø	S	. P21360 pichia angu	strepto	P45458 glycine max
QI QI		MASZ_MYCTU	MASZ_MYCLE				Ω.					MASZ RHIME	MASZ BRUME	MASZ_BRUSU	MASZ_CORGL	MASZ_COREF	MASZ BRAJA	MASZ BACHD	MAZ2_PSESM	MASZ ECOL6	MASZ_SHIFL	MASZ_ECOLI		GCP_CAEEL				MASY EMENI		MASZ_YEAST		- 1	SY_STR	MASY_SOYBN
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P13244 brassica na Q43827 raphanus sa P24571 cucurbita m	P77947 streptomyce P08216 cucumis sat P17815 ricinus com	P19927 escherichia Q50612 mycobacteri P39180 escherichia	P25062 halobacteri Q8kft1 chlorobium P17432 gossypium h
MASY_BRANA	MASY_STRAE	MBHL_ECOLI	CSG HALVO
MASY_RAPSA	MASY_CUCSA	SEA2_MYCTU	IF2_CHLTE
MASY_CUCMA	MASY_RICCO	AG43_ECOLI	MASY_GOSHI
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ALIGNMENTS

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NCBI_TaxID=1769;
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                                                                                                                                                                                                                                                                                                                                                                                   241
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                                                                                                                                                                                                                                                                                                                                       INARFALNAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVP 181
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                                                                                                                                                                              100.0%; Score 3810; DB 1; Length 741; 100.0%; Pred. No. 2.5e-241; ive 0, Mismatches 0; Indels 0.
                                                                                                                                 339 339 CATALYTIC BASE (BY SIMILARITY) 633 633 CATALYTIC ACID (BY SIMILARITY) 741 AA, 80403 MW, A92F54E0FE8B7C64 CRC64;
                                                                  Pfam; PF01274; Malate synthase; 1.
TIGRPAMS; TIGRO1345; malate syn G; 1.
Transferase; Glyoxylate bypass; Tricarboxylic acid cycle;
Complete proteome; 3D-structure.
ACT SITE 633 633 CATALYTIC BASE (BY SIMILARITY SEQUENCE 741 AA, 80403 MW.
                                TIGR, WI1885; -..
Tuberculist; Rv1837c; -.
HAMMSP, MF 00641, -i, alate synthase.
InnerPro; IPR001465; Malate synthase.
InterPro; IPR006253; Malate synthG.
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F70722; F70722.
1N8I; 18-DEC-02.
1N8W; 18-DEC-02.
                                                                                                                                                                                         Similarity
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:- PATHWAY: Glyoxylate bypass; second step.
-:- SUBDNIT: Monomer (By similarity).
-:- SUBCELLUIAR LOCATION: Cytoplasmic (By similarity).
-:- SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          WEDLINE=21128732; PubMed=11234002;
Cole S.T., Edifmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Fellwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Barrell B.G.,
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82.0%; Pred. No. 4.3e-196;
Live 54; Mismatches 72; Indels 5;
                                                                                                                                                                                        GLCB OR ML2069 OR MLCB1788.27.
Mycobacterium leprae.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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638 638 CATALYTIC ACID (BY SIMILARITY)
731 AA; 80141 MW; 3878CADA45D8416C CRC64;
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HAMAD, MP 00641,.
InterPro; IPR001465; Malate synthase.
InterPro; IPR001653; Malate synthG.
Ffam; PF01274; Malate synthase, 1.
TIGRPAMS; TIRR01345; malate syn G; 1.
TIGRPAMS; TIRR01345; malate syn G; 1.
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                                                     30-MXY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Malate synthase G (EC 2.3.39)
GLCB OR ML2069 OR MLCB1788.27.
731 AA
PRT;
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STANDARD;
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PIR; T44752; T44752.
HSSP; P37330; 1D8C.
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ACT_SITE 340
ACT_SITE 638
SEQUENCE 731 AA;
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LNARFALNAANARWGSLYDALYGTDTIPETEGAEKGSEYNKIRGDKVIAYARKFMDQAVP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PATHWAY: Glyoxylate bypass; second step.
SUBUNIT: Monomer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
                                                  ILIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLA
                                                            AAVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDAIV----DTDGS
                                                                                                                                                                                                      BYDNDCQSILGYVVRWYDQGIGCSKVPDIHNVALMEDRATLRISSQLLANWLRHGVITSE
                                                                                                                                 MVRKGTMKSQPWILLAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAG
                                                                                                                                                                                                                               ASTAWVPSPTAATLHALHYHQVDVAAVQQGLAGKRRATIEQLLIIPLAKELAWAPDEIRE
                           EDVLGLPQNTMKIGIMDEERRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGP
                                                                                                                                                                     DVRASLERMAPLVDRQNAGDVAYRPMAPNFDDSIAFLAAQELILSGAQOPNGYTEPILHR
                                                                                                                                                                                                                                                                                                               LSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPT-SVLLINHGLHIE
                                                                                                                        EVFEGIMDALFIGLIAIHGLKASDVNGPLINSRIGSIYIVKPKMHGPAEVAFICELFSRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Characterization of a chromosomal locus that affects pathogenicity hodococus fascians.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate = S-malate
                                                                                                                                                                                                                                                                                                                                                                                                                  15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Malate synthase G (EC 2.3.3.9).
GLCB OR VICA.
Rhodococcus fascians.
Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
NCBI_TAXID=1828;
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Goethals K.;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQIDKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKVDAWHGEHAGAEYDRAAYKAFLKEIGYLLDEPADFQIHTSGVDTEITTTAGPQLVVPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLPQNTMKIGIMDEERRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMVRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLPINTLKVGIMDEERRTIVNLKACIQAASERVVFINTGFLDRTGDBIHTSMEAGPVVRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LNARFALNAANARWGSLYDALYGTDVI PETDGAEKGPTYNKVRGDKVI AYARKFLDDSVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GIMDALFIGLIAIHGLKASDVNGPLINSRIGSIYIVKPKMHGPAEVAFICELFSRVEDVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAGASTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 724;
                                                                                                                                                         EMBL, AJ301559, CAC35701.1;
HSSP, P37330, 1D8C.
HAMAP, MF_00641;
InterPro; IPR004655; Malate synthase.
InterPro; IPR06553; Malate_synthase.
InterPro; IPR06553; Malate_synthase.
ITGREAMS; TTGROH45; malate_syn G; I.
Transferase; Glyoxylate bypass; Tricarboxylic acid cycle.
ACT_SITE 340 340 CATALYTIC BASE BY SIMILARITY).
SEQUENCE 724 AA; 78609 NW; F889FEB83890995E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              69.1%; Score 2634; DB 1;
69.0%; Pred. No. 1.6e-164;
iive 82; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 69.0
Matches 499; Conservative
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597 596 657 656

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LSSGSFGDATGFTVQDGQLVVALPDKS-TGLANPGQFAGYTGAAESPTSVLLINHGLHIE
                                                                                                                                                                                                300 AAVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 ILIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLA
                                                                                                                                           242 IQIDPSSPVGQIDAAGVKDVLMEAALTIIMDCEDSVAAVDADDKVVIXRNWLGLMKGDLA
                                                                                                                                                                                                                             302 BEVSKGGSTFTRIMNPDRVYTRADGSELTLHGRSLLFVRNVGHLMTNDAILDKDGNBVPE
                                                                                                                                                                                                                                                                                                  360 GIMDALFIGLIAIHGLKASDVNGPLI--NSRIGSIYIVKPKWHGPAEVAFICELFSRVED
                                                                                                                                                                                                                                                                                                                                         362 GIQDGLFTSLIAIH-----DLNGNTSRKNSRTGSVYIVKPKMHGPEEAAFTNELFGRVED
                                                                                                                                                                                                                                                                                                                                                                                                 418 VLGLPQNTMKIGIMDEERRITVNLKACIKAAADRVVFINTGFLDRIGDEIHTSMEAGPMV
                                                                                                                                                                                                                                                                                                                                                                                                                                              417 VLGLPRNTLKVGIMDEERRITVNLKACIKAAKDRVVFINTGFLDRIGDEIHTSMEAGAVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                478 RKGTMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  538 TAWVPSPTAATLHALHYHQVDVAAVQQGLAGKRRATIEQLLTIPLAKELAWAPDEIREEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               598 DNNCQSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRHGVITSADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     597 DNNAQGILGYVVRWIDQGVGCSKVPDINDVGLMEDRATLRISSQLLANWLRHGVISQEQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     658 RASLERMAPLVDRQNAGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTEPILHRRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22423060; PubMed=12534463;
Nelson K.E., Wehnel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Nelson K.E., Wehnel C., Paulsen I.T., Dodson R.J., Holmes I
Bartins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes I
Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,
Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
Lauber J., Stjepandic D., Hobelsel J., Straetz M., Heim S.,
Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Prīteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadaceae, Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comparative analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence and comparative analysis of metabolically versatile Pseudomonas putida KT2440."; Environ. Microbiol. 4:799-808(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Malate synthase G (BC 2.3.3.9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATHWAY: Glyoxylate bypass; second step. SUBUNIT: Monomer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas putida (strain KT2440)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       718 REFKAR 723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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  181
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PSEPK
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-!- SUBDMIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; PubMed=10984043;
MEDLINE-20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.-T., Brwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate = S-malate +
                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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CATALYTIC ACID (BY SIMILARITY).
3669670A9E38D391 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 725;
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HAMAP, MF 00641, -1, 1.

InterPro, IPR006253, Malate_synthag.

InterPro, IPR006253, Malate_synthag.

InterPro, IPR0174, Malate_synthag.

TIGRPAMS, TIGRO1345, malate_syn G; 1.

TIGRPAMS, TIGRO1345, malate_syn G; 1.

Transferase, Glyoxylate bypass, Tricarboxylic acid cycle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.4%; Score 2569; DB 1; Length 7 69.1%; Pred. No. 2.9e-160; ive 77; Mismatches 139; Indels
                                                                                                                                              15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Malate synthase G (EC 2.3.3.9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE004485; AAG03871.1; -. PIR; H83586; H83586.
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                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            opportunistic pathogen."
Nature 406:959-964(2000)
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                                                                                                                                                                                                                                                                               Pseudomonas aeruginosa.
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631 6
725 AA;
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ACT_SITE 340 3
ACT_SITE 631 6
SEQUENCE 725 AA;
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les 502; Conserv
                                                                                                                                                                                                                                                          GLCB OR PA0482.
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                                                                            PSEAE
MASZ PSEAE
Q91636;
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STANDARD;
                                                                                                                                              Pseudomonas fluorescens.
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      -FKAR
                                                                                                                                     GLCB OR FC2.4
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                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
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                                                                                                                                                                                                                       Length 725
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CATALYTIC ACID (BY SIMILARITY)
8363F218E6116AE1 CRC64;
                                                                                                                              TIGR; PP0356; -.
HAWAP; MF 00641; -; 1.
Transferase; Glyoxylate bypass; Tricarboxylic acid cycle;
Transferase; Glyoxylate bypass; Tricarboxylic acid cycle;
                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                    66.7%; Score 2541; DB 1; 67.1%; Pred. No. 1.9e-158; iive 95; Mismatches 139;
                                                                                                                     EMBL; AE016775; AAN65987.1; -.
TIGR; PE0356; -.
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631 631 CZ
725 AA; 78346 MW;
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ACT_SITE 340 3
ACT_SITE 631 6
SEQUENCE 725 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:- PATHWAY: Glyoxylate bypass; second step.
-:- SUBUNIT: Monomer (By similarity).
-:- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-:- SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
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CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate = S-malate
                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas
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HSGN: p37330; 1DBC.
HAMAP; MF 00641; -; 1.
InterPro; IPR001465; Malate_synthase.
InterPro; IPR006253; Malate_synthG.
Pfam: PF01274; Malate_synthG.
Pfam: PF01274; Malate_synthges; G; 1.
TIGRPAMS; TIGR01345; Malate_syn G; 1.
TIGRPAMS; TIGR01345; Malate_syn G; 1.
Transferase; Glyoxylate bypass; Tricarboxylic acid cycle.
Transferase; Glyoxylate bypass; Tricarboxylic acid cycle.
Transferase; Glyoxylate bypass; Tricarboxylic acid cycle.
Transferase; Glyoxylate bypass; Tricarboxylic acid cycle.
Transferase; Glyoxylate bypass; Tricarboxylic acid cycle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Artiguenave F.M., Delecu M., Vilagines R., Danglot C.;
"A functional glyoxylate bypass is mandatory for utilization
alkanes by Pseudomonas fluorescens.";
Submitted (MAR-1997) to the EMBL/Genbank/DDBJ databases.
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66.7%; Pred. No. 1.5e-155;
iive 85; Mismatches 152;
                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Malate synthase G (EC 2.3.3.9).
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Matches 483; Conservative
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us-09-688-672a-2.rsp

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AE016857; AAO54024.1;
PSPTO0480; -.
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725 AA;
                                                   Complete proteome.
ACT_SITE 340
ACT_SITE 631
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15-SEP-2003
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Best Local S:
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                                                                                                NCQSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRHGVITSADVRA 659
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-i- SUBINIT: Monomer (By similarity).
-i- SUBCELLUIAR LOCATION: Cytoplasmic (By similarity).
-i- SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
                                            EEVAKGGKTFTRTMNPDRVYTGVDGQDVTLHGRSLLFVRNVGHLMTIDAILDKAGNEVPE
                                                                                                                                                   NLPRNTLKVGIMDEERRTTVNLKACIKAASERVVFINTGFLDRTGDEIHTSMEAGAMVRK
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    IQIDASTPVGQTDAAGVKDVLMEAALTTIMDCEDSVAAVDADDKVVIYRNWLGLMKGDLA
                                                                              GIMDALFIGLIALHGLKASDVNGPLINSRTGSIYIVKPKMHGPAEVAFTCELFSRVEDVL
                                                                                                                                   GLPQNTMKIGIMDEERRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMVRK
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                              AAVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFE
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Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M.,
Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M.,
Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Daugherty S.,
Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T.,
White O., Fraser C., Collmer A.;
"Complete sequence of Pseudomonas syringae.";
"Complete sequence of Pseudomonas syringae.";
submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Malate synthase G 1 (EC 2.3.3.9).
GLCB1 OR GLCB-1 OR PSPTO0480.
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                                                                   340 CATALYTIC BASE (BY SIMILARITY)
631 CATALYTIC ACID (BY SIMILARITY)
79143 MW, F1993264E8083660 CRC64;
TIGK: ESTLOURSU;
HAMAP: MF 0041: -; 1.
Transferase: Glyoxylate pypass; Tricarboxylic acid cycle;
                                                                                                                                                   Match 65.3%; Score 2489; DB 1; Length 7 Local Similarity 65.3%; Pred. No. 4.8e-155; es 473; Conservative 97; Mismatches 150; Indels
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(Rel: 42, Last sequence update)
(Rel. 42, Last annotation update)
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535 598 655 718

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ASLERMAPLVDRQNAGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTEPILHRRRR
                       IMDALFTGLIAIHGLKASDV--NGPLINSRTGSIYIVKPKWHGPAEVAFTCELFSRVEDV
                                                                                                                                                      LGLPQNTMKIGIMDEERRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMVR
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Nester E.W.,
The genome of the natural genetic engineer Agrobacterium tumefaciens
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MEDINE-21608551. PubMed=11743194;
GOOGNOR B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmiel K., Gordon J., Vaudin M., Tartchouk O., Eppp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Cielo C., Slater S.;
Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens C58.",
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-!- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate = S-malate
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                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
STRAIN=MAFF303099;
MEDLINE=Z1082930; PubMed=11214968;
MEDLINE=Z1082930; PubMed=11214968;
MEDLINE=Z1082930; PubMed=11214968;
MEDLINE=Z1082930; PubMed=11214968;
MEDLINE=Z1082930; PubMed=IIZ14968;
MEDLINE=Z1082930; PubMed=IIZ14968;
MARCHIAM Y., Kiyokawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumoto M., Matsumoto M., Matsumoto M., Matsumoto M., Matsumoto M., Matsumoto M., Takawa C., Namada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti";
DNA Res. 7:331-338(2000).
-:- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate = S-malate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PATHWAY: Glyoxylate bypass; second step.
-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
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63.4%; Score 2416; DB 1; Length 721;
Best Local Similarity 64.4%; Pred. No. 2.8e-150;
Matches 467; Conservative 86; Mismatches 164; Indels
Malate synthase G (EC 2.3.3.9).
GLCB OR MLR4664.
Rhizobium loti (Mesorhizobium loti).
Bacteria, Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC BASE (BY SIMILARITY).
CATALYTIC ACID (BY SIMILARITY).
65376311A7E1BFDF CRC64;
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InterPro; IPR001465; Malate_synthase.
InterPro; IPR00553; Malate_synthG.
Pfam; PP01274; Malate_synthG.
TIGRFAMS; TIGR01345; malate_syn_G; 1.
Transferase; Glyoxylate_bypass; Tricarboxylic acid cycle;
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629
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ACT_SITE 338 3
ACT_SITE 629 6
SEQUENCE 721 AA;
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183 SGSFGDATGFTVQDGQLVVALPDKSTGLANPGQ-FAGYTGAAESPTSVLLINHGLHIEIL 241
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Matches 464;
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                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                            SUBCELLUIAR LOCATION: Cytoplasmic (By similarity). SICB subfamily. SIMILARITY: Belongs to the malate synthase family.
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CATALYTIC ACID (BY SIMILARITY)
69P304D5D6F8EFFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAD; MF_00641; -; 1.
InterPro; IPR001465; Malate_synthase.
InterPro; IPR006253; Malate_synthG.
Pfam; PF01274; Malate_synthase; 1.
TIGRRAMS; TIGR01345; malate syn G; 1.
Transferase; Glyoxylate bypass; Tricarboxylic acid cycle;
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EMBL; AE007947; AAK85871.1; ALT_INIT.
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PIR; F97364; F97364.
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ACT_SITE 346
ACT_SITE 637
SEQUENCE 731 AA;
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606 AQGILGYVVRWVDQGVGCSKVPDINNIGLMEDRATLRISAQHMANWLRHGVVTBAQIIKT 665
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                                                                                                                       LERMAPLVDRQNAGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTEPILHRRREF
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-!- SUBUNIT: Monomer (By similarity).
-!- SUBCOLLUTAR LOCATION: Cytoplaemic (By similarity).
-!- SIMILARITY: Belongs to the malate synthase family. GloB subfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 RVSVGNIRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQAQ
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HAMAP; MF 00641; -; ...
InterPro; IPRO0145; Malate synthase.
InterPro; IPRO0145; Malate synthG.
Pfam; PF01274; Malate synthG.
Pfam; PF01274; Malate synthase; 1.
TIGR10374; Malate synthase; 1.
TIGR10
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
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"Malate synthase gene from Rhizobium leguminosarum.";
Submitred (OCT-2001) to the EMBL/GenBank/DDBJ databases.
--- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate =
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15-SEP-2003 (Rel. 42, Last annotation update)
Malate synthase G (EC 2.3.3.9).
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15-SEP-2003 (Rel. 42, Last sequence update)
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15-SEP-2003 (Rel. 42, Last sequence update)
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16-SEP-2003 (Rel. 42, Last annotation update)
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18-SEP-2003 (Rel. 42, Last annotation update)
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CRWKDVGSFAVKDGALVVRSIDGEQAMLTDGKHFAGYRGDAAAPTHILLKONGIHIBIV
                                                                            IDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAAA
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-!-PTHWAY: Glyoxylate bypass; second step.
-!-SUBUNIT: Monomer (By similarity).
-!-SUBUNIT: Monomer (By similarity).
-!-SUBCELLDLAR LOCATION: Cytoplasmic (By similarity).
-!-SIMILARITY: Belongs to the malate synthase family. GlcB subf.
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between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). 180 300 540 009 121 181 240 300 360 360 420 417 480 477 537 597 9 61 61 241 VLDATTPIGKADAAGISDVVLESAITTIMDCEDSIAAVDAEDKVLVYRNWLGLMKGDLEE EVTKGGRAFTRRINPDRAYTAPDGATLTLPGRSLMLVRNVGHLMTNPAVLDRDGEEVPEG TWKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGWWTWTELMADMVETKIAQPRAGASTAW 62 QIDKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPVL NARFALNAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVPL SSGSFGDATGFTVQDGQLVVALPD-KSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEI LIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAA DHKQAPWISAYENWNVDVGLECGLSGHAQIGKGMWAMPDLMAAMLEOKIVHPKAGANTAW VPSPTAATLHALHYHQVDVAAVQQGLAGKRRATIEQLLTIPLAKELAWAPDEIREEVDNN COSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWIRHGVITSADVRAS 598 AQGILGYVVRWVDQGVGCSKVPDINNVGIMEDRATLRISAQHMANWLHHGIVSEAQIVET DRVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQA AVDKDGTAFLRVLNRDRNYTAPGGGOFTLPGRSLMFVRNVGHLMTNDALVDTDGSEVFEG IMDALFIGLIAIHGLKASDVNGPLINSRTGSIYIVKPKMHGPABVAFTCELFSRVEDVLG LPQNTMKIGIMDEERRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMVRKG LERMAPLVDRONAGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTEPILHRRRREF Gaps 5; ; Score 2351.5; DB 1; Length 723; ; Pred. No. 4.6e-146; 94; Mismatches 169; Indels 5; REMIL, ALS91782; CAC41449.1; -. RMAPP, MF 00644; -. RMAPP, MF 006455; Malate synthase.

R InterPro; IPRO01465; Malate synthase.
R InterPro; IPRO01465; Malate synthase, 1.
R TiGREAMS; TIGRO145; malate syn GG; 1.
R Transferase; Glyoxylate bypass; Tricarboxylic acid cycle; Complete proteome.
R Ocmplete proteome.
R ACT SITE 338 338 CATALYTIC BASE (BY SIMILARITY).
R ACT SITE 629 629 CATALYTIC BASE (BY SIMILARITY).
SEQUENCE 723 AA; 78853 MW; A0E95E8A5164BB58 CRC64; 338 338 CATALYTIC BASE (BY SIMILARITY) 629 629 CATALYTIC ACID (BY SIMILARITY) 723 AA, 78853 MW, AOE95E8AS164BBS8 CRC64; 61.7%; Query Match 61.7%, Best Local Similarity 62.9% Matches 455; Conservative 62 122 121 182 301 361 361 418 478 541 601 241 301 421 481

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                                                                                                                                                                                                                                                                                        427 PNTLKIGIMDEERRITVNLKEAIRAKDRVVFINIGFLDRIGDEIHISMEAGPMIRKGDM 486
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-:- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-:- SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
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                                                                            DPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAAAV
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Brucellaceae; Brucella.
NCBI_TaxID=29461;
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15-5EP-2003 (Rel. 42, Last sequence update)
15-5EP-2003 (Rel. 42, Last annotation update)
Malate synthase G (EC 2.3.3.9).
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SEQUENCE FROM N.A.
STRAIN=16M / ATCC 23456 / Biotype 1;
MEDLINE=20020109; PubMed=11756688;
DelVecchic V.G., Kapadral V., RedKar R.J., Patra G., Mujer C., Los T.,
Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
Selkov E., Blzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
Haselkorn R., Kyrpides N., Overbeek R.;
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-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLUTAR LOCATION: Cytoplaemic (By similarity).
-!- SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
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-!- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate = S-malate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The genome sequence of the facultative intracellular pathogen
Brucella melitensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60.8%; Score 2318; DB 1; Length 728; 61.8%; Pred. No. 7.2e-144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC BASE (BY SIMILARITY)
CATALYTIC ACID (BY SIMILARITY)
B1313A617979270D CRC64;
                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAWAP, MF_00641; -; 1.
InterPro; IPR001465; Malate_synthase.
InterPro; IPR006253; Malate_synthG.
IPfam; PF01274; Males synthase; 1.
IIGR1345; Malate synt G; 1.
TIGR1345; TigR01345; Malate syn G; 1.
Transferase; Glyoxylate bypass; Tricarboxylic acid cycle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97; Mismatches 174;
                                                                                                                                                                       15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Malate synthase G (BC 2.3.3.9)
Brucella melitensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE009480; AAL51561.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79985 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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636
                                                                                                                                                                                                                                                                                                                                            Brucellaceae; Brucella.
NCBL_TaxID=29459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF3299; AF3299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      728 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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636
                      718 KAK
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SEQUENCE
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Best Local
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Q8YIR3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate = 5-malate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- ENZYME REGULATION: Inhibited by oxalate, glycolate and ATP.
-!- PATHWAY: Glyoxylate bypass; second step.
-!- SUBUNIT: Monomer.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TDRVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQ
                                                                                                                                                                                                                                                                                                                                                    STRAIN=ATCC 13059 / AS019;
Lee H.S., Sinskey A.J.;
Lee H.S., Sinskey A.J.;
"Molecular characterization of aceB, a gene encoding malate synthase
in Corynebacterium glutamicum.",
J. Microbiol. Biotechnol. 4:256-263(1994).
                                                                                                                                                                                                                                                                                      analysis
":
                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Malate synthase G (EC 2.3.9).
GLCB OR ACEB OR CGL2329.
Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria, Actinobacteria, Actinobacteriaes, Corynebacterineae, Corynebacterineae, Corynebacterineae, Corynebacterium.
NCBI_TaxID=1718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMEL; X78491; CAA55243.1; -

R FIRL; L27123; AAA68074.1; -

R FIR; 140715; 140715.

R FIR; 140715; 140715.

R HSSP; B37330; 1D8C.

R HSAMAP; MF 00641; -; 1

R InterPro; IPR001465; Malate synthas.

R InterPro; IPR001465; Malate synthas.

R TGREAMS; TIGR01346; Malate synthas.

R TGREAMS; TIGR01346; Malate synthas; I TGREAMS; TIGR01346; Malate synthas.

R TGREAMS; TIGR01346; Malate synthas; I TGREAMS; TIGR01346; Malate syn G; 1.
                                                                                                                                                                                        [1] _
SEQUENCE FROM N.A., SEQUENCE OF 1-10, AND CHARACTERIZATION.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
MEDLINE=95111631; PubMed=7812449;
Reinscheid D.J., Eikmanns B.J., Sahm H.;
Malate synthase from Corpusabacterium glutamicum: sequence of the gene and biochemical characterization of the enzyme.
Microbiology 140:3099-3108(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC BASE (BY SIMILARITY)
CATALYTIC ACID (BY SIMILARITY)
72AA0663AE7C87F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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61.3%; Pred. No. 5.8e-142;
ive 90; Mismatches 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               [3]
SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
Nakagawa S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :06
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646 CZ
7 82231 MW;
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Matches 444; Conservative 9
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646
638 AA;
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INIT MET 0
ACT SITE 355
ACT SITE 646
SEQUENCE 738 AA;
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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NADHPIGKTDFAHIADVVLESAISTIQDCEDSIAAVDAEDKVAVYRNWIGIANAGKLEDTF
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                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                          4,
                                                                                                                                                                                                                                           SIMILARITY).
SIMILARITY).
CRC64;
                                                                                                                                                                                                                                                                                                                     Length 728
                                                                                                       HAMAP, MISTORIA; -; 1.

INTERPROF, TRR001465; Malate synthase.

INTERPROF, TRR001465; Malate synthase.

Ffam; PF01274; Malate synthase; 1.

TIGRFAMS; TIGR01445; Malate syn G; 1.

Transferase; Glyoxylate bypass; Tritcarboxylic acid cycle; Complere proceome.

ACT SITE 345 345 CATALYTIC BASE (BY SIMILARITY ACT SITE 636 536 CATALYTIC ACID (BY SIMILARITY SEQUENCE 728 AA); 79966 WW; F95569D002A14EDE CRC64;
                                                                                                                                                                                                                                                                                                               Query Match 60.7%; Score 2313; DB 1; Length 7
Best Local Similarity 61.6%; Pred. No. 1.5e-143;
Matches 443; Conservative 97; Mismatches 175; Indels
                                                                                                                                                                                                                                                                                                                                                  97;
                                                                                                                                                                                                                                     345 345 CA
636 636 CA
728 AA; 79966 MW;
                                                                         EMBL; AE014458; AAN30550.1;
TIGR; BR1648; -.
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AQIDKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPV 120

61

738 AA

STANDARD;

RESULT 14 MASZ_CORGL ID MASZ_CORGL

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLERWAPLVDRQNAGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTEPILHRRRE 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      265 QIDPTHPIGKEDXTGLKDILLESAITTIMDFEDSVAAVDAEDKTLGYRNWFLLNTGELTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             441 LPRHTLKVGVMDEERRISVNLDACIMEVADRLAFINIGFLDRIGDEIHTSMEAGAMVRKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TDRVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLIPQNQALLNARDELQ
                                                                                                                                                                                                                                                                                                                                                                                                        26 TERVIVGGMQVAKVLRDFLTESVLPRVGVDAERFWNGFGDIVRDMTPRNRELLARRDELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                       AQIDKWHRRRVIBPIDMDAYRQFLTBIGYLLPBPDDFTITTSGVDABITTTAGPQLVVPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIDPESQVGTTDRAGVKDVILESALTTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMINDAIVDTDGSEVFBG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMDALFTGLIAIHGLKASDVNGPLINSRTGSIYIVKPKMHGPAEVAFTCELFSRVEDVLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LPQNTMKIGIMDEERRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMVRKG
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             GlcB subfamily
                                                                                                                                                                                                                                                                                                                                                       Gaps
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9
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                                                                                                                                                                                                                                                                362 CATALYTIC BASE (BY SIMILARITY)
653 CATALYTIC ACID (BY SIMILARITY)
83491 MW, F9550473EC4E9A09 CRC64;
                                                                                                                                                                     HAMAP; NE_00641; -; 1.
InterPro; IPR001465; Malate_synthase.
InterPro; IPR006253; Malate_synthG.
Pfam; PF01274; Malate_synthase; 1.
TIGRPAMs; TIGR01345; malate_syn_G; 1.
Transferase; Glyoxylate bypass; Tricarboxylic acid cycle;
                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                            Length
              Belongs to the malate synthase family.
(By similarity).
                                                                                                                                                                                                                                                                                                                          59.7%; Score 2273; DB 1;
61.5%; Pred. No. 6.5e-141;
ive 90; Mismatches 182;
                                                                                                               entities requires a license agreement ({ or send an email to license@isb-sib.ch)
  Cytoplasmic
                                                                                                                                                                                                                                                                                                                                                     90;
                                                                                                                                                        EMBL; AP005221; BAC19041.1; -.
  LOCATION:
                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                        362 3
653 6
748 AA;
                                                                                                                                                                                                                                                       Complete proteome.
ACT_SITE 362
ACT_SITE 653
SEQUENCE 748 AA;
                                                                                                                                                                                                                                                                                                                                         Local Similarity
es 444; Conserv
    SUBCELLULAR
                 SIMILARITY:
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                                                                                                     LSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEI
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                                              LNAR FALNAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The entire genomic sequence of Corynebacterium efficiens YS-314.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate = S-malate
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A., Nishio Y.,
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Bacteria; Actinobacteria; Actinobacteridae; ActinomyCetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H.,
Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Malate synthase G (EC 2.3.3.9).
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-!- SUBUNIT: Monomer (By similarity).
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Search completed: November 21, 2003, 16:04:15 Job time : 11.7256 secs

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us-09-688-672a-2.rspt

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RESILT 1
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q9ae55 rhodococcus	Q9i636 pseudomonas	Q98dk4 rhizobium l	Q8uj85 agrobacteri	Q937w7 rhizobium l	Q92ta4 rhizobium m	Q8yir3 brucella me	Q8fz50 brucella su	Q8fnb3 corynebacte	Q9kb03 bacillus ha	Q8fdn6 escherichia	Q8pgr6 xanthomonas	Q8pdu8 xanthomonas	Q9u3q5 caenorhabdí	017353 caenorhabdi	Q8x609 escherichia
SUMMARIES	ID	Q9AESS	091636	Q98DK4	080785	Q937W7	Q92TA4	Q8YIR3	Q8FZ50	Q8FNB3	Q9KB03	Q8FDN6	Q8PQR6	QSPDUS	Q9U3Q5	017353	609X8Ö.
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ALIGNMENTS

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LT 1	55	Q9AE55	1000 JULY 1001	01-JUN-2001	01-MAR-2003	Malate synth		Rhodococcus fascians.	Bacteria; Ad	Corynebacte	NCBI_TaxID=1828;		SEQUENCE FR	STRAIN=D188;	Vereecke D.M.,	Goethals K.;	"Characterization of	Rhodococcus	Submitted ((EMBL; AJ301			InterPro, Il	-	TIGREAMS; T.		Query Match	Best Local Sim: Matches 499;	-		IOT S	61 AQ:	
RESULT	Q9AE55	A S) E	TO	Ę	DE	Z	SO	00	ပ္ပ	XO:	Z.	КP	RC	RA	RA	RH	R	RL	DR	DR	DR	DR	DR	보 2	ÇX Q	g.	n ⊠ San	ć	ŝ	QQ	δχ	

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Last annotation update)
                                                                                                                                                                                                                              67.4%; Score 2569; DB 16;
69.1%; Pred. No. 3.7e-158;
ive 77; Mismatches 139;
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EMBL, AE004485, AAG03871.1, -.
HSSP, P37330, 1D8C.
InterPro, IPR001465, Malate_synthase.
InterPro, IPR006553, Malate_synthG.
Pfam, PF01274, Malate_synthase, 1.
TIGRPAMS, TIGR01345, malate_syn_G; 1.
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     GKVDAWHGEHAGAEYDRAAYKAFLKEIGYLLDEPADFQIHTSGVDTEITTTAGPQLVVPV 121
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STRAIN=ATCC 15692 / PAO1;
MEDLINE=ZOR47337; PubMed=10984043;
MEDLINE=ZOR47337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete gnome sequence of Pseudomonas aeruginosa PAO1, an
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Bacteria, Proteachacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadacee, Pseudomonas.
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Nature 406:959-964 (2000)
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InterPro; IPR006253; Malate synthG.
Pfam; PF01274; Malate synthase; 1.
IIGRFAMs; TIGR01345; malate_syn_G; 1.
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SEQUENCE 744 AA;
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SEQUENCE FROM N.A.
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MEDLINE=21082930; PubMed=11214968;

MEDLINE=21082930; PubMed=11214968;

MEDLINE=21082930; PubMed=11214968;

Manchine A., Nakamura Y., Sato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashina K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;

"Complete genome structure of the nitrogen-fixing symbiotic bacterium
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                    Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                  Length
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                                                                                                                                                                                                                                                                                         721 AA; 78058 MW; 65376311A7E1BFDF CRC64;
                                                                                                                                                                                                                                                                                                                 Query Match
63.4%; Score 2416; DB 16;
Best Local Similarity 64.4%; Pred. No. 3.1e-148;
Matches 467; Conservative 86; Mismatches 164;
                                                                                                                                                                                                                 EMBL; AP003004; BAB51267.1; -.
InterPro; IPR001465; Malate synthase.
InterPro; IPR006553; Malate synthG.
Pfam; PF01274; Malate synthase; 1.
TIGRPAMS; TIGR01345; malate_syn_G; 1.
                                                                                                                                                                                           Mesorhizobium loti.";
DNA Res. 7:331-338(2000)
                                                                                                                                                                                                                                                                               Complete proteome. SEOUENCE 721 AA:
                                                                                  SEQUENCE FROM N.A.
                                                         NCBI_TaxID=381;
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ASLERMAPLVDRQNAGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTEPILHRRRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDITNE=21608550; PubMed=11743193; Monks D.E., Kitajima J.P., Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Elsen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M., J., McClelland B., Palmieri A., Raymond C., Rouse G., Saemphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Nester E.W.,
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Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Goodner B., Hinkle G., Gattung S., Miller M., Blanchard M.,
Gourollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz F
Rlanegan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Cielo C., Slater S.,
"Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens C58.";
EMBL; AE00899; AAL41078.1;
EMBL; AE007947; AAK85871.1;
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01-JUN-2002 (TrEMBLET: 21, LEST SEQUENCE UDGATE)
Malate synthase G.
GLCB OR ATU0047 OR AGR C 78.
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium.
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                                                                                                      63 IDDWYRRHG-APADMDEYQSFLREIGYLLPEGSDFQVSTQNVDPEIASIAGPQLVVPVMN 121
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                                                                                                                                                       122 ARYALNAANARWGSLYDALYGIDAIPESDGAEKGKSYNPKRGEKVIAWVRDFLDISAPLO 181
                                                                                                                                                                                              SGSFGDATGFTVQDGQLVVALPDKSTGLANPGQ-FAGYTGAAESPTSVLLINHGLHIEIL 241
                                                                                                                                                                                                                 IDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAAA 301
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                                     362 MDAAITGLIALYDIGPS---GRRKNSRTGSMYVVKPKWHGPEEVAFAVEIFSRVEDALGL
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MEDLINE=21396507; PubMed=11481430;
Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DRC-2003 (TrEMBLrel. 2), Last annotation update)
01-MAR-2003 (TrEMBLrel. 2), Last annotation update)
Probable malate synthase G protein (EC 4.1.3.2).
GLCB OR R00062 OR SMC02581.
GLCB OR R00062 OR SMC02581.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium.
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AKQA 722
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NCBI_TaxID=382;
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ARPATILLGKNGLHTEIŲIDPSTEIGKSDRAGISDVILESALTTIMDCEDSVAAVDAEDK
                                                                                                                                                                                   MVETKIAQPRAGASTAWVPSPTAATLHALHYHQVDVAAVQQGLAGKRATIEQLLTIPLA
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                                                                                                                                                               VLGYRNWLGLNKGDLAAAVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHL
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                                            GDKVIAYARKFLDDSVPLSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhizobium leguminosarum (biovar viciae).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Malate synthase gene from Rhizobium leguminosarum.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
BMBL, AN059637; AAL17965.1;
InterPro; IPR00465; Malate synthase.
InterPro; IPR005253; Malate synthase.
Ffam; PF01274; Malate synthase; 1.
TIGRPAMS; TIGR01345; malate syn G; 1.
SEQUENCE 723 AA; 79677 WW; 4E879906CFD64444 CRC64;
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Last annotation update)
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Garcia de los Santos A., Hynes M.F.;
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Best Local Similarity
Matches 464; Conserv
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REMBL, AL591782; CAC41449:1;
RINTERPO: IPR001465; Malate synthase.
RINTERPO: IPR006253; Malate synthase.
RIGROMS: TIGR01345; malate synthase, 1.
PIGRN1345; Malate synthase, 1.
M. Lyase; Complete proteome.
Q SEQUENCE 723 AA; 78853 MW; AOB95E8A5164BB58 CRC64;
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Best Local Similarity 62.9%; Pred. No. 4.8e-144;
Matches 455; Conservative 94; Mismatches 169; Indels
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SEQUENCE FROM N.A.

C STRAIN=16M / ATCC 23456 / Biotype 1;

X MEDLINE=20020109; PubMed=1175668ar R.J., Patra G., Mujer C., Los T.,

DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,

La DelVecchio V.G., Rapatral V., Redkar R.J., Lykidis A., Reznik G.,

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A Haselkorn R.; Kyrpides N., Overbeek R.;

The genome sequence of the facultative intracellular pathogen

The genome sequence of the facultative intracellular pathogen

The genome Sci. U.S.A. 99:443-448 (2002).

B InterPro: IRR004869; Malate_Synthase.

DR InterPro: IRR004865; Malate_Synthase.

DR TIGRRAMS, TIGR01345; malate_Synthase.

DR TIGRRAMS, TIGR01345; malate_Synthase.

DR TIGRRAMS, TIGRO1345; malate_Synthase.
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Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales.
Brucellaceae; Brucella.
NCBI_TaxID=29459;
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                                                                          Last sequence update)
Last annotation update)
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                                                    Created)
O8YIR3
O8YIR3
Q8YIR4
O8YIR5
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01-MAR-2002 (TrEMBLrel. 20, L.
01-MAR-2003 (TrEMBLrel. 20, L.
MALate synthase G (EC 4.1.3.2)
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Lyase, Complete proteome.
SEQUENCE 748 AA; 83491 MW;
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                                                                                                                                               RMAAIVDKQNEGDPLYRPMAADFDKSIAFQAACDLVFKGREQPNGYTEPVLHRRRLELK 725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SelfAllNB-22247741; PubMed=12271122; Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F., Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanam M.J., Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R., Nelson W.C., Ayodeju B., Kraul M., Shetty J., Malek J.F., Madupu R., Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L., Hover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.; "The Brucella suis genome reveals fundamental similarities between animal and plant pathogens and symbionts."; Proc. Natl. Acad. Sci. U.S.A., 99:13148-13153(2002).
SPTAATLHATHYHKIDVAAVQEKLKSRPRAKLDDILSVPVAVRPNWTPDDIQHEIDNNAQ
                                     SILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRHGVITSADVRASLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 VSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQAQI
                                                                                                                         RMAPLVDRQNAGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTEPILHRRRREFK
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
NCBI_TaxID=29461;
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Last sequence update)
Last annotation update)
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hes 175;
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                                                                                                                                                                                                                                                                       PRELIMINARY;
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STRAIN=1330 / Biovar 1;
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SEQUENCE 728 AA
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QNTMKIGIMDEBRRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMBAGPMVRKGTM
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Corynebacterineae, Corynebacteriaceae, Corynebacterium.
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ò	361 IMDALFTGLIAIHGLKASDVNGPLINSRTGSIYIVKPKMHGPAEVAFTCELFSRVEDVLG 420	δ	126 ALN
đ		<u>ස</u>	
ζ	421 LPQNTMKIGIMDEERRITVNLKACIKAAADRVVFINTGFLDRIGDEIHTSMEAGPMVRKG 480	δ	
qq	441 LPRHTLKVGVMDEERRTSVNLDACIMEVADRIARINTGFLDRTGDEIHTGMBAGAMVRKA 500	<u>අ</u>	
ò	481 TMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTWTELMADMVETKIAQPRAGASTAW 540	8 8	
ą	501 DMQTAPWKQAYEDNNVDAGIQRGLPGKAQIGKGWAMTELMGEMLEKKIGQLREGANTAW 560	QQ .	
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	Malate synthase. BH2133.	qu	663 AKV
90 00	Bacillus halodurans. Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.	8	
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8 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	STEADURGE FROM N.A.	QQ	723 AKE
	medilibergolisosi; Pudaki Y., Takaki Y., Maeno G., Sasaki R., Masui N., Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,	RESULT Q8FDN6 ID Q8	LT 11 N6 Q8FDN6
	acillus	AC	Q8FDN6; 01-MAR-2003
	halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28 41317-4331 (2000) FMRH: APONISTA: PREPRESS: 1	TO C	01-MAR-2003 01-MAR-2003
	HSSP; P37333; 1D8C. InterPro; IPR001465; Malate_synthase.	OGNE	Malace Synth GLCB OR C370: Escherichia
	InterPro; IPR006253; Malate_synthG. Pfam; PP01274; Malate_synthase; 1.		Bacteria, Pro Enterobacter
	renr.ca.s, increase. Complete procedme. SEQUENCE 727 AA, 81208 MW, CE18B45930E5EAES CRC64:	R R CX	NCBI_TaxID=Z. [1] SEQUENCE FROM
Mee	59.2%; Score 2256.5; DB 1 / 60.7%; Pred. No. 7.1e-138; cvative 95; Mismatches 184;	R R R R R R R R R R R	STRAIN=06:H1 MEDLINE=2238 Welch R.A., 1 Rasko D., Bu
ò	VGNLRIARVLYDFVNNBALPGTDIDFDSFWAGVDKVVADLTPQNQALLNARDELQAQIDK 65	RA RA RT	Mayhew G.F., Mobley H.L.T "Extensive mo
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55.H1 / CFT073 / ATCC 700928;

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=2388234; PubMed=12471157;

A. Burland V., Plunkett G. III, Redford P., Roesch P.,

Burland V., Liou S.-R., Boutin A., Hackett J., Stroud D.,

J.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

H.L.T., Donnenberg M.S., Blattner F.R.;

H.L.T., Donnenberg M.S., Blattner F.R.;

ive mosalc structure revealed by the complete genome sequence athogenic Escherichia coli.";

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Stat. Acad. Sci. U.S.A. 99:17020-17024 (2002).

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riaceae; Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     DKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPVLNA
                                                                                                                                                                                                                          RFALNAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVPLSS
                                                                                                                                                                                                                                                                                                                             GSYQDVVAFKVVDKQLRIQLKNGKETTLRTPAQFVGYRGDTAAPTCILLKNNGLHIELQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DALFTGLIAIHGLKASDVNGPLINSRTGSIYIVKFKMHGPAEVAFTCELFSRVEDVLGLP
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                                                                                                                                                                                                                                                                                              GSFGDATGFTVQDGQLVVALPD-KSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEILI
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                                                                                     4 VSVGNIRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQAQI
                                                    Gaps
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01-07-2002 (TrEMBLrel. 22, Last sequence update)

01-07-2002 (TrEMBLrel. 22, Last sequence update)

01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

Malate synthase.

MAS OR XAC0256.

Xanthomona axonopodis (pv. citri).

Bacteria, Proteobacteria; Gammaproteobacteria; Xanthomonadales;

Xanthomonadeae; Xanthomonas.
                                                    15;
                  Length 723;
                                                    173; Indels
                    DB 16;
                  Score 2168.5; DB 1
Pred. No. 3.6e-132;
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                                                   Mismatches
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                                                    113;
                  56.9%;
                                                    Conservative
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                                    Similarity
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                                                 422;
                  Query Match
Best Local S
Matches 422
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RC STRAIN=306 / ATCC 13902 / XV 101;

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Guaggio R.B., Monteiro-Vitorallo C.B., Van Sluys M.A., Almeida N.F.,
RA Canarotte G., Canavan P., Cardozo J., Chambergo F., Capina L.B.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.B., El-Dorry H.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Formighieri E.C., Machado M.C., Greggio C.C., Gruber A.,
RA Kasuyama A.M., Kishi L.T., Leite R.P., Lemoss E.G.M., Lemos M., M. M.
RA Martins E.C., Machado M.J., Madeira A.M. B.N., Martinez-Rossi N.M.,
RA Martins E.C., Machado M.J., Manck C.F.M., Miyaki C.Y., Moon D.H.,
RA Pereira H.A., Rossi A., Sena M.A.D., Silva C., Ca Souza R.F.,
RA Spinola L.A.F., Taxita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Trutfi D., Tsai S.M., White F.F.,
R. "Comparison of the genomes of two Xanthomonas pathogens with differing R. Nather M. Martine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----RGDLSFDAPNGKHYALRPEAERAVLIVRPRGWHLDEKHVLI--DGQPLAGGLFDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPTDPKMVINALNSGAKVFMADFEDSTAPT-----WRNLLA-GORTLVAAV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80A47F8D32B7C848 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 279.5; DB 16;
Pred. No. 9.2e-10;
....rhes 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           465 LWOWLHHGOHLDDGTAIDQHLLOATLRALPARL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
7.3%; Score 279.5;
Best Local Similarity 24.9%; Pred. No. 9.2e
Matches 123; Conservative 59; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro, IPRO06252, Malate_synthA.
InterPro, IPRO01465, Malate_synthase.
Pfam, PF01274; Malate synthase, 1.
IIGRFAMs, TIGR01344, malate_syn_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59271 MW;
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EMBL; AE011650; AAM35148.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         536 ASTAWVPSPT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     692 LAAQELILSGAQO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   538 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome
SEQUENCE 538 AA
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540

PRT;

PRELIMINARY;

QBPDU8;

SEQUENCE FROM N.A.

us-09-688-672a-2.rspt

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GFRNNISVTLGYLDYWL-RGVGCVPLDN-----LMEDLATAEISRAQLWQWLHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Pred. No. 0.00013;
58; Mismatches 186; Indels
                                                                                                                                                                                                                                                                                                                                                                              Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOCITRATĒ LYĀSE; 1.
101848 MW; AAF64B820B82D1B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of the nematode C.elegans: A platform
      D-GNGC--VP-IHN--LMEDAATAEISRAQLWQWLHHG 474
                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Wentowe begaca..."
investigating biology.";
Science 282:2012-2018(1998),
EMBL, 2831216, CAB62784.1;
EMBL, 2831216, CAB62784.1;
NormPep; CO8F11.14; CE23529,
InterPro; IPRO00524; Isocit.lyase,
InterPro; IPRO00524; Isocit.lyase,
InterPro; IPRO00528; Malate_SynthA.
InterPro; IPRO06252; Malate_SynthA.
InterPro; IPRO01465; Malate_SynthA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGRFAMS; TIGRO1346; isocit_lyase; TIGRFAMS; TIGRO1346; isocit_lyase; TIGRFAMS; TIGRO1344; malate_syn_A; PROSITE; PS00161; ISOCITRATE_LYASE; SEQUENCE 907 AA; 101848 MW; APPA
                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00463; ICL; 1.
Pfam; PF01274; Malate synthase; ProDom; PD001857; ISoCit_lyase_p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.4%;
                                                                                                                                       (TrEMBLrel. 13, C
(TrEMBLrel. 13, I
(TrEMBLrel. 23, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 23.73
                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                           Caenorhabditis elegans.
                                                                                                                                                                                                   C08F11.14 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                      NCBI TaxID=6239;
                                                                                                                                              01-MAY-2000
                                                                                                                                                                                    01-MAR-2003
                                                                                                                                                                 01-MAY-2000
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Matches
                                                                 RESULT 14
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                                                                                                                                                                                                           Caralla Anc. Reinach F.C., Farah C.S., Furlan L.R.,
Ad Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
Ad Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
Alves L.M.C., Ad Amaral A.M., Bertolini M.C., Canargo L.E.A.,
Alves L.M.C., Go Amaral A.M., Cardozo J., Chambergo F., Ciapina L.P.,
Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
A rata J.B., Ferraira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
A rata J.B., Ferraira A.J.S., Ferreira R.C.C., Gruber A.,
Ratavyana A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
Antins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
Apreira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
Spinola L.A.R., Takita M.A., Tamura R.E., Taixeira E.C., Tezza R.I.D.,
Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
Sctubal J.C., Kitajima J.P.;
Achipana Spathogens with differing
Host specificities."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223 LPKLQSWEBAALWETALAHIEAMLGLPHGQIKVTVLIETLPAVFENDEILHALRARIVGL 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 AESPISVLLINHGLHIEILIDPESQVGTIDRAGVKDVILESAITTIMDFEDSVAAVDAAD 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283 KVLGYRNWLGINKGDLAAAVDKDGTAFLRVLNRDRNYTAPGGGQFTL---PGRSLMFVRN 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----WRNILLA-GORTLAAAVRGELT------FDAPNGKHYALRPEHERAVLIVRP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                340 VG-HLMTNDAIVDTDGSEVFEGIMDALFTGLIAIHG---LKASDVNGPLINSRIGSIYIV 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283 NCGRWDYIFSYLKT-FRAHPDRVLPERGOVIMTOPFLKAYSELLIKTCHRRGAHAMGGMA 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRAQVGKGMWTWTELMADMVETKIAQPRAGASTAWVPSPT-------AATLHALH 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YHQVDVAAVQQGLAGKRRATIEQLLTIPLAKELAWAPDEI-REEVDNNCOSILGYVVRWV 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NTGFLDRTGDEIHTSMEAGP---MYRKGTM-KSQPWILAYED-----HNVDAGLAAGFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 VERNDV------HITSDMLIATP------PGGITRAGFEGNVEVCVRYLAAWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AELPAAL----QDRRIEI-----TGPTDPKMVINALNSGAKVFMADFEDSTAPT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 RGWHLDEKHVLI--DGQPMAGGLFDA---ALFAFHNARTLMAKD-RGP-----YLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              396 KPKMHGPAEVAFTCELFSRVEDVLGLPQNTMKIGIMDEERRTTVNLKACIKAAADRVVFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               342 AQIPINHDEAANEQAMARVRADKLREVSAGHDGTWVAHPALIPVAMAVFDEHMPTAHOHH
                                                                                               Xanthomonas campestris (pv. campestris).
Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                540 AA; 59271 MW; 60CA577ED1C66947 CRC64;
  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOGVECSKVPDIHDVALMEDRATLRISSOLLANWIRHG 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.8%; Score 258; DB 16; 36.4%; Pred. No. 2.3e-08; ative 54; Mismatches 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AE012119; AAM39556.1; -.
InterPro; IPR006222; Malate syntha.
InterPro; IPR001465; Malate synthase.
Pfam; PF01274; Malate synthase; I.
TIGRFAMs; TIGR01344; malate syn A; I.
                                                                                                                                         Xanthomonadaceae; Xanthomonas
  222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 417:459-463(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome.
                                                         Malate synthase.
MLS OR XCC0237.
                                                                                                                                                            NCBI_TaxID=340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               420 GLPQNIMKIGIMDEERRITVNLKACIKAAADRVVFINTGFLDRIGDEIHTSMEAGPMVRK 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 GTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWL--GLNKGDLAAAVDKDG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              625 GLSRGTIKCTVLIEHLLATFQLHEITHSLKDHVVGLNCGRWDFFCSHRHQISMTAFFMRN 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              685 YSLE----LIKTCHORGIHAMGGMAAHIPIKHDQIANDKAFALVTSDKOREVTDGHDGT 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             307 TAFLRVLNRDRNYTAP-GGGQFTLPGR-SLMFVRNVGHLMTNDAI----VDTDGSEVFEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                480 GTMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAGASTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----LFDFGLFVFHNAKA-----LISKGSGP-YFYLPKLQNABBAQLWSDVFKFTEDKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WVPSPTAATLHALHYHQVDVAAVQQGLAGKRRATIEQLLTIPLA--KELAWAPDEIREEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 IMDALFT-GLIAIHGLKASDVNGPLINSRTGSIYIVKPKWHGPAEVAFTCELFSRVEDVL
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----AVRNNISYTHPTTKKEYKLDEKHAVLMVRPRGWHLTEKHVQIHNQPTSGT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D--NNCQSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             483 GPPDRKSVINALNSGANVFMTDFEDSNSPT------WRNOIEGOVNMYD---
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34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INDAIV---DIDGSEVFEGIMDALFT-GLIAIHGLKASDVNGPLINSRIGSIYIVKPKMH 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 INAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAY--ARKFLDDSVPLSSG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 SFGDATGFTVQDGQLV------VALPD--KSTGLANPGQFAGYTGAAESPTSV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLINHGLHIEILIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRN 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             290 WL--GLNKGDLAAAVDKDGTAFLRVLNRDRNYTAP-GGGQFTLPGR-SLMFVRNVG-HLM 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----NTEFNPRRLRLLSKRNQVQADINNSLWFPDFNKETEVLRSDQ--GWKG-AEIPRDL 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                               Caenorhabditis elegans.
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.2%; Score 198.5; DB 5; Length 968;
23.8%; Pred. No. 0.00044;
tive 70; Mismatches 222; Indels 183;
                                                                                                                                                                                                                                                                                                                                    "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 968;
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Blanchard M., Kramer J., Gibson A.;
Blanchard M., Kramer J. elegans cosmid COSE4.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
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                                   968 AA
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InterPro; IPR006554; Isocit lyase.
InterPro; IPR000918; Isocit_lyase_ph.
InterPro; IPR006552; Malate synthä.
InterPro; IPR001465; Malate_synthase.
                                   PRT;
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE-99069613; Pubmed-9851916;
                                                               01-MAY-2000 (TrEMBLrel. 05, Crt 01-MAY-2000 (TrEMBLrel. 13, Lat 01-MAR-2003 (TrEMBLrel. 23, Las Hypothetical 108.6 kDa protein. C05E4.9.
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Matches 148; Conservative
                                 PRELIMINARY;
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Best Local Similarity
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STRAIN=Bristol N2;
Waterston R.;
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401 GPAEVAFTCELFSRVEDVLGLPQNTMKIGIMDEERRTTVNLKACIKAAADRVVFINTGFL 460
                                                                                      653 SABEAQLWADVFKYTEDKLGLARGTIKCTVLIEHLLASFQLHEIIHALKDNIVGLNCGRW 712
                                                                                                                                                                                                                                 -----GASTAWVPSPTAATLHALHYHQ 556
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----LFDFGLFVFHNAKA-----LIAQGSGP-YFYLPKLQ 652
                                                                                                                                                                                713 DYIFSYİKİFQNHRKFLLPDRFQIGMTAPFMR-------NYSLEVIKACHLRĞ
                                                                                                                                        -----AGPMVRKGTMKSQPWILAYBDHNVDAGLAAGFSG
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  609 EKHVLIHNQPTSGS--
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Perfect score:

Sequence:

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Run on:

Scoring table:

Minimum DB 8 Maximum DB 8

Database

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C. glutamicum prot
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B. lacufermentum
B. flavum AK. Bre
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B. lactofermentum
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Feedback inhibitio
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C. glutamicum aspa
Propionibacterium
Methylophilus meth
Aspartokinase II.
Blifdobacterium lo
M. tuberculosis an
M. tuberculosis re
M. gonorrhoea emi
Listeria monocytog
H. pylori GHPO 774
Procein with aspar
Staphylococus epi
Listeria monocytog
Human ORFX protein
Glycine max aspart
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/label= Histidine_tag
/note= "Nickel chelating region used for purifying
the_fusion protein"
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                                                                                                                          AAW06586
AAW61152
AAR63570
AAR63571
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AAR40846
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AAY39178
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ABP40380
ABB47953
ABP08315
AAE04359
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/label= Mo2_region
  Mycobacterium tuberculosis
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 Misc-difference 49
 WO200124820-A1
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 M. tuberculosis Tb
Mycobacterium poly
Corynebacterium th
Modified Corynebac
Amino acid sequenc
C. Sulutamicum meta
C. glutamicum meta
C. glutamicum prote
Corynebacterium gl
                                                                                 November 21, 2003, 15:50:31; Search time 25.6707 Seconds (without alignments) 2621.664 Million cell updates/sec
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| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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2193
1 VQKYGGSSVADAERIRRVAE.....SAATRRPRCTRGRDGRWACQ 424
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            GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Match Length DB
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1619.5 1248.5 1227.5 1224.5 1224.5 1224.5 1224.5

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Result . 0 N

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The present invention relates to the isolation of Mycobacterium tuberculosis antigen polypeptides (e.g. Tb24) and the nucleic acids encoding them. The invention describes compounds and methods for the diagnosis of tuberculosis or for inducing protective immunity against tuberculosis. The compounds comprise at least one immunity against tuberculosis. The compounds comprise at least one immunity against tuberculosis. The compounds comprise at least one immunity against concoding such polypeptides. The Mycobacterium proteins and nucleic acid molecules encoding them can be used in diagnostic kits for the detection of Mycobacterium infection in parients and biological samples. The Compounds of the invention and antibodies directed against the Mycobacterium infections. The nucleic acids encoding the Mycobacterium proteins may be used in vaccines for immunisation against Mycobacterium polypeptide for MO-2.

Mycobacterium polypeptide for MO-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An isolated polypeptide comprising a Mycobacterium antigen, e.g., from Mycobacterium tuberculosis, useful in a vaccine for enhancing an immune response to and inhibiting development of a Mycobacterium infection
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                                                             Tuberculosis, Mycobacterium infection, gene therapy, anti bacterial;
immunostimulant, MO-2.
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Pred. No. 3.8e-142;
8; Mismatches 34;
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                                                                                                                                                                      Location/Qualifiers
                    Mycobacterium polypeptide for MO-2.
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85.1%;
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08-AUG-2000; 2000US-0223828
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Best Local Similarity 85.1
Matches 338; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           808
                                                                                                                                                                                                                                                                                                                                                                                consisting of a His tag for purification, antigen MtB81 and antigen Mo2. Compositions comprising at least 2 heterologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially humans) against infection by Mycobacteria. The compositions contain at least 2 heterologous antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease frequently affecting patients with acquired immunodeficiency disease, AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          809 ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRRRQHRHGAAERLQGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     989 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRRRQHRHGAAERLQGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRQDRHHLHLLLPQTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLIGAGMRSHPGVTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEEGRVVLVAGFQGVSQDTXDVTTLGRGGSDTTAVAMAAALGADVCELYTDVDGIFSADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 869 LEEGRVVLVAGFOGVSODTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FCEALAAVGVNIELISTSEDORSRCCAATPNWTRPWSRCMKRSGSAATRRPRCTRGRDGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                    Lodes ML;
                                                                                                                                                                                                                                                          Vaccinating against Mycobacteria infections in mammals using fusion
                                                                                                                                                                                                                                                                                                                                                                   represents Mycobacterium fusion protein antigen TbF14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 2193; DB 22; Length 1172; 100.0%; Pred. No. 5.5e-195; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                 Dillon DC,
                                                                                                                                                                                                                                                                                 proteins comprising combinations of heterologous antigens
                                                                                                                                                 McNeill PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU08233 standard; Protein; 421 AA.
                                                                                                                                                 Houghton RL,
                                                                                                                                                                                                                                                                                                                          Claim 3; Fig 3; 168pp; English.
                                           99US-0158338
99US-0158425
2000WO-US28095
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Best Local Similarity 100.
Matches 424; Conservative
                                                                                                                                                                                          WPI; 2001-290576/30.
N-PSDB; AAS03794.
                                                                                                        (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1172 AA;
                                                                                                                                                 Reed S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WACQ 1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WACQ 424
10-OCT-2000;
                                                             07-OCT-1999;
                                           07-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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305 D----GTTD--ITFTCPRSDGPRAMELLKKWQQQGDWTNVLYDDQVGKVSLVGAGMKSH 357
     185 RIVPNAQKLERLSFEEMLELAAVGSKILVLRSVEYARAFNVPMRVRSSYSNDPGTLIAGS 244
                                                                                             245 MEDIPMEEAVLTGVATDKSEAKVTVLGIPDKPGEAAKVFRALADAEINIDMVLQNVSSVE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a modified aspartokinase from Corynebacterium aspartokinase (e.g., AAB2607) and to DNA encoding the modified aspartokinase (e.g., AAB2607) and to DNA encoding the modified modified to remove its sensitivity to feedback inhibition by L-threonine or L-lysine. This is achieved by substituting the wild-type Thr 311 with any other amino acid, for example, in AAB25007 Thr 311 is substituted by Ile. The invention also relates to expression vectors and host coryneform bacteria contraining the modified DNA, and to the preparation of L-lysine using coryneform bacteria transformed with the modified aspartokinase-encoding DNA. Culturing coryneform bacteria transformed with the modified aspartokinase DNA of the invention provides efficient production of L-lysine. The present sequence represents a modified corynebacterium glutamicum aspartokinase of the invention, T3111.
                                                                                                                                                 295 ERLQGRGRQDRHHLHLLPQTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLIGAGMRSH
                                                 241 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRR-----ROHRHGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding modified aspartokinase without synergistic feedback inhibition by L-lysine and L-threonine for efficient production cL-lysine by coryneform bacterium fermentation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aspartokinase; AK; lysine synthesis; feedback inhibition;
L-lysine; L-threonine; insensitive; product inhibition;
coryneform bacterium; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified Corynebacterium glutamicum aspartokinase, T311I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Wild-type Thr replaced with Ile"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yonetani Y,
                                                                                                                                                                                                                                              355 PGVTATFCEALAAVGVNIELISTSE 379
                                                                                                                                                                                                                                                                                               358 PGVTAEFMEALRDVNVNVELISTSE 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 29-30; 33pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                    A.
                                                                                                                                                                                                                                                                                                                                                                                                                 AAB29607 standard; Protein; 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ochiai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-APR-2000; 2000WO-JP02456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterium glutamicum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-687179/67.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB29607;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                            296 VLQNVSKVEKGKTDITFTCSRDVGPAAVEKLDSLRNEIGFSQLLYDDHIGKVSLIGAGMR 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 120
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IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRRRQHRHGAAE---- 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                        RLQGRGRQDRHHLHLLPQTS---GPPPWKNWTRSETRSASTQLLYDDHJGKVSLJGAGMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 VOKYGGSSLESAERIRNVAERIVATKKAGNDVVVVCSAMGDTTDELLDLAAAVNPVPPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIVENARKLDTUTFEEMLEMAACGAKULMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDITDDLLDLAQQVCPAPPPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a gene from a high temperature-resistant coryneform microbe that encodes a heat-resistant lysin biosynthetic enzyme enzyme has aspartate-semialdehyde dehydrogenase activity and can be used for growing amino acid-producing microbes. The present amino acid sequence corresponds to an enzyme of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A heat-resistant lysin biosynthetic system enzyme gene of a high temperature-resistant coryneform microbe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corynebacterium thermoaminogenes lysin biosynthetic enzyme lysC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22; Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heat-resistant, lysin biosynthesis, enzyme; coryneform;
aspartate-semialdehyde dehydrogenase; lysC.
                                                                                                                                                                                          SHPGVTATFCEALAAVGVNIELISTSEDQRSRCCAAT 389
                                                                                                                                                                                                                       SHPGVIATFCEALAAVGVNIELISTSEIRISVLCRDT 392
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65.2%; Pred. No. 1.5e-107;
iive 58; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Page 21-22; 27pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                AAG64046 standard; Protein; 421 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterium thermoaminogenes.
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N-PSDB; AAH45374.
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                                                                                             296
                                                                                                                                                                                                                                                                                                                                                                                                              AAG64046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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Best Local 8
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Corynebacterium glutamicum
                                                                                                                               Matches 251; Conservative
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                                                                                                                       Local Similarity
                                                                                                 421 AA;
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Misc-difference
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                                       ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA
                                                                                          LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCE1YTDVDG1FSADP
                                                                                                  RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
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                              VOKYGGSSVADAERIRRVAERIVATKKOGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPR
                                                                                                                                                                                                                                                                                                                                bacteria; chemical compound; L-amino acid; vitamin; lysC;
                                                                                                                                                                                                                                                                                                                   Amino acid sequence of a aspartate kinase carrying T3111 mutation
                27;
 DB 21; Length 421;
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56.0%; Score 1227.5; DB 21
64.0%; Pred. No. 1.3e-105;
iive 56; Mismatches 58;
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                                           The specification describes Coryneform bacteria which produce chemical compounds, which instead of a single copy of an open reading frame (ORF), gene or allale naturally present at a desired locus have at least two copies of the ORF, gene or allele, preferably in tandem arrangement. The modified bacteria are is useful for producing chemical compounds including L-amino acids, vitamins, nucleosides and nucleotides. The present sequence is encoded by a lysC gene, and represents an aspartate kinase carrying the Tilli mutation. Tandem duplications of the lysC gene are used to construct the bacteria of the invention.
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64.0%; Pred. No. 1.3e-105;
ive 56; Mismatches 58; Indels
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Page 105-106; 109pp; English.
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                                                                                            L-lysine, has at
in question at a
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                                                                                      Coryneform bacteria to produce chemical compounds e.g. least two copies of open reading frame, gene or allele particular desired site
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                                        Thierbach
                                                                                                                                   Claim 15; Page 102-103; 109pp; English.
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                                        Moeckel
06-AUG-2001; 2001US-309877P
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Best Local Similarity 64.0
Matches 251; Conservative
                                        Kreutzer C,
                                                           WPI; 2003-278476/27.
N-PSDB; ABZ77391.
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AAU71863-AAU71222 represent the novel C glutamicum metabolic pathway proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                          Kim J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding metabolic pathway proteins from Corynebacterium glutamicum, useful for producing methionine and lysine in Corynebacterium and Brevibacterium -
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                                                                                                                                                                                                                                                                                                                                                                          Haberhauer G,
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                                                                                                                                                                                                                                                                                                                                                                          Zelder O,
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                                                                                                                                                                                                                                                                                                                                                                          Schroeder H,
                                                                                                                                                                                                    09-MAR-2000; 2000US-187970P
23-JUN-2000; 2000US-0606740
                                                                                                                                      22-DEC-2000; 2000WO-IB02035
                                                                                                                                                                                                                                                                                                                                                                              Kroeger B,
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N-PSDB; AAS96084.
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WO200166573-A2
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99DE-1031424
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                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                         RESULT 9
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                                                                                                                                                                                                                                                The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a marant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium coryneform bacterium coryneform bacterium and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, thanins, saccharides and organic acids, in the exemplification of the invention.

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 EMDMLLTAGERISNALVAMAIESLGAEAQSFTGSQAGVLTTERHGNARIVDVTPGRVREA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS 240
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                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VQKYGGSSLESAERIRNVAERIVATKKAGNDVVVVCSAMGDTTDELLELAAAVNPVPPAR
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                                                                                                                                                                                                                                                                                                                                                  Yokoi
                                                                                                                              Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 17; SEQ ID NO: 3781; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                    Ochiai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.8%; Score 1224.5; DB 22
64.0%; Pred. No. 2.5e-105;
live 55; Mismatches 59;
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Ikeda M, Ozaki A;
                                                                                                     C glutamicum protein fragment SEQ ID NO: 3781.
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                       AAG90027 standard; Protein; 421
                                                                                                                                                                                                                                                                                                                          (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                        99JP-0377484.
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03-AUG-2000; 2000JP-0280988.
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                                                                                                                                                                   Corynebacterium glutamicum.
                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                  Mizoguchi F
Senoh A,
                                                                                                                                          organic acid synthesis.
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                                                                                                                                                                                                                                                                                                                                                                                         2001-376931/40.
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N-PSDB; AAH65246.
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Tateishi N,
                                                  AAG90027;
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Best Local S
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RESULT 8
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241 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA------RRRRQHR 290
                                                                                                                                                                                                                    245 MEDIPVEEAVLTGVATDKSEAKVTVLGISDKPGEAAKVFRALADAEINIDMVLQNVSSVE 304
                                                                                                                                                                                                                                                                                                          291 HGAAERLQGRGRQD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 347
                                                                                                                                                                                                                                                                                                                                                                                   -----TNVLYDDQVGKVSLV 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium glutamicum MP protein sequence SEQ ID NO:26.
                                                                                                                                                                                                                                                                                                                                                            348 GAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
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                           ---TNVLYDDQVGKVSLV 350
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        HGAAERLQGRGROD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a mutant version of the C. glutamicum asparto-kinase (AK) alpha suburit. The mutation is at position 279 and is a corresponds to the substitution of a non-acidic amino acid, pref. Ala. This mutation causes removal of the enzyme from additional feedback inhibition. Inhibition by Thr is removed completely and the synergic inhibition of Lys and Thr is also removed. The new AK has increased heat stability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA
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                                                                                                                                                                                                                                                                                                              Mutant, C. glutamicum, aspartokinase, AK; alpha; beta, subunit; substitution, non-acidic; amino acid; Ala; additional; enzyme; feedback inhibition; synergic inhibition; heat stability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15; Length 421;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                     305 DGTTDITFTCPRSDGRRAMEILKKLÖVQG-----NW
                                                                                        GAGMKSHPGVTAEFMEALRDVNVNIELISTSE
                                                                      348 GAGMRSHPGVTATFCEALAAVGVNIELISTSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 14-16; 28pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                 AAR51469 standard; Protein;
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Best Local Similarity 64.0
Matches 251; Conservative
                                                                                                                                                                                                                                                                                 AK alpha subunit T279A.
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                                                                                                                                                                                                                                                  (first
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Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IKDVPMEDPILITGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA------RRRRQHR 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic pathway (MP) proteins given in AAAF954 to AAB80211. The C. glutamicum MP nucleic acids are useful for the production of fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, including status acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids from Corynebacterium glutamicum encoding metabolic pathway proteins, useful for producing fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, and purine and pyrimidine bases.
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64.0%; Pred. No. 2.5e-105;
.ive 55; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            Zelder O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; Page 193-194; 1737pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Schroeder
9DDE-1032928
9DDE-1033004
9DDE-1033005
99DE-1033005
99DE-1040764
99DE-1040766
99DE-1040766
99DE-104033
99DE-1041379
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99DE-1042076
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99DE-1042129.
2000US-0187970.
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Best Local Similarity 64.0
Matches 251; Conservative
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03-SEP-1999;
09-MAR-2000;
                                                   14-JUL-1999;
12-AUG-1999;
27-AUG-1999;
27-AUG-1999;
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27-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
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03-SEP-1999;
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03-SEP-1999
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RESULT 11 AAR51465

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LEEGRVVLVAGFOGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 180
                                                                                                                                                                                                                             245 MEDIPVEEAVLTGVATDKSEAKVTVLGISDKPGEAAKVPRALADAEINIDMVLQNVSSVE 304
                                                                                                                                                                                                                                                                                                             305 DGTTDITFTCPRADGRRAMEILKKLÖVQĞ----NW------TNVLYDDQVGKVSLV 350
                                                                                                                                                                                                                                                                            HGAAERLQGRGRQD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 347
             LDEGKICIVAGFOGVNKETRDVTTLGRGGSDTTAVALAAALNADVCEIYSDVDGVYTADP
                                                                                                                                  181 RIVRNARKLDTVTFBEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The primers given in AAQ84968-69 were used in the PCR amplification of C. glutamicum ATCC 13869 DNA to isolate the DNA sequences given in AAQ84970-71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Variant of phospho-enol pyruvate carboxylase - not substantially inhibited by aspartic acid, is used for efficient production of amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 55.8%; Score 1223.5; DB 16; Length 421; Best Local Similarity 64.0%; Pred. No. 3.1e-105; Matches 251; Conservative 55; Mismatches 59; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phosphoenolpyruvate-carboxylase; Corynebacterium glutamicum.
                                                                                                                                                                                                         241 IKDVPMEDPILTGVAHDRSBAKVTIVGLPDIPGYAAKVFRAVA-
                                                                                                                                                                                                                                                                                                                                               348 GAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
                                                                                                                                                                                                                                                                                                                                                                         Ë
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 48-51; 77pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR71416 standard; Protein; 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sugimoto M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93JP-0209775.
93JP-0209776.
94JP-0153876.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)

 glutamicum protein.

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N-PSDB; AAQ84970.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09506114-A1
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240
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                                                                                     291 HGAAERLOGRGROD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 347
                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents a mutant version of the C. glutamicum asparto-kinase (AK) alpha subunit. The mutation is at position 279 and corresponds to the substitution of a non-acidic amino acid, pref. Ala. This mutation causes removal of the enzyme from additional feedback inhibition. Inhibition by Thr is removed completely and the synercic inhibition of Lys and Thr is also removed. The new AK has increased heat stability.
                  241 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA------RRRRQHR
RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VOKYGGSSVADAERIRRVAERIVATKKQGNDVVVVSAMGDTTDDLLDLAQQVCPAPPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mutant, C. glutamicum, aspartokinase, AK, alpha, beta, subunit, substitution, non-acidic, amino acid, Ala, additional, enzyme, feedback inhibition, synergic inhibition, heat stability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 15; Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The mutant aspartokinase gene - used to produce AK which is removed from feedback inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 55.8%; Score 1223.5; DB 15; Lengt. Local Similarity 64.0%; Pred. No. 3.1e-105; Les 251; Conservative 55; Mismatches 59; Indels
                                                                                                                                                                                                         379
                                                                                                                                                                                                                                        GAGMKSHPGVTAEFMEALRDVNVNIELISTSE 382
                                                                                                                                                                                                                                                                                                                                                                                                                                      AK alpha subunit T279A from clone ATCC 13869.
                                                                                                                                                                                                         GAGMRSHPGVTATFCEALAAVGVNIELISTSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 22; 28pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                 AAR51465 standard; Protein; 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= T279A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92JP-0110292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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N-PSDB; AAQ61599.
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Best Local S
Matches 251
                               185
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181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     291 HGAAERLQGRGRQD-RHHLHLLP--QTSGPPPWRWWTRSETRSASTQLLYDDHIGKVSLI 347
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                                                                                                                                                                                                                                                                                                              121 LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 180
                                                                                                                                                                                                                                                                                                                                               184
                                                                                                                                                                                                                   64
                                                                                                                                                                                                                                                                                                                                                                                             IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA------RRRRQHR
                                                                                                                                                                                                                                                  61 ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA
                                                                                                                                                                                                                                                                 1 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR
                                                                                                                                                                                                                 s vokyggsslesaerirnvaerivatkkagndvvvvcsamgdttdellelaaavnPvPPar
                                                                                                                                                                                                                                                                                                                                                                             RIVRNARKLDTVTFEEMLEMAACGAKVLMIRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                                       Gaps
inhibition, by substituting the respective alpha and/or beta subunit (ARR86307/08) residues Ala 279 and/or 30 with another amino acid, and homoserine dehydrogenase (HD) gene (AAT03321) which encodes an attenuated HD (AAR86306), by substituting the residues Leu 23 and/or Val 104 with another amino acid, esp. Phe or Ile.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant DNA encoding aspartokinase in Coryneform bacterium
                                                                                                                      55.8%; Score 1223.5; DB 16; Length 421; 64.0%; Pred. No. 3.1e-105; ive 55; Mismatches 59; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L-lysine; aspartokinase; lysC gene; coryneform bacterium;
Corynebacterium glutamicum; fodder; feedstuff.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yoshihara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351 GAGMKSHPGVTAEFWEALRDVNVNIELISTSE 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brevibacterium lactofermentum ATCC 13869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96JP-0325658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW68147 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayakawa A, Nakamatsu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AJIN ) AJINOMOTO CO INC. (AJIN ) AJINOMOTO KK.
                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-416006/36.
N-PSDB; AAV41300.
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                                                                                                                                       1 Similarity
251; Conserv
                                                                                            421 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-NOV-1998
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                                                                                                                        Query Match
Best Local S:
Matches 251
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                                                                                               Sequence
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                                                                                                                                                                                                                                                                    HGAAERLQGRGRQD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 347
                                                                                                                                                                                                                                                                                                                                   | :|||| :|||||:
|-----TNVLYDDQVGKVSLV 350
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                                 64
                   IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA--------RRRRQHR
   VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR
                                                                BLDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA
                                                                                                                                                                                       RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coryneform bacteria with increased L-lysine prodn. efficiency are produced by integrating a Coryneform aspartokinase (AK) gene (AAT03326) which encodes an AK free of L-Lys and L-Thr feedback
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High L-lysine production using transformant coryneform bacteria having attenuated or deficient homoserine dehydrogenase gene and introduced feedback inhibition free asparto:kinase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aspartokinase, homoserine dehydrogenase, L-lysine production, coryneform bacteria, feedback inhibition free, attenuated, ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "opt. substituted to remove L-Lys and
L-Thr feedback inhibition"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterium glutamicum aspartokinase alpha-subunit.
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                                                                                                                                                                                                                                                                                                                                   | : : | | | | | DGTTDITFTCPRADGRRAMEILKKLQVQG-----NW-
                                                                                                                                                                                                                                                                                                                                                                              GAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
                                                                                                                                                                                                                                                                                                                                                                                                     GAGMKSHPGVTAEFMEALRDVNVNIELISTSE 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Pages 55-57; 77pp; Japanese.
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279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR86307 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-320579/41.
N-PSDB; AAT03326.
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Misc-difference
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Yoshihara

Sugimoto M,

97EP-0121443. 96JP-0325659

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The present invention describes a recombinant DNA autonomously replicable in cells of coryneform bacteria (CB), comprising a DNA sequence coding for an aspartokinase (AK) in which feedback inhibition by L-lysine and L-threonine is desensitised, a DNA sequence coding for a dinydrodipicolinate synthase (DHPR), a DNA sequence coding for dinydropicolinate synthase (DHPR), a DNA sequence coding for aspartate decarboxylase (DAMD) and a DNA sequence coding for aspartate aminotransferase (AAT). The present sequence is wild-type lyst from Brevibacterium lactofermentum. The DNA and related products from the present invention, can be used for improving L-lysine productivity by CB. The L-lysine produced can be used as a fodder
                                                                                                                                                                                                                                                    Recombinant DNA autonomously replicable in coryneform bacteria used to produce L-lysine, codes for e.g. aspartokinase, di:hydropicolinate reductase and synthase and di:amino-pimelate
                                                                                                                                                                                                                                                                                                                                                     Claim 2; Page 22-23; 59pp; English.
                                                                                                                     (AJIN ) AJINOMOTO CO INC
                                                                                                                                                          Araki M, Nakamatsu T,
                                                                                                                                                                                                 WPI; 1998-379060/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 AA;
                                                                                                                                                                                                                    N-PSDB; AAV40254
                                                                                                                                                                                                                                                                                                                  decarboxylase
                                         05-DEC-1997;
                                                                              05-DEC-1996;
    22-JUL-1998
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                                                                     This is the wild-type alpha subunit of Brevibacerium lactofermentum CATCC 1369 (Corynebacterium glutamicum) aspartokinase, an enzyme involved in the biosynthesis of L-lysine, but which is subject to feedback inhibition. A claimed recombinant DNA molecule that is autonomously replicable in coryneform bacteria comprises a DNA sequence coding for an aspartokinase in which feedback inhibition. By L-lysine and L-threonine is desensitised, and a DNA sequence coding for a diaminopimelate decarboxylase. This mutant aspartokinase preferably has residue Ala-279 of the alpha subunit (see AAW68152) and residue Ala-30 of the beta subunit (see AAW68152) and residue Ala-30 of the beta subunit (see AAW68152) and maino acid that is not Ala and is not an acidic amino acid. The host coryneform bacteria are used in a claimed method for producing L-lysine, which is useful as a fodder additive. They show improvements in L-lysine yield without
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 421;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 19;
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64.0%; Pred. No. 3.1e-105;
iive 55; Mismatches 59;
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                                       Claim 2; Page 17-18; 50pp; English
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used in preparation of L-lysine
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                                                     Gaps
                                                  27;
  DB 19; Length 421;
55.8%; Score 1223.5; DB 19; Lengt 64.0%; Pred. No. 3.1e-105; ive 55; Mismatches 59; Indels
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                                                  251; Conservative
                           Similarity
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Search completed: November 21, 2003, 16:03:11 Job time : 27.6707 secs

Brevibacterium lactofermentum, lysC, L-lysine, coryneform bacterium, aspartokinase, feedback inhibition, dihydropicolinate reductase, diaminopimelate decarboxylase, aspartate aminotransferase.

Brevibacterium lactofermentum

EP854189-A2

Brevibacterium lactofermentum lysC protein.

13-0CT-1998

Sequence (Sequence equence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence

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Sequence 30, Application US/08311731A

Patent No. 6583266
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR TITLE OF INVENTION: DIGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VOKYGGSSVADAERIRRVAERIVATKKOGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR
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COMPUTENT: END P. COMPATIBLE
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CLASSIFICATION NUMBER: G0044/7125
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TELEPHONE: 617/720-3441
INPORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 anino acids
TYPE: anino acids
TYPE: Anino acids
TYPE: Anino acids
                                                                                            US-08-532-828B-6
US-08-596-86-8
US-08-596-104-8
US-09-109-452A-1124
US-09-1107-532A-6090
US-09-1107-532A-6090
US-09-1107-532A-64941
US-09-252-991A-22037
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US-09-324-542-114
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US-08-311-731A-30
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Sequence 5, Appl
Sequence 11, App
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Sequence 8, A
Sequence 20,
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1 VQKYGGSSVADAERIRRVAE.....SAATRRPRCTRGRDGRWACQ 424
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                                  GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-08-596-366-6
US-08-985-908-5
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US-08-852-730-14
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US-08-985-91A-29720
US-09-252-991A-29720
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US-09-072-596-222
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US-08-887-534A-23
US-08-887-534A-23
US-08-8887-534A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                           November 21, 2003, 15:58:31
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
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Gaps

17;

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Query Match
55.8%; Score 1223.5; DB 1
Best Local Similarity 64.0%; Pred. No. 1.1e-116;
Matches 251; Conservative 55; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348 GAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         351 GAGMKSHPGVTAEFMEALRDVNVNIELISTSE 382
  ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Corynebacterium glutamicum
STRAIN: ATCC13869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA

ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS TEXT EDITOR
CURRENT APPLICATION UNDER: US/08/700,359
FILING DATE: 08-OCT-1996
CLASSIFFCATION: 435
PRICK APPLICATION NUMBER: UP-35019
FILING DATE: 04-MAR-1994
ATTORNEY/AGENT: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 9, Application US/08700359
; Patent No. 5766925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 24,618
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US-08-532-828B-3
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                                                                                                                                                                               125 LDEGRIVLVAGFQGVSQDTRDITTLGRGGSDTTALAMAAALGADVCEIYIDVDGIFSADP 184
                                                                                                                                                                                                                                       181 RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS 240
                                                                                                                                                                                                                                                               185 RVVHNARKLDTVTFEEMLEMAACGAKVLMIRCVEYARRHNI PVHVRSSYADKPGTVIVGS 244
                                                                                                                                                                                                                                                                                                                                                  245 IKDVPMEDPILITGVAHDRSEAKVTIVGIPDIPGYAAKVFRAVA-----DADVNIDM 295
                                                                   61 ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 120
                                                                                                                                                                                                                                                                                                                          241 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRRRQHRHGAAE---- 295
                                                                                                                                                                                                                                                                                                                                                                                                          296 RLQGRGRQDRHHLHL---LPQTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLIGAGMR 352
                                                                                                         65 ELDMLLTAGERISNALVAMAIESFGAQARSFTGSQAGVITTGTHGNAKIIDVTPTRLQFA 124
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5 VQXYGGSSVADADRIRRVAERIVQTKKQGNDIVVVVSAMGDTTDDLLDLAQQVCPEPPAR 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                353 SHPGVTATFCEALAAVGVNIELISTSEDORSRCCAAT 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08532828B
| Patent No. 5688671
| GENERAL INFORMATION:
| APPLICANT: GOING: Wasakazu
| APPLICANT: GGNA, Yuri
| APPLICANT: SUZUKI, Tomoko
| APPLICANT: TANAKA, Akiko
| APPLICANT: TANAKA, Akiko
| APPLICANT: MATSU, Hiroshi
| TITLE OF INVENTION: MUTANT ASPARTOKINASE GENE
| NUMBER OF SEQUENCES: 24
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
21P: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS TEXT EDITOR
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/532,828B
TILING DATE: 27-OCT-1995
TILING DATE: 27-OCT-1995
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CLASSIFICATION: 435
PRIOR APPLICATION DATA.
APPLICATION NUMBER: JP 5-101450
FILING DATE: 27-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELERAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acids
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MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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US-08-532-828B-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291 HGAAERLQGRGRQD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30S DGTTDITFTCPRADGRRAMEILKKLQVQG-----NW-----TNVLYDDQVGKVSLV 350
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                                                                                                                                                                                                                                                                                            65 EMDMLLTAGERISNALVAMAIESLGAEAQSFTGSQAGVLTTERHGNARIVDVTPGRVREA
                                                                                                                 1 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPR
                                                        Gaps
                                                        27;
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DB 1; Length 421;
                                                     59; Indels
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APPLICANT: SUGINOTO,
APPLICANT: SUGINOTO,
APPLICANT: SUZUKT, TOMOKO
APPLICANT: SUZUKT, TOMOKO
APPLICANT: TANAKA, AKIKO
APPLICANT: MATSUT, HIROSHI
TITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 22
CORRESPONDENCES: 22
CORRESPONDENCES: 22
CORRESPONDENCES: 09LON, SPIVAK, MCCLELLAND, MAIER & NEUS
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 40C
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us-09-688-672a-4.rai

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RESULT 5
US-08-967-104-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEEGRIVILVAGFOGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 IKDVPMEDPILTGVAHDRSBAKVTIVGLPDIPGYAAKVFRAVA-------RRRRQHR 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             291 HGAABRLOGRGROD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 347
                                                                                                                                                                                                                                                                           9
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Patent No. 5876981

GENEAL INFORMATION:

APPLICANT: SUGINOTO, Masakazu

APPLICANT: SUGINOTO, Masakazu

APPLICANT: SUZUKI, Tomoko

APPLICANT: MATSUI, Hiroshi

APPLICANT: IZUI, Katsura

ITILE OF INVENTION: ITS GENE, AND PRODUCTION METHOD OF AMINO ACID

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: P.C.

ADDRESSEE: P.C.

ADDRESSEE: P.C.

ADDRESSEE: P.C.

ATREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE # 400
                                                                                                                                                                                                                                                                                         5 VQKYQGSSLESAERIRNVAERIVATKKAGNDVVVVCSAMGDTTDELLELAAAVNPVPPAR
                                                                                                                                                                                                                                                                     1 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPR
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                      27;
                                                                                                                                                                                                        DB 1; Length 421;
                                                                                                                                                                                                    ; Score 1223.5; DB 1; Length
; Pred. No. 1.1e-116;
55; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSE: P.C.
STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE # 400
STREET: VISS JEFFERSON DAVIS HIGHWAY, SUITE # 400
STATE: VIRGINIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 22202,
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/08/596,366
FILING DATE: 29-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             348 GAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGMKSHPGVTAEFMEALRDVNVNIELISTSE 382
REFERENCE/DOCKET NUMBER: 1
TREECOMMUNICATION INFORMATION
TELEPHONE: 703-413-3000
TELEFRX: 703-413-2220
                                                                                                                                                                                                      55.8%;
                                                                                                    TYPE: amino acid
; TOPOLOGY: linear
; MOLECTLE TYPE: protein
US-08-700-359-9
                                                                                                                                                                                                Query Match
Best Local Similarity 64.0°
Matches 251; Conservative
                                                             INFORMATION FOR SEGID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
US-08-596-366-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 RIVPNAQKLEKLSFEEMLELAAVGSKILVLRSVEYARAFNVPLRVRSSYSNDPGTLIAGS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA-------RRRRQHR 290
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APPLICANT: SUGUKI, Tomoko
APPLICANT: SUZUKI, Tomoko
APPLICANT: MATSUI, Hiroshi
APPLICANT: IZUI, Katsura
TITLE OF INVENTION: MUTANT PHOSPHOENOLPYRUVATE CARBOXYLASE,
TITLE OF INVENTION: ITS GENE, AND PRODUCTION METHOD OF AMINO ACID
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER, & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27;
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 19 5-209775
FILING DATE: 24-AUG.1993
PRIOR APPLICATION NUMBER: 19 5-209776
FILING DATE: 24-AUG.1993
PRIOR APPLICATION NUMBER: 24-BUG.1994
PRIOR APPLICATION NUMBER: 19 6-153876
FILING DATE: 05-JUL.1994
ATTORNEY/AGENT INFORMATION:
NAME: 08LOW, NORMAR P.
REFERENCE/DOCKET NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-784-0 PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
DENGTH: 421 anino acids
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amino acid
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Best Local Similarity 64.04
Matches 251; Conservative
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MOLECULE TYPE: protein
US-08-596-366-6
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MASAKAZU SUGIMOTC, YASUHIKO YOSHIHARA, AND TSUYOSHI NA
FOR PRODUCING L-LYSINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIVENARKLDTVT FEEMLEMAACGAKVLMLRCVEYARRHNI PVHVRSSYSDRPGTVVVGS
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                                                                                                                                                                                                                     SEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3; Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.8%; Score 1223.5; DB 3 64.0%; Pred. No. 1.1e-116; ive 55; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             348 GAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
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                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,908
FILING DATE: 05-DEC-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-325659
FILING DATE: 05-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRALION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                         ; Sequence 5, Application US/08985908
; Patent No. 6004773
                                                                                                            Patent No. 6004773
GENERAL INFORMATION:
APPLICANT: MASAYUKI ARAKI, P
TITLE OF INVENTION: METHOD I
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 703413-2220
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
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amino acid
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Best Local Similarity 64.03
Matches 251; Conservative
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STREET: 17
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                                                                       US-08-985-908-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 55.8%; Score 1223.5; DB 2; Length 421; Best Local Similarity 64.0%; Pred. No. 1.1e-116; Matches 251; Conservative 55; Mismatches 59; Indels 27; Gaps
SSEE: P.C.
F: 1755 JEFFERSON DAVIS HIGHWAY, SUITE # 400
ARLINGTON
VIRGINIA
                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  348 GAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 10-784-0 PCT TELEPHONE: (703) 413-220
TELEFAX: (703) 413-220
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                       PILING DATE:
CLASSIPICATION NOMBER: US/US/98',104
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/596,366
FILING DATE: 29-APR-1996
APPLICATION NUMBER: UP 5-209775
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 5-209776
FILING DATE: 24-AUG-1993
PRIOR APPLICATION NUMBER: UP 6-153876
FILING DATE: 05-UUL-1994
ATTORNEY/AGBAT INFORMATION:
NAME: OBLON, NORMAN F.
NAME: OBLON, NORMAN F.
REGISTATION NUMBER: 24,618
                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 421 amino acids amino acid
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                                                                                                               ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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             ADDRESSEE:
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                                                                                             COUNTRY:
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Sequence 5, Application US/08985916
Fatent No. 6221636
GENERAL INFORMATION:
APPLICANT: ATGUSH HAYAKAWA, MASAKAZU SUGIMOTO, YASUHIKO YOSHIHARA, AND TSUYOSHI
TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
COUNTRY: VA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HGAABRLQGRGRQD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----TNVLYDDQVGKVSLV 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
COMPUTER: BM PC compatible
CORREATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,916
FILING DATE: 05-DEC-1997
APPLICATION 1435
PRIOR APPLICATION NUMBER: US/08/985,916
ATTING DATE: 05-DEC-1996
ATTING DATE: 05-DEC-1996
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64.0%; Pred. No. 1.1e-116;
tive 55; Mismatches 59;
351 GAGMKSHPGVTAEFMEALRDVNVNIELISTSE 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 24,618
TELEPHONE: 703-413-3000
TELEFA. 703-413-2220
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity 64.0%
Matches 251; Conservative
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APPLICANT: SEIKO HIRANO, MASAKAZU SUGIMOTO, EIICHI NAXANO,
APPLICANT: MASAKA IZUL, ATSUSHI HAYAKAWA, YASUHIKO YOSHIHARA, AND TSUYOSHI
APPLICANT: MASAKA IZUL, ATSUSHI HAYAKAWA, YASUHIKO YOSHIHARA, AND TSUYOSHI
APPLICANT: MAKAYATSU
ITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE
NUMBER OF SEGUENCES:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, NAIER AND NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, NAIER AND NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
STATE: VA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
ARREST AND MATE:
ALING DATE: O5-07-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IKDVPMEDPILITGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA------RRRRQHR 290
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APPLICALL...
FILING DATE: 05-07-179,
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-142812
FILING DATE: 05-001-1996
ATTORNEY AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEPHONE: 703-413-3220
TELEPHONE: 703-413-3220
                                                                                                                 Sequence 14, Application US/08852730 Patent No. 6090597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SECILE 2015 NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: 421 amino acids TYPE: amino acids TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 64.0%
Matches 251; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-08-852-730-14
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NS-09-252-991A-29720

Sequence 29720, Application US/09252991A

Sequence 29720, Application US/09252991A

Sequence 29720, Application US/09252991A

Sequence 29720, Application US/09252991A

Sequence 29720, Application UND SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINGAR FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1998-02-18

PRIOR PLING DATE: 1998-02-18

PRIOR PLING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 29720

LENGTH: 461
                                                                                                                                                  30S DGTTDITFTCPRADGRRAMEILKKLQVQG-----NW------TNVLYDDQVGKVSLV 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----HRHGAAERLQGRGRQDRHHLHLLPQTSGPPPWKNWTRSETRSASTQLLYDDH 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -ANIGAREAIGDIN 389
185 RIVPNAQKLEKLSFEEMLELAAVGSKILVLRSVEYARAFNVPLRVRSSYSNDPGTLIAGS 244
                                                                  291 HGAAERLQGRGRQD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VOKYGGSSVADAERIRRVAERIVATKKQGNDVVVVSAMGDTTDDLLDLAQQVCPAPPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                          241 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     341 IGKVSLIGAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IAKVSIVGVGMRSHAGVASRMFEALAKESINIQMISTSE 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.5%; Score 823; DB 4; I 42.6%; Pred. No. 1.3e-75; iive 80; Mismatches 105;
                                                                                                                                                                                                           348 GAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
                                                                                                                                                                                                                                                 351 GAGMKSHPGVTAEFMEALRDVNVNIELISTSE 382
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US-07-684-135A-2
; Sequence 2, Application US/07684135A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 42.65
Matches 170; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-252-991A-29720
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                                                                                                                                                                                                                                                                                                                              SSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
T: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 55.6%; Score 1219.5; DB 1
Best Local Similarity 63.8%; Pred. No. 2.8e-116;
Matches 250; Conservative 55; Mismatches 60;
                                                                                                                                                               GENERAL INPORMATION:
APPLICANT: STGIMOTO, MASAKAZU
APPLICANT: GGAWA, YURI
APPLICANT: SUZUKI, TOMOKO
APPLICANT: TANAKA, AKIKO
APPLICANT: TANAKA, AKIKO
APPLICANT: MATSUI, HITOSHI
TITE OF INVENTION: MUTANT ASPARTOKINASE GENE
NUMBER OF SEQUENCES: 24
351 GAGMKSHPGVTAEFMEALRDVNVNIELISTSE 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

WEDUNG TYPE: READABLE FORM:

WEDUNG TYPE: Ploppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOFTWARE: MS-DOS TEXT EDITOR

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/532,828B

FILING DATE: 27-OCT-1995

CLASSIFICATION: 435

RAPPLICATION DATA:

APPLICATION NUMBER: UP 5-101450

FILING DATE: 27-APR-1993

ATTORNEY/ASDRT INFORMATION:

REGISTRATION NUMBER: 24,618

REGISTRATION NUMBER: 24,618

REGISTRATION NUMBER: 10-764-0 PCT

TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : Corynebacterium glutamicum
AJ3463
                                                                                                                           Sequence 4, Application US/08532828B Patent No. 5688671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SP
STREET: 1755 S. JEFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM:
                                                                                      RESULT 9
US-08-532-828B-4
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COUNTRY: USA ZIP: 98104-7092
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                                        JS-09-056-556-227
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APPLICANT:
APPLICANT;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Schendel Frederick J. and
APPLICANT: Schendel Frederick J. and
APPLICANT: Flickinger, M. C.
TITLE OF INVENTION: Bacillus MGA 3 Aspartokinase
TITLE OF INVENTION: II Gene
NUMBER OF SEQUENCES: 2
CORRESPONDENCES: 2
CORRESPONDENCES: 2
APPRESED: Merchant & Gould
STREET: 3100 No. 5243039west Center
STREET: Minneapolis
STRATE: Minneapolis
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 RGRQDRHHLHLLPQTSGPPPWKNWTRSETRSASTQLLYDD-
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US-07-684-135A-2
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ZIP: 55402

ZOP: TEADDBLE FORM:
COMPUTER READDBLE FORM:
COMPUTER: Diskette, 3.5 inch, 720 Kb
COMPUTER: No. 5243039thgate 386
OPERATING SYSTEM: DOS 4.0
COMTWARE: WordPerfect 5.0
                                                                                                                                                                                                                                                                                                                   SOFTWARE: WordPerfect - 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/684,135A
FILING DATE: 19910412
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Woessner, Warren D.
REGISTRATION NUMBER: 80,440
REFERENCE/DOCKET NUMBER: 600.216-US-
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TEMMETH: 411 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: Polypeptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 411 amino acids
TYPE: AMINO ACID
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Best Local S
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TREATME
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                                                                              APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: DILLON, COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J. 31,392
REGISTRATION NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (206) 622-4900
                                                                                                                                                                                                 ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 EEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAM 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAM 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
35.1%; Score 770; DB 4;
Best Local Similarity 100.0%; Pred. No. 6.5e-71;
Matches 156; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 227, Application US/09056556 Patent No. 6350456 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 222, Application US/09072596; Patent No. 6458366; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 227: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 156 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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Sequence 2225, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5.225
                                                                                                                                                                                                                                                                                                                                      241 IKDVPMEDPILIGVAHDRSEAKVTI-VGLPDIPGYAAKVFRAVARRRRQHRHGAAERLQG 299
                                                                                                                                                                                                               121 LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      315 VDMIVQNVEEDGTTDFTFTVNRVDLAKAEKILNETA-----KN---IGAREVSTR----D 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----RROHRHGAAERLOGRGRODRHHLH-LLPQTSGPPPWKNWTRSETRSASTOLLYDD 339
                                                                                                                                               61 ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA
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                                                                                                                                                                                                                                                                                                          181 RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSS-------
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                           1 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR
                                                                     17 VOKYGGTSMGTPERILNVARRVKRWHDHGHKVVVVVSAMSGETNRLLALÁKAITETPDPR
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                                                                                                                                                                                                                                                                                                                                                                                                      229 YSDRPGTVVVGSIKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARR---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        340 HIGKVSLIGAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  363 DIVKVSIVGVGMRSHAGVASKMFTALADEGINILMISTSE 402
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US-09-134-001C-5225
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ORGANISM:
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Patent No. 6526368

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUNANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
                           TUBERCULOSIS
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APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 770; DB 4; Length 156; Pred. No. 6.5e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
RESTERATION:
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                           3: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAM 157
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; ORGANISM: Acinetobacter baumannii
US-09-328-352-6511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (206) 622-490
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 amino acids
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Best Local Similarity 100.
Matches 156; Conservative
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                                                                                                                                                                Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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US-09-328-352-6511
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LENGTH: 438
                                                                                                                                                                                      COUNTRY:
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us-09-688-672a-4.rapb

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RESULT 1
US-09-793-306-163
                                                                                                                                                                                                    November 21, 2003, 16:08:22 ; Search time 16.537 Seconds (without alignments) 4680.740 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                           US-09-688-672A-4
2193
1 VQKYGGSSVADAERIRRVAE.....SAATRRPRCTRGRDGRWACQ 424
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1: /cgn2_6/prodata/1/pubpaa/PCT_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubpaa/PCT_NEW PUB.pep:*
3: /cgn2_6/prodata/1/pubpaa/PCT_NEW PUB.pep:*
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10: /cgn2_6/prodata/1/pubpaa/USO9_PUBCOMB.pep:*
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18: /cgn2_6/prodata/1/pubpaa/USO08_PUBCOMB.pep:*
18: /cgn2_6/prodata/1/pubpaa/USO08_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 163, App Sequence 24, Appl Sequence 24, Appl Sequence 5, Appli Sequence 2, Appli Sequence 10, Appl Sequence 227, App Sequence 227, App Sequence 222, App Sequence 229, App Sequence 27, Appl Sequence 29, Appl Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 23, Appli Sequence 23, Appli	
σı	US-09-793-306-163 US-09-738-626-3781 US-09-746-660A-24 US-10-226-136-5 US-10-067-974-16 US-10-067-974-16 US-10-10-067-974-16 US-10-193-022 US-10-193-02-222 US-09-812-17-290 US-09-813-17 US-09-890-813-17 US-09-890-813-6 US-10-301-997-23 US-10-9891-813-6 US-10-9891-813-6 US-10-9891-813-6 US-10-9891-813-6	
DB		
% Query Match Length DB	 44444444444490000004 14444440000000004	
% Query Match		
Score	10224.5 10224.5 10224.5 10224.5 10211.	
Result No.		

equence 16, aduence 7, a squence 34, equence 12, aduence 142, aduence 1425	Sequence 5718, Ap Sequence 6962, Ap Sequence 40, Appl Sequence 40, Appl Sequence 60, Appl Sequence 60, Appl Sequence 60, Appl Sequence 114, App Sequence 114, App Sequence 116, App Sequence 160, Appl Sequence 160, Appl Sequence 160, Appl Sequence 160, Appl Sequence 17, Appl Sequence	
US-09-890-813-16 US-10-226-136-7 US-10-022-832-34 US-09-890-813-12 US-10-156-761-142	US NO NO NO NO NO NO NO NO NO NO NO NO NO	
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110 118 119) #

ALIGNMENTS

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sequence 163, Application US/09793306

; Batent No. US20020098200A1

; GENERAL INFORMATION:

; APPLICANT: Campos-Neto, Antonio

; APPLICANT: Ovendale, Pamela

APPLICANT: Ovendale, Pamela

APPLICANT: Ovendale, Pamela

APPLICANT: Corixa Corporation

; APPLICANT: Corixa Corporation

; APPLICANT: Corixa Corporation

; TITLE OF INVENTION: of Tuberculosis

TITLE OF INVENTION: of Tuberculosis

; FILE REFERENCE: 014058-008740US

; TITLE OF LINVENTION: of Tuberculosis

; FILE REFERENCE: 014058-008740US

; CURRENT FILING DATE: 2001-02-26

; PRIOR APPLICATION NUMBER: US 60/185,037

; PRIOR FILING DATE: 2000-08-08

; NUMBER OF SEQ ID NOS: 164

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 163

; LENGTH: 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: MO-2 (aspartokinase)
US-09-793-306-163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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291 HGAAERLQGRGRQD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Pompelus, Markus
APPLICANT: Roger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Belder, Oskar
APPLICANT: Alder, Oskar
APPLICANT: Hang-Schick
APPLICANT: Heng-Schick
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APPLICANT: Hang-Schick
APPLICANT: MTABOLIC PATHWAY PROTEINS
TITLE OF INVENTION: OCRYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
TITLE OF INVENTION: MARBER: US/09/146,660A
TITLE OF INVENTION: MARBER: US/09/140A
TITLE OF INVENTION NUMBER: 09/601124
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 1999-06-25
PRIOR PELICATION NUMBER: 60/142101
PRIOR PLING DATE: 1999-06-25
PRIOR PELICATION NUMBER: 60/142101
PRIOR PLING DATE: 1999-06-25
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                                                                                                                  241 IKDVPMEDPILIGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA-----
                                                                                                                                                                                                                                                           GAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
                                                                                                                                                                                                                                                                                                                                                                                 351 GAGMKSHPGVTAEFMEALRDVNVNIELISTSE 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24, Application US/09746660A Publication No. US20030049804A1 GENERAL INFORMATION:
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Best Local Similarity 64.09
Matches 251; Conservative
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                                                                                                                  IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRRQHRHGAAE----
                                                                              LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCELYTDVDGIFSADP
                                                                                                                                                                                     RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNI PVHVRSSYSDRPCTVVVGS
                                                                                                                                                                                                                          185 RIVRNARKLDTVTFEEMLEMAGAKGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             356 SHPGVTATFCEALAAVGVNIELISTSEIRISVLCRDT 392
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APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZGGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHKO
APPLICANT: TYKZI, HARUHKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: TKEDA, MASATO
APPLICANT: OZAKI, AKI
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484.
PRIOR PILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 3781, Application US/09738626; Publication No. US20020197605A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) ORGANISM: Corynebacterium glutamicum
US-09-738-626-3781
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Sequence 2, Application US/10067974

Publication No. US20030055232A1

Publication No. US20030055232A1

GENERAL INFORMATION:

APPLICANT: Li, Linia-
APPLICANT: Trei, Kelli J.

TITLE OF INVENTION: Polymucleotide Constructs for Increased Lysine Production

TITLE REPERENCE: 1533.264001

CURRENT APPLICATION NUMBER: US/10/067,974

CURRENT FILING DATE: 2002-02-08

FRIOR FILING DATE: 2001-02-08

NUMBER OF SEQ ID NOS: 25

NUMBER OF SEQ ID NOS: 25
                                                                                                                                                     HGAAERLQGRGRQD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 347
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                                                                                  241 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA--------RRRRQHR 290
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                                                                                                                                  LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP
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63.8%; Pred. No. 3.3e-108;
ive 55; Mismatches 60;
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Best Local Similarity 63.83
Matches 250; Conservative
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US-10-067-974-2
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                     RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                     241 IKDVPMEDPILIGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA------RRRRQHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE. OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR CITY: ARLINGTON STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/226,136

FILING DATE: 23-Aug-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KOBAYASHI, Masaki
YOSHIHARA, Yasuhiko
NAKAMTSU, TSUYOShi
OF INVENTION: METHOD OF PRODUCING L-LYSINE
OF SEQUENCES: 24
                                                                                                                                                                        305 DGTTDITFTCPRSDGRRAMEILKKLÓVQG-----NW---
                                                                                                                                                                                                               GAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
                                                                                                                                                                                                                                                   GAGMKSHPGVTAEFMEALRDVNVNIELISTSE 382
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APPLICATION NUMBER: US/08/952,976
FILING DATE: 8-DEC-1997
APPLICATION NUMBER: UP 7-140614
FILING DATE: 07-0UL-1955
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPRONE: 703-413-3000
FORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                  SUGIMOTO, Masakazu
IZUI, Masako
HAYAKAWA, Atsushi
NAKANO, Eiichi
                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/10226136
Publication No. US20030054506A1
GENERAL INFORMATION:
APPLICANT: OTSUNA, Seiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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Best Local Simi
Matches 251;
                                                                                                                                                                                                                                                                                                       RESULT 4
US-10-226-136-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.2%; Score 1144.5; DB 1560.2%; Pred. No. 3.4e-101; tive 54; Mismatches 75;
  305 DGTTDITFTCPRXDGRRAMEILKKLQVQG-----NW
                                                                                                                                                                                                                                          APPLICANT: ONURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, UUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIKAWA, HIROSHI
APPLICANT: SHIRAM, HIROSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TILLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR PLING DATE: 2001-06-30
NUMBER: OF SEQ ID NOS: 15109
SEQ ID NO 12993
                                                          348 GAGMRSHPGVTATFCEALAAVGVNIELISTSE
                                                                                351 GAGMKSHPGVTAEFMEALRDVNVNIELISXSE
                                                                                                                                                                                        Sequence 12093, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 227, Application US/10084843 publication No. US20030143243A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 IDMVVQNVSAASTGLTDIS---
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Matches 239; Conserv
                                                                                                                                                                        US-10-156-761-12093
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US-10-084-843-227
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APPLICANT: Li, Lining-Yew
APPLICANT: Li, Lining-Yew
APPLICANT: Trei, Kelli J.
TITLE OF INVENTION: POlymucleotide Constructs for Increased Lysine Production
FILE REFERENCE: 1533.264001
CURRENT APPLICATION NUMBER: US/10/067,974
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 06,267,183
PRIOR FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELDMLITAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 IKDVPMEDPILIGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA-------RRRROHR 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291 HGAAERLQGRGRQD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 347
                              305 DGTTDITFTCPRADGRRAMEILKKLQVQG----NW-----TNVLYDDQVGKVSLV 350
      HGAAERLQGRGRQD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VOKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 15; Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.2%; Score 1211.5; DB 1563.5%; Pred. No. 1.2e-107; cive 55; Mismatches 61;
                                                                                348 GAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
                                                                                                      351 GAGMKSHPGVTAEFMEALRDVNVNIELISISE 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: MISC_FEATURE
) LOCATION: (380)...(380)
OTHER INFORMATION: May be either Thr or Ile
US-10-067-974-16
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OTHER INFORMATION: May be either Ser
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US-10-067-974-16
IS-10-067-974-16
; Sequence 16, Application US/10067974
; Publication No. US20030055232A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 63.5
Matches 249; Conservative
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LOCATION: (345)..(345)
OTHER INFORMATION: May be
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NAME/KEY: MISC_FEATURE
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                                                                                                                                                                              FFDMLJTAGERISMALLAMAIKNLGHSAQSFTGSQAGVITDSVHNKARIIDVTPGRIRTA
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                                                                                                                                               ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA
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                                            1 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPR
Gaps
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Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
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      AFFILLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.1%; Score 770; DB 12; Length 156; 100.0%; Pred. No. 7.4e-66; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER REALDS. 1035
COMPUTER REALDS. 1039 disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION ADATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNYY/AGENT INFORMATION:
                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLF
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 EEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAM 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 227:
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Publication No. US20030135026A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 156 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                   STATE: Washington
COUNTRY: USA
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Best Local Similarity 100.0
Matches 156, Conservative
                                                                                                                                                                                                                                                                                                                                                       ZIP: 98104-7092
APPLICANT:
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US-10-193-002-222
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62 LDMLLTAGERISNALVAMAIESLGAHARSFIGSQAGVITTGTHGNAKIIDVTPGRLQTAL 121
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                                                                                           METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                              CITY: Seattle
STATE: Washington
COUNTRY: USE
COMPUTE: Bashington
COMPUTE: Blopy disk
MEDIUM TYPE: Flopy disk
COMPUTE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
FILING DATE: 10-Jul-2002
CLASSIFICATION NOTHER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION ADATA:
APPLICATION ADATA:
APPLICATION VUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INDOMATION:
NAME: WAXI, DAVID J.
REGISTRATION NUMBER: 31392
REGISTRATION NUMBER: 31392
REGISTRATION NUMBER: 31392
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                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 290, Application US/09882227
Publication No. US20030158396A1
GRNERAL INFORMATION:
GRNERAL INFORMATION:
APPLICANT: Kleanbus, Harold
APPLICANT: Miller, Charles
APPLICANT: Tomb, Jean-Prancois
APPLICANT: Tomb, Jean-Prancois
APPLICANT: Goomen, Raymond P.
TITLE OF INVENTION: Identification of Polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 EEGRVVLVAGFOGVSODTKDVTTLGRGGSDTTAVAM 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 35.1%; Score 770; DB 12; Best Local Similarity 100.0%; Pred. No. 7.4e-66; Matches 156; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 222:
US-10-193-002-222
Twardzik, Daniel R.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND
TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 222:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 156 amino acids
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STRANDEDNESS: single
                                                                                                                                                NUMBER OF SEQUENCES:
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203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 ECMSTRIFSAYLNKIRVKARQYDAFDIĞFİTTDEFGNADİLEATYPAVAKRLHGDWIQDP 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDR-PGTVVVGSIKD 243
                                                                                                                                                                                                                                                                                                         325 KAEPVPYLTFDEAAELAYFGAQVLHPQSMRPARESDIPVRVKMSYNPKAPGTLIT---KA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -------PSKLWSRELIQQASEL----DHVVEELEKIAVVNLLQNRSIIS 483
97 VMKFGGSSVASADRMKEVATLILSFPEE--RPIVVLSAMGKTTNKLLLAGEKAVSCGVIN 144
                                                                                             204
                                                                                                                                   ERISNALVAMAIESLGAHARSFIGSQAGVITIGIHGNAKIIDVI----PGRLQ-TALEEG 124
                                                                                                                                                                                                         125 RVVLVAGFOGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADPRIVR 184
                                                                                                                                                                                                                                             265 AIAIVTGFLGKARKSCAVTTLGRGGSDLTATTIGKALGLPEIQVWKDVDGVLTCDPNIYP 324
                                                                                                                                                                                                                                                                                   185 NARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDR-PGTVVVGSIKD 243
                                                                                                                                                                                                                                                                                                                                                           244 VPMEDPILTGVAHDRSEAKVTIVGLPDIP--GYAAKVFRAVARRRRQHRHGAAERLQGRG 301
                                                                                                                                                                                                                                                                                                                                                                                                 382 RDMSKAVLÍSIVLKRNVIMLDÍASTRMLGQYGFLÁKVFSIFEELGISVDVVATSEVSVSL 441
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                                                                                             145 VSSIEELCFIKDLHLRTVDQLGVDGSVISKHLBELEQLLKGIAMMKELTKRTQDYLVSFG
                                                         --DLAQQVCPAPPREL----DMLLTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346 LIGAGMRSHPGVTATFCEALAAVGVNIELIS------TSEDQRSRCCAA 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
16.2%; Score 356; DB 10;
Best Local Similarity 29.9%; Pred. No. 2.7e-25;
Matches 101; Conservative 57; Mismatches 116;
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TITLE OF INVENTION: Aspartate Kinase
FILE REFERENCE: Bal430 PCT:
CURRENT APPLICATION NUMBER: US/09/890,813
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/172944
PRIOR PILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 8, Application US/09890813; Publication No. US20020183486A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Zea mays
US-09-890-813-8
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US-09-890-813-8
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     Encoding No. US20030158396Alel Helicobacter Polypeptides in
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TIVKTQ------IEBTKQALKPFLAQMDSIDYDENIAKVSIVGVGMKSHSGVASIAF 350
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larity 27.0%; Pred. No. 2.6e-27;
Conservative 71; Mismatches 165; Indels 11
                                                                                                                                                                                                                                                                                       Length 394;
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                                                                                                                                                                                                                                                                                   Query Match 30.7%; Score 673; DB 12; Length 39-Best Local Similarity 40.1%; Pred. No. 5.8e-56; Matches 151; Conservative 83; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17, Application US/09890813; Publication No. US20020183486A1; GABERAL INFORMATION:
APPLICANT: E.I. of Pont de Nemours and Company; TITLE REFERENCE: BB1430 PCT
CURRENT FILING NUMBER: US/09/890,813; CURRENT FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/172944; SOFTWARE: Microsoft Office 97; SEQ ID NOS: 24
SSEQ ID NO 17;
TITLE OF INVENTION: Encoding No. US2002015813
TITLE OF INVENTION: Genome
FILE REFERENCE: 06132/047002
CURRENT APPLICATION NUMBER: US/09/882,227
CURRENT FILING DATE: 2001-06-15
PRIOR PELING DATE: 1997-07-29
NUMBER OF SEQ ID NOS: 638
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO. 290
LENGTH: 394
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351 KALAKDNINIMMISTSE 367
                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Helicobacter pylori
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TYPE: PRT
ORGANISM: Glycine max
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Best Local Simi
Matches 128;
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US-09-890-813-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           324 AKTVPYLTFEEATELAYFGAQVLHPQSMRPAREGDIPVRVKNSYNPKAPGTLITRQ-RDM 382
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WAKFGGSSVSSARMAEVAGLILTFPEE--RPVVVLSAMGKTTNNLLLAGEKAVGCGVIH 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCELYTDVDGIFSADPRIVRN 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 ARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDR-PGTVVVGSIKDV 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 PMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRRRQHRHGAAERLQGRGRQD 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RHHLHL-----LPQTSGPPPWKNWTRSETRSASTQLLYDDHIGK------ 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 VSEIBEWNWVKSLHIKTVDELGLPXICNTSLYELEQLLKGIAMMKELTPRTSDYLVSFGE 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTAL----EEGR 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------VCPAP-----VCPAF 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16.0%; Score 350; DB 10; Length 560; 26.4%; Pred. No. 1e-24; ive 76; Mismatches 155; Indels 104;
                                                                                   381 RDMDKVVLTSIVLKSNVTMLDİVSTRMLGQYGFLARVF 418
                                                   244 VPMEDPILTGVAHDRSEAKVTIVGLPDIP--GYAAKVF 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        344 --VSLIGAGMRSHPGVTATFCEALAAVGVNIELIS 376
                                                                                                                                                      US-09-890-813-6
Sequence 6, Application US/09890813
Publication No. US20020183486A1
GENERAL INFORMATION:
APPLICANT: E.I. du Pont de Nemcurs and Company:
TITLE OF INVENTION: Aspartate Kinase
FILE REFERENCE: B81430 PCT
CURRENT APPLICATION NUMBER: US/09/890,813
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/172944
PRIOR FILING DATE: 1999-12-1
NUMBER: OF SEQ ID NOS: 24
SOFTWARE: Microsoft Office 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (168)
NAME/KEY: UNSURE
LOCATION: (384)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: UNSURE
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                  324
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RESULT 14 US-10-301-997-23 ; Sequence 23, Application US/10301997

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200 MAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVVGSIKDVPMEDPILTGVAHDRS 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RHHLHLLPQTSGPPPWKNWTRSETRSASTQLLY--DDHIGKVSLIGAGMRSHPGVTATFC 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 FHQISMILET-----LKNQYEALAYKINEHYVKISLIGSGMRDMSGVASKAF 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 QELTTLGRGGSDTTAVALAVS-NQIPCEIYTDVDGVYATDPRLLPKAKRLDIVSYEEMME
                                                                                                                                                                       ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41;
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14.3%; Score 314.5; DB 12; Length 262;
Best Local Similarity 33.9%; Pred. No. 8.7e-22;
Matches 87; Conservative 47; Mismatches 82; Indels 41;
                     AL INFORMATION:
APPLICANT: Holden, David W.
TITLE OF INVENTION: ANTI-BACTERIAL METHODS AND MATERIALS
UNMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/301,997
FILING DATE: 22-No. US20030148346A1-2002
CLASSIFICATION: vUnknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 28341/33996
                                                                                                                                                                                                                                                          STATE: Illinois
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/527,431
FILING DATE: «Unknown»
APPLICATION NUMBER: US/08/887,534
FILING DATE: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                  ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (312) 474-6300
TELEPAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 23, Application US/09989339; Publication No. US20030088886A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 262 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: (312) 474-6600 INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363 EALAAVGVNIELISTSE 379
Publication No. US20030148346A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                     CITY: Chicago
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US-09-989-339-23
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APPLICANT: Falco, Saverio Carl
APPLICANT: Famodu, Layo
APPLICANT: Famodu, Layo
APPLICANT: Ramaker, Michael
APPLICANT: Ramaker, Michael
APPLICANT: Ranaker, Michael
APPLICANT: Tarczynski, Mitchell C.
APPLICANT: Tarczynski, Mitchell C.
APPLICANT: Tarczynski, Mitchell C.
APPLICANT: Tarczynski, Mitchell C.
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APPLICANT: Tarczynski, Mitchell C.
APPLICANT: Tarczynski, Mitchell C.
APPLICANT: Tarczynski, Mitchell C.
APPLICANT: Tarczynski, Mitchell C.
TITLE OF INVENTION: PLANT METHIONINE CONTENT OF THE SEEDS OF PLANTS
FILE REPERENCE: BB-1067-B
CURRENT APPLICATION NUMBER: US/09/989,339
CURRENT APPLICATION NUMBER: 08/703,829
PRIOR PELLING DATE: 1996-08-27
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Microsoft Office 97
SOFTWARE: Microsoft Office 97
SOFTWARE: MICROSOft Office 97
TYDE: RRT
TYDE: RRT
CREATING BScherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 KLDAIRNIQFAILERLRYPNVIREEIERLLENITVLAEAAALATSPALTDELVSHGELMS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 NALVAMAIESLGAHARSFTGSQAGVITTGTHGNAK----IIDVTFGRLQTALEEGRVVL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 VAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADPRIVRNARK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     189 LDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGSIKDVPMED 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 VSKFGGTSVADFDAMNRSADIVLS---DANVRLVVLSASAGITNLLVALAEGLEPGERFE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----APPPRELDMLLTAGERIS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
14.2%; Score 310.5; DB 11; Length 449;
Best Local Similarity 30.2%; Pred. No. 4.6e-21;
Matches 102; Conservative 55; Mismatches 118; Indels 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                297 PLFRALALRRNQTLITLHSLNMLHSRGFLAEVFGILAR 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249 PILTGVAHDRSEAKVTIVGLPDI--PGYAAKVFRAVAR 284
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Search completed: November 21, 2003, 16:38:11 Job time: 18.537 secs

us-09-688-672a-4.rpr

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

November 21, 2003, 15:57:31 ; Search time 8.84535 Seconds (without alignments) 4609.825 Million cell updates/sec Run on:

US-09-688-672A-4 2193 1 VQKYGGSSVADAERIRRVAE.....SAATRRPRCTRGRDGRWACQ 424 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		40			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
1	615.	· [ı Q	i N	079	įΩ
8	545.		N	N	719	spartokinase
m	•	7.	N	N	242	spartate kinas
4	229	56.1	421	~1	S15276	ctate kinase
Ŋ	4	4	N	Ŋ	538	w
φ	$^{\circ}$	7	\leftarrow	N	353	
7	٠	7.	0	N	576	hetic
αο	∞	'n.	\leftarrow	~	394	
ወ	7	'n.	0	N	164	ate kinas
10	•	S.	0	C)	226	cate kina
11	9	4,	0	~	36	artate kinas
12	9/	4.	0	7	7	okir
13	7	4,	Н	N	93	okinase II
14	742.5	<u>ب</u>	0	N	10	aspartate kinase (
15	₹.	ς.	$\overline{}$	ď	39	aspartokinase - Aq
16	4	3	0	N	2.4	Η
17	₹.	ش	m	C)	36	H
18	O	ζ,	0	N	34	
19	•	ς,	0	N	37	aspartate kinase (
20	711		0	0	~	aspartokinase - He
21	0	ď.	О	N	8	Н
22	0	ď.	\vdash	7	35	[im
23	0	α,	0	~	22	artokinase II
24		ä	$^{\circ}$	7	7	artate
25	S	ω.	3	N	F306	artate kinase
26	S		3		Н	K prote
27	m	œ,	σı	~	8231	rtokinase, a
28	œ	ŝ	0	N	8991	artokinase II
29	9	'n	Η.	0	8394	aspartokinase I (a

aspartate kinase (aspartokinase I (a	aspartate kinase (aspartokinase I (a	aspartate kinase (aspartokinase (lys	aspartokinase [imp	aspartate kinase (aspartate kinase -	aspartate kinase (aspartate kinase -	aspartokinase I/ho	thra bifunctional	aspartokinase I-ho	aspartokinase I, h	achartokinace T/ho
C46665	AB1617	D97845	AD1254	C64371	E71635	D97123	D69337	F75405	AH0056	T48575	AC0502	DEECK	B90629	B85480	78008
C)	0	2	8	7	0	0	7	7	0	N	7	H	7	7	ç
404	403	401	403	473	446	9 9 9	462	473	813	569	820	820	820	820	n C G
24.3	23.9	23.7	23.1	22.4	21.9	21.1	20.1	20.1	17.9	17.2	16.9	16.8	16.8	16.8	7 7
~		_	9(492	480.5	462	440.5	440	91.5	377	20.5	369.5	69.5	69.5	7 2
532 2	524	520	2	4.	48		4		m		'n	36	3	36	2

ALIGNMENTS

RESULT	1
probabl	provis. provise ask protein - Mycobacterium tuberculosis (strain H37RV) C.Species: Mycobacterium tuberculosis
C; Date:	C;Date: 17.1/101-10208 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C:Accession: P70794
R,Cole,	Parkhill, J. Devlin, K.;
Rajandr	Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A; Autho A; Title A: Refer	A,Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. Ajitle: Deighering the biology of Mycobacterium tuberculosis from the complete genome & A.Peference number: 200600. MITD: 98396987. PMID: 9634230
A; Acces	AACCESSION: F70794
A; Molec	Abbacatas: preminiary; macher acta bequence not shown; transfacton not shown A;Molecule type: DNA
A; Restu A; Cross A; Exper	ues: 1-421 COUZA -references: GRAL022121; GB:AL123456; NID:g3261559; PIDN:CAA18031.1; PID:g296013: imental source: strain H37Rv
C,Genet A,Gene:	
C; Super F; 3-406	C;Superfamily: aspartate kinase; aspartate kinase homology F;3-406/Domain: aspartate kinase homology <dki></dki>
Query Ma Best Loc Matches	Query Match Best Local Similarity 85.1%; Pred. No. 2.2e-112; Matches 338; Conservative 7; Mismatches 35; Indels 17; Gaps 3;
ζŎ	1 VOKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPR 60
qa	5 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR 64
δλ	61 ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 120
qo	65 ELDMLLTAGERISNALVAMAIESLGAHARSFIGSQAGVITTGTHGNAKIIDVTPGRLQTA 124
δy	121 LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 180
역 입 .	125 LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 184
δ	181 RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS 240
q _Q	185 RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS 244
۸۵	241 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRRRQHRHGAAE 295
qa	245 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVADADVNIDM 295
ζŏ	296 RLQGRGRQDRHHLHLLPQTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLIGAGMR 352
qq	296 VLQNVSKVEDGKTDITFTCSRDVGPAAVEKLDSLRNEIGFSQLLYDDHIGKVSLIGAGMR 355

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Query Match
Best Local Similarity 77.6
Matches 302; Conservative
A;Residues: 1-421 <CIR>
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Holroyd,
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N.Alternate names: aspartokinase alpha chain
N.Alternate names: aspartokinase alpha chain
N.Alternate names: aspartokinase alpha chain
C.Speciase: Mycobacterium smegmatis
C.Speciase: Mycobacterium smegmatis
C.Speciase: Mycobacterium smegmatis
C.Saccassion: $42422; $31801
N.A.: Pascopella, L.; Bloom, B.R.; Jacobs Jr., W.R.
Nol. Microbiol. 11, 629-639, 1994
A.Title: Isolation and characterization of the aspartokinase and aspartate semialdehyde
A.Areference number: $42421; MUID:94254720; PMID:7910936
A.Molecule type: DNA
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                                                                                                                          departokinase [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Accession: G87199
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.;
R; Davies, R.W.; Devlin, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Ruther, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.;
A;Acference number: A86909; MulD:21128732; PMID:11234002
A;Accession: G87199
A;Accession: G87199
A;Accession: G87199
A;Residues: 1-421 <STO>
A;Residues: 1-421 <STO>
A;Coss-references: GB:AL450380; NID:g13093941; PIDN:CAC31839.1; GSPDB:GN00147
C;Genetiask
C;Superfamily: aspartate kinase; aspartate kinase homology
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                    SHPGVTATFCEALAAVGVNIELISTSEIRISVLCRDT 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 1545.5; DB 2; Pred. No. 3.5e-107; 18; Mismatches 43;
  SHPGVTATFCEALAAVGVNIELISTSEDQRSRCCAAT
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80.4%;
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Best Local Similarity 80.4%
Matches 319; Conservative
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A,Molecule type: DNA
A,Molecule type: DNA
A,Esidues: 329-321 <SER>
A,Cross-references: EMBL:X82928; NID:g599716; PIDN:CAA58100.1; PID:g599717
B,Kalinowski, J.; Bachmann, B.; Thierbach, G.; Puehler, A.
Mol. Gen. Genet. 224, 317-324, 1990
A,Title: Aspartokinase genes lysC-alpha and lysC-beta overlap and are adjacent to the A,Reference number: S12250; MUID:91094767; PMID:1980002
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A; Residues: 1-421 - 6PDS.
A; Cross-references: EMBL:X57226; NID:g40509; PIDN:CAA40502.1; PID:g580983
A; Experimental source: ATCC 13032
R; Serebrijski, I.; Mojcik, F.; Reyes, O.; Leblon, G.
Submitted to the EMBL Data Library, November 1994
A; Description: Two loci of Corynebacterium glutamicum ATCC17965 that complement lakeference number: S49977
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A,Cross-references: EMBL:217372, NID:g44506, PIDN:CAA78984.1, PID:g581352 A,Note: the authors translated the initiation codon GTG for residue 1 as Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA
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                                                  C)Genetics:
A)Start codon: GTG
C,Superfamily: aspartate Kinase, aspartate Kinase homology
C,Superfamily: aspartate Kinase, phosphotransferase
E;1-421/Product: aspartate Kinase alpha chain #status predicted <ASA>
E;2-406/Domain: aspartate kinase homology <ADKI>
E;250-421/Product: aspartate kinase homology <ADKI>
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Roman, S.; Yuan, Y.; Brady, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J., Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog A; Reference number: A82950; MUID:20437337; PMID:10984043
A; Reference number: A82950; MUID:20437337; PMID:10984043
A; References: DNA
A; Residues: 1-412 <STO>
A; Cross-references: GB:AE004525; GB:AE004091; NID:g9946805; PIDN:AAG04293.1; GSPDB:GN001: C; Genetics:
A; Experimental source: strain PA01
C; Genetics:
A; Gene: 1ysC; PA0904
C; Superfamily: aspartate kinase; aspartate kinase homology
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    VDEGNVAIVAGFQGVSQDSKDITTLGRGGSDTTAVALAAALDADVCEIYTDVDGVFTADP
                                               RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                                                                                                      292 GAAERLOGRGRODRHHLHLLPQTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLIGAGM
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Typesides: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Accession: T3583
R;Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, June 1999
A;Reference number: Z21576
A;Accession: T35383
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Reference tupher
A;Residues: DAA
A;Residues: 1,425 cMIR>
A;Residues: 1,425 cMIR>
A;Residues: 1,425 cMIR>
A;Cross-references: EMBL:AL079348; PIDN:CAB45482.1; GSPDB:GN00070; SCOEDB:SC66T3.26c
C;Genetics
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C;Genetics
C;Superfamily: aspartate kinase; aspartate kinase homology
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                                                                                                                                                      Length 421;
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Best Local Similarity 61.6%; Pred. No. 3.9e-77;
Matches 239; Conservative 54; Mismatches 79; Indels 10
                                                                                                                                                                                               58; Indels
C,Genetics:
A,Gene: lysC-alpha
A,Start codon: GTG
C,Superfamily: aspartate kinase, aspartate kinase homology
C,Keywords: alternative initiators; phosphotransferase
F;3-406/Domain: aspartate Kinase homology <DKI>
                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
56.1%; Score 1229.5; DE
Best Local Similarity 64.3%; Pred. No. 1e-83;
Matches 252; Conservative 55; Mismatches 5
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aspartate kinase (EC 2.7.2.4) II - Bacillus stearothermophilus NiAlternate names: aspartckinase II C;Species: Bacillus stearothermophilus C;Species: Bacillus stearothermophilus C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 18-Jun-1999 C;Accession: JC4640 K; Da Rossi, E.; Riccardi, G. R;Cantoni, R.; Labo, M.; De Rossi, E.; Riccardi, G. A;Title: Sequence of the Bacillus stearothermophilus gene encoding aspartokinase A;Reference number: JC4640; MUID:96186919; PMID:8635739
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A.Accession: S76164
A.Accession: S76164
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-600 < KAN-2
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NyAlternate names: lysine-sensitive aspartckinase II
NyAlternate names: lysine-sensitive aspartckinase II
NyContains: aspartckinase II alpha chain; aspartckinase II beta chain
CySpecies: Bacillus sp.
CyDate: 21-Jan-1994 #sequence revision 24-Feb-1995 #text_change 18-Jun-1999
CyDate: 21-Jan-1994 #sequence revision 24-Feb-1995 #text_change 18-Jun-1999
CyDate: 21-Jan-1994 #sequence revision 24-Feb-1995 #text_change 18-Jun-1999
CyDate: 21-Jan-1994 #sequence revision 24-Feb-1995 #text_change 18-Jun-1999
CyDate: 21-Jan-1994 #sequence revision 28, 2806-2814, 1992
Appl. Environ. Microbiol. 58, 2806-2814, 1992
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                                           (strain PCC 6803)
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Pred. No. 7.6e-53;
83; Mismatches 118;
                                                Synechocystis sp.
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Best Local Similarity 43.9
Matches 183; Conservative
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S76764
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A;Note: sequence modified after extraction from NCBI backbone
A;Note: sequence extracted from NCBI backbone (NCBIN:117802)
A;Accession: B48946
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Accession: C48946
A;Molecule type: protein
A;Accession: C48946
A;Molecule type: protein
A;Accession: C48946
A;Molecule type: protein
A;Accession: C48946
A;Molecule type: protein
A;Accession: C48946
A;Molecule type: protein
A;Accession: C48946
A;Molecule type: protein
A;Residues: 246-253 <6C3>
A;Note: this material was purified beta chain; the beta chain apparantly was not blocked
C;Comment: The amino terminal Met of the beta chain is preceded by a strongly predicted
C;Comment: The amino terminal Met of the alpha chain is preceded by a strongly predicted
C;Comment: The amino terminal Met of the alpha chain region. This suggests that expres
C;Comentics:
C;Comentics:
C;Comentics:
A;Start codou: GTG
C;Superfamily: aspartate kinase; aspartate kinase homology
C;Keywords: alternative initiators; heterotetramer; lysine biosynthesis; phosphotransfere
F;2-45/Froduct: aspartate kinase homology velta:
F;2-46-411/Product: aspartokinase II beta chain #status predicted <BET>
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|---QNRINVDIIIQSA-----TDAETTNLSFSIKSDDLEETMAVLENNKNLLNYQGI 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.8%; Score 785; DB 2; 42.1%; Pred. No. 1e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 42.13
Matches 170; Conservative
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Ï.

A,Molecule type: DNA
A,Residues: 1-407 < cAN.^
A,Fesidues: 1-407 < cAN.^
A,Cross-references: GB:L46351, NID:9928810; PIDN:AAB06216.1, PID:9928811
C,Comment: This enzyme is the first key enzyme in the biosynthetic pathway of the aspart:

c,Superfamily: aspartate kinase, aspartate kinase homology C,Keywords: aspartic proteinase; phosphotransferase

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aspartokinase, alpha and beta chains NWB1498 [imported] - Neisseria meningitidis (strain G;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Accession: P81076
R;Tettelin, H:; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Pleischmann, R.D.; Dougherty, B.A.; H.; Oin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. A;Authors: Canadi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, B.R.; Rappuoli, R.; Ve A;Reference number: A81000; MUD:2017575; PMID:10710307
A;Accession: F81076
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A;Access
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A;Residues: 1-405 <TET>
A;Cross=references: GB:AE002499; GB:AE002088; NID:G7226737; PIDN:AAF41854.1; PID:G722674
A;Cross=references: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB1498
C;Superfamily: aspartate kinase; aspartate kinase homology
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A;Cross-references: GB:AP001517; GB:BA000004; NID:g10175500; PIDN:BAB06815.1; GSPDB:GN00
A;Experimental source: strain C-125
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R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir: Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
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C;Superfamily: aspartate kinase; aspartate kinase homology
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Best Local Simi
Matches 161;
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aspartate kinase (EC 2.7.2.4) alpha and beta chains Cj0582 [imported] - Campylobacter je_C'Species: Campylobacter jejuni
C'Species: Campylobacter jejuni
C'Species: Campylobacter jejuni
C'Accession: B1.Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C'Accession: B21405
R'Parkhill, J'; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C'W.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; Vanyliet, A.; Whitehead, S.; Barrell
Nature 403, 665-669, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype
A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: B91405
A;Molecule type: DNA
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A;Cross-references: GB:AL139075; GB:AL111168; NID:g6967817; PIDN:CAB75218.1; PID:g6968045
A;Experimental source: serotype 02, strain NCTC 11168
                                                       7;
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                                                                                                                                                                                                                                                                                                                                                                                           240
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                                                                                                                                                                                           ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 120
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                                                                                                                              121 LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP
                                                                                                                                                                                                                                                                                                                       RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
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                                                                                                1 VOKYGGSSVADAERIRRVAERIVATKKOGNDVVVVVSAMGDITDDLLDLAQQVCPAPPR
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DMDVILLSSGERVISALLSIALNEKGCPAISFSGRKAGIITDSVPTKARIHHIDTKAIKSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 VQKYGGTSVGTLERIEAVANRVIQSAQQGNQLVVVVSAMSGVTNTLIEQABYFSKTPNGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             337 -----YDDHIGKVSLIGACMRSHPGVTATFCEALAAVGVNIELISTSE 379
                                                     73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 412;
                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: 1ysC; Cj0582
C;Superfamily: aspartate kinase; aspartate kinase homology
C;Reywords: phosphotransferase
     34.5%; Score 757.5; DB 2;
42.0%; Pred. No. 1.1e-48;
ive 64; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.9%; Score 742.5; DB 2;
39.9%; Pred. No. 1.4e-47;
ive 89; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -EEGTMEONLLVRGIAFENDVTKVTVHGLP
Query Match
Best Local Similarity 42.0%
Matches 173; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 39.9
Les 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300 RGRODRHHLHLLP--
                                                                                                                                             Ŋ
                                                                                                                                                                                             61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
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E81405
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181 RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS 240

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aspartckinase - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 18-Jun-1999
C;Accession: B70399
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
Wature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUDD:98196666; PMID:9537320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-415 <AQF:
A;Cross-references: GB:AE000726; NID:g2983612; PIDN:AAC07182.1; PID:g2983613; GB:AE00065
A;Experimental source: strain VF5
                                                                                                                                                                         --NENINVDMIIQNVGVDGATNLGFTVPQNELELAKNAMQKILSSKTTIESDSAVLKVSI 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 IKDVPMEDPILIGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRRQHRHGAA----- 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 -EDEVMEKVAVRGITVDTKETRFTVVRVPDKPGIAAEIFKAL------GDAHIVVDM 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295 -- ERLOGRGRODRHHLHLLPQTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLIGAGMR 352
                                                               241 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRRRQHRHGAAERLQGR 300
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                                                                                        241 -KEDGMEQALVSGIALDKNQARVTLRNIEDKPGIAAEIFSVLA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Genetics:
A;Gene: lysC
C;Superfamily: aspartate kinase; aspartate kinase homology
F;3-400/Domain: aspartate kinase homology <DKI>
                                                                                                                                                                                                                                347 IGAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
                                                                                                                                                                                                                                                         341 VGVGMKSHSGVASKAFKALADEGINIGMISTSE 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHPGVTATFCEALAAVGVNIELISTSE 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 GRODRHHLHLLPQTSGPPPWKNW---
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Best Local Similarity 42.43
Matches 164; Conservative
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Search completed: November 21, 2003, 16:09:51 Job time : 9.84535 secs

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Mon Nov 24 15:01:49 2003
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P97048 mycobacteri 981403 mycobacteri 981411 corynebacte 981511 corynebacte 069077 psemdomnas 997151 thermus the 059229 bacillus st 05721 aquifex ac 025827 helicobacte 08495 bacillus su 057991 methanococc 027827 helicobacte 004795 bacillus su 057991 methanococc 027037 rickettsia 027037 serratia ma 027051 rickettsia 027051 rickettsia 027051 rickettsia 027051 methanococc 027051 methanococc 027051 cocherichia 027051 chlamydia fr 099512 chlamydia fr 099512 chlamydia fr 09520 buchnera ap 084367 chlamydia fr 099510 chlamydia fr 090561 chlamydia fr 09510 chlamydia fr 09510 chlamydia fr 09510 chlamydia fr 09510 chlamydia fr 09510 chlamydia fr 09510 chlamydia fr 09510 chlamydia fr 09521 chlamydia fr 09521 chlamydia fr 09521 chlamydia fr November 21, 2003, 15:51:11; Search time 4.99955 Seconds (without alignments) 3988,226 Million cell updates/sec Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. US-09-688-672A-4 2193 1 VQKYGGSSVADAERIRRVAE......SAATRRPRCTRGRDGRWACQ 424 Description GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd. Total number of hits satisfying chosen parameters: 127863 segs, 47026705 residues AK_RICPR AKIH SERMA AKIH ECOLI AKH HARIN AKH DAUCA AKS BCOLI AKK GHUR AKH BUCAI AK CHUR AKHI MAIZE AKH BUCAP AKH BUCAP AKH BUCAP AKH GHUR SUMMARIES Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries AK MYCTU
AK MYCSM
AK COREF
AK COREL
AK PSEAE
AK THETH
AKZ BACSP
AKZ BACSP
AK ARLEV
AK HELEV
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AKI MELEV OM protein - protein search, using sw model BLOSUM62 Gapop 10.0 , Gapext 0.5 Minimum DB seq length: 0 Maximum DB seq length: 200000000 DB SwissProt_41:* % Query Match Length D Perfect score: Score Scoring table: Database : Searched: Sequence: Result No. Run on:

	bartonella	methanococc	fusobacteri	bifidobacte	agrobacteri	anabaena sp	zymomonas m	streptomyce	xanthomonas	mycobacteri	xanthomonas
Q911a3	Q8rt65	058656	Q8r6g5	P59295	Q8ufm1	Q8yxk5	Q9x5e9	091086	P59009	P94989	P59008
ARGB_STRCO	PYRH BARBA	PYRH METUA	PYRH FUSNN	ARGB_BIFLO	PYRH_AGRTS	PYRH ANASP	PYRH ZYMMO	ARGB_STRCL	PYRH XANCP	ARGB MYCTU	PYRH_XANAC
7	Н	Н	Н	Н	Н	Н	Н	Н	н	H	Н
306	239	226	239	318	241	242	242	302	240	294	240
8.0	8.0	6.9	6.8	9	6.7	9.9	9.9	9.9	6 5	6.5	9
175	174.5	151	150	149	146	145.5	145.5	145	143.5	143	141.5
		9	7	ω	σ	40	Н	N	m	44	S

ALIGNMENTS

AKŽYBAST AKŽH ECOLI AK SCHPO

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356 SHPGVTATFCEALAAVGVNIELISTSEIRISVLCRDT 392
                                                      AK MYCSM
ID AK M
                                           RESULT
                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMID outstation the burppean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           296 RLQGRGRQDRHHLHLLLPQTS---GPPPWKWWTRSETRSASTQLLYDDHIGKVSLIGAGMR 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     296 VLÓNVSKVEDGKTDITFTCSRDVGPAAVEKLDSLRNEIGFSQLLYDDHIGKVSLIGAGMR 355
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                                                                                                                                                                                                                                                                                                                                                                                                                         Transferase, Kinase, Diaminopimelate biosynthesis,
Lysine biosynthesis, Alternative initiation; Complete proteome.
CHAIN 1 421 ASPARTOKINASE, ISOFORM ALPHA.
CHAIN 250 421 ASPARTOKINASE, ISOFORM BETA.
INIT MET 250 250 FOR ISOFORM BETA.
CONFLICT 288 336 DANVIDMILATORYSEVEDGYDITFICSRDVGPAAVEKLDS
CONFLICT 288 CYSOFORMWINSETRSASI (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IRISVICRDTELDKAVVALHBAFGLGGDEBATVYAGTGR
-> PORSRCCAATPWNTRPWRRCMKRSGSAATRRPRCTRGR
056732380D2085A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Gaps
               Comment=2 isoforms, Alpha/Aspartokinase alpha subunit (shown here) and Beta/Aspartokinase beta subunit, may be produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 73.7%; Score 1615.5; DB 1; Length Best Local Similarity 85.1%; Pred. No. 3e-106; Matches 338; Conservative 7; Mismatches 35; Indels
                                        alternative initiation;
SIMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 353 SHPGVTATFCEALAAVGVNIELISTSEDQRSRCCAAT 389
                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00696; aakinase; 1.
Pfam; PF01842; ACT; 2.
TIGRFAMs; TIGR00656; asp_kin_monofn; 1.
TIGRFAMs; TIGR00657; asp_kinases; 1.
PROSITE; PS00324; ASPARTOKINASE; 1.
                                                                                                                                                                                                                                                                             Tuberculist, Rv3709c, -.
Tuberculist, Rv3709c, -.
InterPro, IPR001048; Aa kinase.
InterPro, IPR002912; ACT.
InterPro, IPR003260; Asp kin monofn.
InterPro, IPR001341; Aspartate_kinase.
 Event=Alternative initiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                           EMBL; AL022121; CAA18031.1; -. EMBL; AE007178; AAK48180.1; -. PIR; F70794; F70794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 AA; 44461 MW;
                                                                                                                                                                                               EMBL; U90239; AAB49995.1; -. EMBL; U90239; AAB49994.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421
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                                                                                                                                                                                        [Contains: Aspartokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- ENZYME REGULATION: FEEDBACK INHIBITION BY LYSINE AND THREONINE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- PATHWAY: FIRST STEP IN THE COMMON BIOSYNTHETIC PATHWAY LEADING FROM ASP TO THE CELL WALL PRECURSOR MESO-DIAMINOPIMELATE, TO LYS, TO MET, TO ILE AND TO THR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TO MET, TO ILE AND TO THR.
--- SUBUMT: Tetramer consisting of 2 isoforms Alpha (catalytic) and isoforms Beta (function not known) (By similarity).
--- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative initiation;
Comment=2 isoforms, Alpha/Aspartokinase alpha subunit (shown
here) and Beta/Aspartokinase beta subunit, may be produced by
alternative initiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cirillo J.D., Weisbrod T.R., Pascopella L., Bloom B.R., Jacobs W.R. Jr., "Isolation and characterization of the aspartokinase and aspartate
                                                                                                          01-NOV-1995 (Rel. 32, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Aspartokinase (EC 2-72.4) (Aspartate kinase) [Contains: Asparto)
alpha subunit (ASK-alpha); Aspartokinase beta subunit (ASK-beta)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               semialdehyde dehydrogenase operon from mycobacteria.";
Mol. Microbiol. 11:629-639(1994).
-!- CATALYTIC ACTIVITY: ATP + L-aspartate = ADP + 4-phospho-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 67.4%; Score 1478.5; DB 1; Length 421; Best Local Similarity 77.6%; Pred. No. 1.2e-96; Matches 302; Conservative 31; Mismatches 35; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; 217372; CAA78984.1; ...

RINE S4422; S4242; S4242; S42422; S42422; S42422; S42422; S42422; S42422; S42422; S42422; S42422; S42422; S42422; S42422; S42422; S42422; S42422; S42422; S42422; S427.

RINE PROS IPRO01212; ACT.

RINE PROS IPRO0144; ASPARTATE Kinase.

R Pfam; PF00696; aakinase; I.

R Pfam; PF00696; aakinase; I.

R TIGREAMS; TIGRO0657; asp kin monofn; 1.

R TIGREAMS; TIGRO0657; asp kin monofn; 1.

R PROSTE; PS00324; ASPARTOKINASE; 1.

R PROSTE; PS00324; ASPARTOKINASE; I.

CHAIN 1 421 ASPARTOKINASE; ISOFORM BETA.

T CHAIN 250 420 FOR ISOFORM BETA.

T INIT MET 250 250 FOR ISOFORM BETA.

SEQUENCE 421, AA; 44458 MW; 926895FC8625E20CD CRC64;
                                                                                                                                                                                                                                                                                                                                               Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                   Corynebacterineae; Mycobacteriaceae; Mycobacterium
    421 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=ATCC 607 / mc(2)6 / NRRL B-692;
MEDLINE=94254720; Pubmed=7910936;
                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
15-SEP-2003 (Rel. 42, Last ann
STANDARD;
                                                                                                                                                                                                                                                                                                          Mycobacterium smegmatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=ATCC 607 /
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56.9%; Sco...
65.2%; Pred. No. ...
... 58; Mismatches
                                                                                                                                                       InterPro; IPR005260; Asp kin monofn.
InterPro; IPR001341; Aspartate_kinase.
Pfam; PP01642; axkinase; 1.
Pfam; PP01842; ACT; 2.
TIGRFAMS; TIGR00556; asp kin monofn; IIGRFAMS; TIGR00557; asp kinases; 1.
PROSITE; PS03324; ASPARTOKINASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            355 PGVTATFCEALAAVGVNIELISTSE 379
                                                                                                EMBL; AB063129; BAB86820.1; -
EMBL; AP062214; BACT7030.1; ALT_INIT.
InterPro; IPR001048; AR Kinase.
InterPro; IPR002912; ACT.
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es 251; Conservative
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                                                                                                                                                                                                                                                                                                                     296 VLQNISKIEDGKTD--ITFTCARDNGPRAVEKLSALKSEIGFSQVLYDDHIGKVSLIGAG 353
                                                        120
                                                                                   EMDMLLTAGERISNALVAMAIESLGAQARSFIGSQAGVITTGTHGNAKIIDVTPGRLRDA 124
 9
                             64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [Contains: Aspartokinase
                                                                                                                                                                                             ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA
                                                                                                                   LEEGRIVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCE1YTDVDGIFSADP
                                                                                                                                         RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                                                                                                                      IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRRRQHRHGAAE----
                                                                                                                                                                                                                                                                                                  RLOG-----RGRODRHHLHLLPQTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLIGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aspartate.

SUZYME REGULATION: FEEDBACK INHIBITION BY LYSINE AND THREONINE.

PATHWAY: FIRST SIEP IN THE COMMON BIOSYNTHEIIC PATHWAY LEADING
FROM ASP TO THE CELL WALL PRECURSOR MESO-DIAMINOPIMELATE, TO LYS,
TO MET, TO ILE AND TO THR.

TO MET, TO ILE AND TO THR.

SUBDINIT: Tetramer consisting of 2 isoforms Alpha (catalytic) and
isoforms Beta (function not known).

ALTERNATIVE PRODUCTS:
EVENT.ALLERNATIVE PRODUCTS:
                      VQKYGGSSVADAERIRRVAERIVETKKAGNDVVVVVSAMGDTTDDLLDLARQVSPAPPPR
 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVSAMGDTTDDLLDLAQQVCPAPPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
Yazuki M., Mahlma J., Itoh T., Yamagishi A., Nishio Y.,
Usuda Y., Sugimoro S.;
The entire genomic sequence of Corynebacterium efficiens YS-314.";
When entire genomic sequence of Corynebacterium efficiens YS-314.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-: CATALYTIC ACTIVITY: ATP + L-aspartate = ADP + 4-phospho-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Comment=2 isoforms, Alpha/Aspartokinase alpha subunit (shere) and Beta/Aspartokinase beta subunit, are produced alternative initiation; SIMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=152794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Aspartokinase (EC 2.7.2.4) (Aspartate kinase)
11-SEC OR ASK OR CE0220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 AA
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Itaya H., Kimura E., Kawahara Y., Sugimoto
"lysC of Corynebacterium efficiens.";
                                                                                                                                                                                                                                                                                                                                                                              MRSHPGVTATFCEALAAVGVNIELISTSE 379
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or send an email to license@isb-sib.ch).
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P26512; 05928;
01-AUG-1992 (Rel.
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Aspartockinase (EC 2.7.2.4) (Aspartate kinase) [Contains: Aspartokinase alpha subunit; Aspartokinase beta subunit).
1Y-SEP-2003 (Rel. 42, Last annotation update)
1S-SEP-2003 (Rel. 43, Last annotation update)
1S-SEP-2003 (Rel. 43, Last annotation update)
1S-SEP-2003 (Rel. 41, Last annotation update)
1S-SEP-2003 (Rel. 42, Last annotation update)
1S-SEP-2003 (Rel. 41, Last annotation update)
1S-SEP-2003 (Rel. 41, Last annotation update)
1S-SEP-2003 (Rel. 42, Last annotation update)
1S-SEP-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 VOKYGGSSLESAERIRNVAERIVATKKAGNDVVVVCSAMGDTTDELLDLAAAVNPVPPAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transferace; Kinase; Diaminopimelate biosynthesis;
Lysine biosynthesis; Alternative initiation; Complete proteome.
CHAIN 1 421 ASPRIOKINASE; ISOFORM ALPHA.
CHAIN 250 250 FOR ISOFORM BETA.
SEQUENCE 421 AA; 44793 MW; FOD638306983CB5F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13;
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Bacteria, Actinobacteria, Actinobacterides, Corynebacterineae, Corynebacterium.
[Orynebacterineae, Corynebacteriaceae, Corynebacterium.
[1]
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Pred. No. 1.7e-80;
B; Mismatches 63; Indels
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RESULT 5
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                                                                                                                                                                                                                                                                              "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.", submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- ENZYME REGULATION: FEEDBACK INHIBITION BY LYSINE AND THREONINE.
-!- PATHWAY: FIRST STREP IN THE COMMON BIOSYNTHETIC PATHWAY LEADING
FROM ASP TO THE CELL WILL PRECURSOR MESO-DIAMINOPIMELATE, TO LYS,
TO MET, TO ILE AND TO THR.
-!-SUBMUTT: Tetramer consisting of two isoforms Alpha (catalytic) and
two isoforms Beta (function not known).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 158-421 FROM N.A.

SEQUENCE OF 158-421 FROM N.A.

MEDLINE=91094767; PubMed=1980000, NCIB 10025;

MEDLINE=91094767; Daybad=1980000, NCIB 10025;

Kalinowski J., Bachmann B., Thierbach G., Puehler A.;

"Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspartate beta-semialdehyde dehydrogenase gene asd in Corynebacterium glutamicum.";

MOI. Gen. Genet. 224:317-324(1990).

-!- CATALYTIC ACTIVITY: ATP + L-aspartate = ADP + 4-phospho-L-
                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-51 FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
MEDLINE=94161495; PubMed=8117072;
Patek M., Krumbach K., Eggeling L., Sahm H.;
"Leucine synthesis in Corynebacterium glutamicum: enzyme activities, structure of leuk, and effect of leuk inactivation on lysine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event=Alternative initiation;
Comment=2 isoforms, Alpha/Aspartokinase alpha subunit (show
here) and Beta/Aspartokinase beta subunit, are produced by
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TIGRPAMS; TIGRO0657; asp_kinases; 1.
PROSITE; PS00324; ASPARTOKINASE; 1.
Transferase; Kinase; Diaminopimelate biosynthesis;
Lysine biosynthesis; Alternative initiation; Complete proteome.
CHAIN 1921
SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
MEDLINE=22065816; PubMed=1956296;
Kalinowski J., Cremer J., Bachmann B., Eggeling L., Sahm H.,
                                                                                                                       the aspartokinase from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY.
                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Appl. Environ. Microbiol. 60:133-140(1994)
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InterPro; IPR002012; ACT.
InterPro; IPR005260; Asp kin monofn.
InterPro; IPR001341; Aspartate_kinase.
Pfam; PF00896; aakinase; 1.
Pfam; PF01842; ACT; 2.
                                                                                       Puehler A.;
"Genetic and biochemical analysis of Corynebacterium glutamicum.";
Mol. Microbiol. 5:1197-1204(1991).
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EMBL, X57226; CAA40503.1; -.
EMBL, AR005274; BAB97644.1; -.
EMBL, X70959; CAA50296.1; ALT_SEQ.PIR; S15276; S15276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alternative initiation;
                                                                                                                                                                                                                                                        Nakagawa S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ::|:|:|: :|||||| |:||||||::||: || || |||||::|: :|: ||:|:|: ||: ||:|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :
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-!- PATHWAY: FIRST STEP IN THE COMMON BIOSYNTHETIC PATHWAY LEADING FROM ASP TO THE CELL WALL PRECURSOR MESO-DIAMINOPIMELATE, TO LYS,
-!- SUBUNIT: Tetramer consisting of 2 isoforms Alpha (catalytic) and isoforms Beta (function not known) (By similarity).
                                                                                                                     ENHANCED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 27;
                                                                                                                                                                                                                                                                                                                                                55.8%; Score 1224.5; DB 1; Length 421; 64.0%; Pred. No. 8.1e-79; ive 55; Mismatches 59; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Bacteriol. 175:4096-4103(1993).
-!- CATALYTIC ACTIVITY: ATP + L-aspartate = ADP + 4-phospho-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corynebacterinea, Corynebacterinea, Corynebacterinea, NCBI_TaxID=28028,
                                                   250 FOR ISOFORM BETA.
301. S--Y: FEEDBACK-RESISTANT AND IEXPRESSION OF THE ASD GENE.
40 C -> V (IN REF. 1 AND 3).
44754 MM; E36B4D0081DE0827 CRC64;
                    ASPARTOKINASE, ISOFORM BETA
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                                                                                                                                                                                                                                                    421 AA;
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301
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CHAIN
INIT MET
MUTAGEN
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Best Local
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16-OCT-2001 (Rel. 40, Last annotation update)
Aspartokinase (EC 2.7.2.4) (Aspartate kinase)
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                                                                                                                             Pseudomonadaceae; Pseudomonas
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Best Local Similarity 42.6'
Matches 170; Conservative
                                                                             Pseudomonas aeruginosa
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SEQUENCE 412 AA;
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                                                    OR PA0904.
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                                                                                                                                                   This SWISS-PRCT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstainnthe the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D-5G: DECREASED SENSITIVITY OF AK ACTIVITY TO CONCERTED FEEDBACK INHIBITION BY LYSINE AND THREONINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
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                   Comment=2 isoforms, Alpha/Aspartokinase alpha subunit (shown here) and Beta/Aspartokinase beta subunit, are produced by alternative initiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27;
                                                                                                                                                                                                                                                                                                                                                        EMBL; L16448; AAA23293.1; -..
R InterPro; IPR001048; Aa kinase.
R InterPro; IPR001912; ACT.
R InterPro; IPR001912; ACT.
R InterPro; IPR001341; Aspartate kinase.
R Pfam; PF00666; aakinase; 1.
R Pfam; PF00666; aakinase; 1.
R TIGRPAMS; TIGR00656; asp_kin_monofn; 1.
R TIGRPAMS; TIGR00657; asp_kin_monofn; 1.
R TIGRPAMS; TIGR00657; asp_kin_monofn; 1.
R TIGRPAMS; TIGR00657; asp_kin_monofn; 1.
R TIGRPAMS; TIGR00657; asp_kin_monofn; 1.
R TIGRPAMS; TIGR00657; asp_kin_monofn; 1.
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                                                                                                    SIMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.5%; Score 1216.5; DE 63.8%; Pred. No. 3e-78; ive 55; Mismatches 6
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  Event=Alternative initiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 AA; 44796 MW;
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Best Local Similarity 63.8%
Watches 250; Conservative
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                                                                                                                                                STRAIN=ATCC 15692 / PAO1;
STRAIN=ATCC 15692 / PAO1;
STRAIN=2043737; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino B., Westbrook-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Febrer K.R., Kas A., Larbig K.R., Spencer D.H., Worng G.K.-S., Wu. Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";
Nature 406:959-964(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aspartate.
-!- PATHWAY: FIRST STEP IN THE COMMON BIOSYNTHETIC PATHWAY LEADING FROM ASP TO DIAMINOPIMELATE, TO MET, TO ILE AND TO THR.
-!- SIMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 198-412 FROM N.A.
STRAIN=ATCC 15692 / PAO1;
Hindle Z., Throup J.P., Francis K.P., Bycroft B.W., Williams P.,
Stewart G.S.A.B.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + L-aspartate = ADP + 4-phospho-L-
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80; Mismatches 105; Indels
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44388 MW; A06ACAA5E914F337 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001048; Aa kinase.
InterPro; IPR002912; ACT.
InterPro; IPR002912; ACT.
InterPro; IPR001341; Aspartate_kinase.
Pfam; PF00696; aakinase; 1.
Pfam; PF01842; ACT; 2.
TIGRPAMs; TIGR00656; asp_kin_monofn; 1.
TIGREAMs; TIGR00657; asp_kin_monofn; 1.
PROSITE; PS00124; ASPARTOKINASE; 1.
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RESULT 8
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303
                                                                                                                                                                                                                          -----HRHGAAERLQGRGRQDRHHLHLLPQTSGPPPWKNWTRSETRSASTQLLYDDH 340
                                                                                                                                                                                                                                                                  304 TIDFIFTVHRNDYLNALE------ILKQTA------ANIGAREAIGDTN 340
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Aspartokinase (EC 2.7.2.4) (Aspartate kinase) [Contains: Aspartokinase alpha subunit (ASK-beta)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=ATCC 33923 / DSM 674 / AT-62;
MEDLINE=95291465; PubMed=7773416;
Mishiyama M., Kukimoto M., Beppu T., Horiouchi S.;
"An operon encoding aspartokinase and purine phosphoribosyltransferase in Thermus flavus.";
                                                                                                241 IXDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRRRQ-------
                                                                                                                                                        244 DEEESMEOPIISGIAFNRDEAKLTIRGVPDTPGVAFKILGPISAANVEVDMIVQNVAHDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- PATHWAY: FIRST STEP IN THE COMMON BIOSYNTHEFIC PATHWAY LEADING FROM ASP TO DIAVINOPIMELATE, TO MET, TO ILE AND TO THR.
-1- SUBUNIT: Tetramer consisting of 2 isoforms Alpha (catalytic) and isoforms Beta (function not known) (By similarity).
-1- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99173891, PubMed=10074061,
Kobashi N., Nishiyama M., Tanokura M.;
Kapartate kinase-independent lysine synthesis in an extremely
thermophilic bacterium, Thermus thermophilus: lysine is synthesized
via alpha-aminoadipic acid not via diaminopimelic acid.";
J. Bacteriol. 181:1713-1718 (1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Microbiology 141:1211-1219(1995).
-!- CATALYTIC ACTIVITY: ATP + L-aspartate = ADP + 4-phospho-L-
                                                                                                                                                                                                                                                                                                                                                                                   341 IAKVSIVGVGMRSHAGVASRMFEALAKESINIQMISTSE 379
                                                                                                                                                                                                                                                                                                                                                     IGKVSLIGAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AK THETH STANDARD, PRT, P97151; P77991; 30-MAY-2000 (Rel. 39, Created) MAY-2000 (Rel. 39, Last sequence 15-SEP-2003 (Rel. 42, Last annocation Aspartokinase (EC 2.7.2.4) (Aspartat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative initiation;
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EMBL; AB013131; BAA2849.1; -.
EMBL; D37928; BAA07146.1; -.
EMBL; D37928; BAA07147.1; -.
InterPro; IPR001048; Aa_kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermus thermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aspartate.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEEGRVVLVAGFQGVSQDTXDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 -KEVAMEMDKAVTGVALDLDHAQIGLIGIPDQPGIAAKVFQALAERGIAVDMIIQGVPGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----RROHRHGAABRLQGRGRQDRHHLHLLPQTSGPPPWKNWTRSETRSASTQ
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MEDLINE=9307380; PubMed=1444390;
Schendel F.J., Flickinger M.C.;
"Cloning and nucleotide sequence of the gene coding for aspartokinase
II from a thermophilic methylotrophic Bacillus sp.";
Appl. Environ. Microbiol. 58.2806-2814(192).
-!- CATALYTIC ACTIVITY: ATP + L-aspartate = ADP + 4-phospho-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last ennotation update)
Aspartokinase 2 (EC 2.7.2.4) (Aspartokinase II) (Aspartate kinase 2)
[Contains: Aspartokinase II alpha subunit; Aspartokinase II beta
R InterPro; IPR002912; ACT.

AR InterPro; IPR001341; Aspartate_kinase.

DR InterPro; IPR001341; Aspartate_kinase.

DR Pfan; PF00696; askinase; 1.

DR TIGRFAMS; TIGR00657; asp_kin_monofn; 1.

DR TIGRFAMS; TIGR00657; asp_kin_monofn; 1.

DR TIGRFAMS; TIGR00657; asp_kin_monofn; 1.

DR TIGRFAMS; TIGR00657; asp_kin_monofn; 1.

DR TIGRFAMS; TIGR00657; asp_kin_monofn; 1.

RW Lyaine biosynthesis; Alternative initiation.

FT CHAIN 1405 ASPARTOKINASE, ISOFORM BETA.

FT CHAIN 245 465 FOR ISOFORM BETA.

TILE 126 126 E -> D (IN STRAIN AT-62).

TANN 126 TANN 06F7B79E90896GEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                333 AILRPDIAKVSIVGVGLASTPEVPAKMFQAVASTGANIEMIATSE 377
                                                                                                                                                                                                                                                                                                                                                                                                         94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus sp. (strain MGA3),
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCGI_TaxID=1409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         335 LLYDDHIGKVSLIGAGMRSHPGVTATFCEALAAVGVNIELISTSE
                                                                                                                                                                                                                                                                                                                                                                 37.3%; Score 819; DB 1;
43.2%; Pred. No. 2.2e-50;
iive 78; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA
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-!- ENZYME REGULATION: LYSINE-SENSITIVE.
                                                                                                                                                                                                                                                                                                                                                                                                       Matches 175; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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059229;
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246
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                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246
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                                                              subunit]
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                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license@siscement (See http://www.isb-sib.ch/announce/or send an email to license@sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRFGTVVVGS 240
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---QNRINVDIIIQSA-----TDAETTNLSFSIKSDDLEETMAVLENNKNLLNYQGI 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEEGRIVVLVAGFOGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 IKDVPME-DPILIGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRRRQHRHGAAERLQG 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 -EEVTMEQNLVVRGVAFEDEITRVTVFGLPNSLTSLSTIFTTLA-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VOKYGGSSVADAERIRRVAERIVATKKOGNDVVVVSAMGDITDDLLDLAQQVCPAPPPR
                                                                        Comment=2 isoforms, Alpha/Aspartokinase II alpha subunit (shown here) and Beta/Aspartokinase II beta subunit, are produced by alcernative initiation.

SIMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY:
PATHWAY: FIRST STEP IN THE COMMON BIOSYNTHETIC PATHWAY LEADING FROM ASP TO DIAMINOPIMELATE AND LYS, TO MET, TO ILE AND TO THR. SUBUNIT: Tetramer consisting of 2 isoforms Alpha (catalytic) and isoforms Beta (function not known).

ALTERNATIVE PRODUCTS:
Event=Alternative initiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56;
                                                                                                                                                                                                                                                                                                                                                                      ASPARTOKINASE 2, ISOFORM ALPHA.
ASPARTOKINASE 2, ISOFORM BETA.
FOR ISOFORM BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                              35.8%; Score 785; DB 1; Length 411; 42.1%; Pred. No. 5.5e-48; tive 81; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----HIGKVSLIGAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESETGLAKVSIVGSGMISNPGVAAKMFEVLALNGIQVKAVSTSE 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGRODRHHLHLLPQTSGPPPWKNWTRSETRSASTQLLYDD------
                                                                                                                                                                                                                                                                                                                                                                                                                           94061572E369CD48 CRC64;
                                                                                                                                                                                                                                  EMBL, M93419; AAA22251.1; -.
InterPro; IPR001048; Aa kinase.
InterPro; IPR002912; ACT.
InterPro; IPR001341; Aspartate kinase.
InterPro; IPR001341; Aspartate kinase.
Pfam; PF00865; aakinase; 1.
Pfam; PF01842; ACT; 2.
TIGREAMS; TIGR00656; asp kin monofn; 1.
TIGREAMS; TIGR00656; asp kin monofn; 1.
PROSITE; PS00324; ASPARTOKINASE; 1.
Transferase; Kinase; Diaminopimelate biosynthesis; lysine biosynthesis; Alternative initiation.
                                                                                                                                                                                                                                                                                                                                                                                                                           44342 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Best Local Similarity
Matches 170; Conserv
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SEQUENCE
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STANDARD;

AK2_BACST P53553;

AK2_BACST ID AK2_B AC P5355.

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                                                                                                           5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- ALTERNATIVE PRODUCTS:

Event=Alternative initiation;

Comment=2 isoforms, Alpha/Aspartokinase II alpha subunit (show here) and Beta/Aspartokinase II beta subunit, may be produced alternative initiation;

-!- SIMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aspartate.

-!- ENZYME REGULATION: DYSINE-SENSITIVE (BY SIMILARITY).

-!- PATHWAY: FIRST STEP IN THE COMMON BIOSYNTHETIC PATHWAY LEADING

-!- SUBDNIT: Tetramer consisting of 2 isoforms Alpha (catalytic) ar isoforms Beta (function not known).
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Aspartokinase Z [EC 2.7.2.4) (Aspartokinase II) (Aspartate kinase (Contains: Aspartokinase II beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52;
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R InterPro; IPR001048; Aa kinase.

R InterPro; IPR001048; Adr.

InterPro; IPR001341; Aspartate_kinase.

R InterPro; IPR001341; Aspartate_kinase.

R InterPro; IPR001341; Aspartate_kinase.

R InterPro; IPR001341; Aspartate_kinase.

R Pfam; PF00696; aakinase; 1.

R Pfam; PF00696; asp kin monofn; 1.

R TICRPAMS; TICR00657; asp kin monofn; 1.

R TICRPAMS; TICR00657; asp kin monofn; 1.

R TICRPAMS; TICR00657; asp kin monofn; 1.

R TICRPAMS; TICR00657; asp kin monofn; 1.

R TICRPAMS; TICR00657; asp kin monofn; 1.

R TICRPAMS; TICR00657; asp kin monofn; 1.

R TICRPAMS; TICR00657; asp kin monofn; 1.

R TICRPAMS; TICR00657; asp kin monofn; 1.

R TICRPAMS; TICR00657; asp kin monofn; 1.

R TICRPAMS; TICR00657; asp kin monofn; 1.

R TICRPAMS; TICR00657; asp kin monofn; 1.

R TICRPAMS; TICR00657; asp kin monofn; 1.

R TICRPAMS; TICR00657; asp kin monofn; 1.

R TICRDAN ASPARTOKINASE 2, ISOFORM BETA ASPARTOKINASE 2, ISOFORM BETA
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Gene 169:135-136(1996).
-!- CATALYTIC ACTIVITY: ATP + L-aspartate = ADP + 4-phospho-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 407;
                                                                                                                                                                                                                                                     Bacillus stearothermophilus.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
NCBI_TaxID=1422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cantoni R., Labo M., de Rossi E., Riccardi G., "Sequence of the Bacillus stearothermophilus gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PROBABLE)
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43.2%; Pred. No. 1.7e-47;
iive 77; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FOR ISOFORM BETA
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Matches 173; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65
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LDEGALVIVAGFQGVT-ETGEITTLGRGGSDTTAVALAAALKAEKCDIYTDVTGVFTTDP 183
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                                                                                         RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
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                                                                                                                                                                                                                                                                                   300 RGRQDRHHLHLLPQTSGPPPWKNWTRSETRSAS------TQLL----
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-!- CATALYTIC ACTIVITY: ATP + L-aspartate = ADP + 4-phospho-L-
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Bacceria; Aquificae; Aquificales; Aquificaceae; Aquifex.
NCBI_TaxID=63363;
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SEQUENCE 415 AA; 45519 MW; E8111750A8C14162 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               340 HIGKVSLIGAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
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PIR, B70399; B70399.
InterPro; IPR001048; Aa kinase.
InterPro; IPR002212; AcT.
InterPro; IPR002261; AcT.
InterPro; IPR001341; Aspartate_kinase.
Pfam; PF010842; ACT; 2.
TIGRFAMS; TIGR00656; asp kin monofn; 1.
TIGRFAMS; TIGR00657; asp kin monofn; 1.
PROSITE; PS00324; ASPARTOKINASE; 1.
PROSITE; PS00324; ASPARTOKINASE; 1.
Tranfferase; Kinase; Diaminopimelate biosynthesis;
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2.4) (Aspartate kinase)
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Gaps

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Length 415;

33.5%; Score 734.5; DB 1; Length 42.4%; Pred. No. 1.9e-44; rive 76; Mismatches 124; Indels

Matches 164; Conservative

Similarity

Query Match Local

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                                                                          VOKFGGTSVGTLERIELCAKRVIKALEKGYKPVVVSSAMAGETDSLIELAKKVHPRPPER
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MEDLINE=99120557; PubMed=9923682;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
Smith D.R., Noonan B., Guil B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nicelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
Trust T.J.,
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16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
LYSC OR JHP1150.
LYSC OR JHP1150.
Bactoria: Proteobacteria: Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacteria;
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Nature 397:176-180(1999).
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Microbiology 142:3067-3078(1996).
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Sanders J., Emmerson P.T., Harwood C.R.;
"The dnaB-phah (256 degrees-240 degrees) region of the Bacillus
subtilis chromosome containing genes responsible for strees responses,
the utilization of plant cell walls and primary metabolism.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VOKYGGSSVADAERIRRVAERIVATKKOGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR
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                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Chen N.-Y., Hu F.M., Paulus H.;
"Nucleotide sequence of the overlapping genes for the subunits of
Bacillus subtilis aspartokinase II and their control regions.";
J. Biol. Chem. 262:8787-8798(1987).
                                                                                                                                                                                                                                                                                                                                                                                24;
                                                                                                                                                                                                                                                                                                                     Length 405;
                                                                                                                                                                                                                                                                                                           Query Match
32.9%; Score 721; DB 1; Length 405.
Best Local Similarity 41.4%; Pred. No. 1.7e-43;
Matches 161; Conservative 84; Mismatches 120; Indels
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                                    408 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         350 MKSHSGVASIAFKALAKDNINIMMISTSE 378
         InterPro; IPR001341; Aspartate_kinase.
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EN 1312 SEQUENCE FROM N.A.

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RA COLLEGE TO NO. SERSIANCES P. BOLOID A. A. DIORIO G.,

RA AREWEGO V. BETTER CO. M.G. CANAGED I. C. GAMONIA D. C., BED. S.,

RA COLLEGE F. BOUTERED M.C. CANAGED I. C. CANAGED S. C. STONE S. A.

COLLEGE V. BOUTERED M.C. CANAGED I. C. CANAGED R. A. DIORIDE R. A.

COLLEGE V. CANAGED M.C. CANAGED S. CANAGED R. A. DIORIGE R. A.

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Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.
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004795; 031759;
01-0CT-1993 (Rel. 27, Created)
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Best Local Similarity
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TIGR; HP1229;
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SEQUENCE FROW N.A.
STRAIN=26695 / ATCC 700392;
MEDLINE=97394467; PubMed=9252185;
MEDLINE=97394467; PubMed=9252185;
MEDLINE=97394467; PubMed O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Loftus B., Ritzderald L.M., Lee N., Adams M.D., Hickey E.K.,
MCKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kalley J.M.,
Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
                                                                                                                                                                                                                                                                              1 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPR
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                                                                                                                                                                                                                                       39; Gaps
      R InterPro; IPR001341; Aspartate_kinase.
R InterPro; IPR001341; Aspartate_kinase.
Pfam; PF00695; Acri. 2.
R Pfam; PF01842; Acri. 2.
R TIGRPAMS; TIGR00656; asp_kin_monofn; 1.
R TIGRPAMS; TIGR00656; asp_kin_monofn; 1.
R TIGRPAMS; TIGR00656; asp_kin_monofn; 1.
R TIGRPAMS; TIGR00656; asp_kin_monofn; 1.
R Transferase; Kinase; Diaminopimelate biosynthesis;
M Transferase; Kinase; Diaminopimelate biosynthesis;
M Transferase; Kinase; Diaminopimelate biosynthesis;
T CHAIN 246 408 ASPARTOKINASE 2, ISOFORM ALPHA.
T CHAIN 246 746 FOR ISOFORM BETA.
T INIT_MET 246 246 FOR ISOFORM BETA.
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                            Score 712.5; DB 1; Length
Pred. No. 6.6e-43;
82; Mismatches 116; Indels
                                                                                                                                                                     166 V -> A (IN REF, 2).
43836 MW, 8E718FCDAAB05B96 CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
AspartoXinase (EC 2.7.2.4) (Aspartate kinase)
LYSC OR HP1229.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          405 AA.
                                                                                                                                                                                                          32.5%;
                                                                                                                                                                                                                        al Similarity 40.0
158; Conservative
InterPro; IPR002912; ACT
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408 AA;
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CONFLICT
SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 TIGRDGKTDLDFTIVKTQ------IEETKQALKPFLAQMDSIDYDENIAKVSIVGVG 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299 GRGRQDRHHLHL-LPQTSGPPPWKNWTRSETRSASTQLL------YDDHIGKVSLIGAG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVG-
                                                                                                                                                                              COMMON BIOSYNTHETIC PATHWAY LEADING
complete genome sequence of the gastric pathogen Helicobacter
                                    pylori.";
Nature 388:539-547(1997)
-!- CATALYTIC ACTIVITY: ATP + L-aspartate = ADP + 4-phospho-L-
                                                                                                                                                                   -!- PATHWAY: FIRST STEP IN THE COMMON BIOSYNTHEFIC PATHWAY FROM ASP TO DIAMINOPIMELATE, TO MET, TO ILE AND TO THR. -!- SIMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.4%; Score 711; DB 1; Length 40 40.6%; Pred. No. 8.4e-43; ive 85; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lysine biosynthesis; Complete proteome.
SEQUENCE 405 AA; 44133 MW; 74723D671FF49395 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transferase, Kinase, Diaminopimelate biosynthesis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351 MRSHPGVTATFCEALAAVGVNIELISTSE 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      350 MKSHSGVASIAFKALAKDNINIMMISTSE 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGRFAMS; TIGRO0656; asp kin monofn; 1.
TIGRFAMS; TIGRO0657; asp_kinases; 1.
PROSITE; PS00324; ASPARTOKINASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001048; Aa kinase.
InterPro; IPR002912; ACT.
InterPro; IPR005260; Asp_kin_monofn.
InterPro; IPR001341; Aspartate_kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE000628; AAD08274.1; -. PIR; E64673; E64673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00696; aakinase; 1.
Pfam; PF01842; ACT; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MINIST FR. 0998AWATA N. MOSZAT I. Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Barelser L., Brans A., Braun M., Brignell S.C., Bron S., Bruschi C.V., Caldwell B.M. Capuano V., Carter N.M., Anderiot S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Deniaco F.V., Deviner K.M., Dusterhoft A., Earlich S.D., Emmerson P.T., Beniaco F.V., Calser P., Offere M. J., Farnaco D. J., Ramano M., Faritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Ghima S.Y., Claser P., Offere M. A., Galler B., Capuano M., Aramana D., Karamata D., Harwood C.R., Henaut A., Hibbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., A., Landen J., Laudber J., Lazarevic V., A., Levine A., Liu H., Masuda S., Mauel C., Medique C., Robayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., Mellado R.P., Liu H., Masuda S., Mauel C., Medique C., Robayashi Y., Robil T.M., Portetelle D., Porwollik S., Prescott A.M., A. Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Rareor M., Ravolta C., Roche B., Rose M., Sadaie Y., Scanlan B., Schleich S., Schroeter R., Schleich S., Schroeter R., Scallan B., Schroeter R., Scallan B., Serior P., Schleich S., Schroeter R., Yosanotti A., Tanaka T., Taraka T., Tarkemaru K., Tanaka T., Taraka T., Tarkemaru K., Tanaka T., Taraka T., Tarkemaru K., Tanaka T., Tarkensenger T., Mannut R., Wedler B., Wedler H., Weitzenegger T., Mannut R., Wedler B., Wedler H., Weitzenegger T., Maritar P., Wipat A., Yamamoco H., Yamane K., Yasumoto K., Yati A., Wannut S., Vandenbol M., Vannut S., Wohikawa H., Danchin A., R. Wallellis S., Wannuce of the Gram-positive bacterium Bacillus R., Mathilise R., Wohilas S., Wannuck S., Wannuck S., Wannuck S., Wannuck S., Wannuck S., Wannuck S., Wannuck S., Wannuck S., Wannuck S., Wannuck S., Wannuck S., Wannuck S., Wannuck S., Wannuck S., Wannuck S., Wannuck S., Wannuck S., Wannuck S., Wannuck S., Wannuck S., Wannuck S., Wannuck S., Wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- PATHWAY: FIRST STEP IN THE COMMON BIOSYNTHETIC PATHWAY LEADING FROM ASP TO DIAMINOPIMELATE AND LYS, TO MET, TO ILE AND TO THR.
-!- SUBUNIT: TETRAMER CONSISTING OF TWO ALPHA (CATALYTIC) AND TWO BETA (FUNCTION NOT KNOWN) CHAINS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY.
                               88-FEB-2003 (Rel. 41, Last annotation update)
Aspartokinase 1 (EC 2.7.2.4) (Aspartokinase I) (Aspartate kinase 1)
[Contains: Aspartokinase I alpha subunit; Aspartokinase I beta
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93252813; PubMed=8098035; Chen N.-Y., Jiang S.-Q., Klein D.A., Paulus H.; Chen N.-Y., Jiang S.-Q., Klein D.A., Paulus H.; Organization and nucleotide sequence of the Bacillus subtilis diaminopimelate operon, a cluster of genes encoding the first three enzymes of diaminopimelate synthesis and dipicolinate synthase."; J. Biol. Chem. 268:9448-9465(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 390:249-256(1997).
-!- CATALYTIC ACTIVITY: ATP + L-aspartate = ADP + 4-phospho-L-
                                                                                                                                                                                                             Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus, NCBI_TaxID=1423;
       30-MAY-2000 (Rel. 39, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98044033; PubMed=9384377;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.
                                                                                   Aspartokinase 1
                                                                                                                                                                                         DAPG OR LSSD.
                                       28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                      subunit]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 APPPRELDMLITAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 AISPREQDLLISCGETISSVVFTSMLLDNGVKAAALTGAQAGFLINDQHTNAKIIEMKPE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VOKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGD-----TTDDLLDLAQQVCP 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAINS-JAL-1 / DSW 2661 / ATCC 43067;
STRAINS-JAL-1 / DSW 2661 / DSW 2661 / ATCC 43067;
BULL C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Barke O.A., FitzCerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.L.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSADPRIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 MTADPRVVENAKPLPVVTYTEICNLAYQGAKVISPRAVEIAMQAKVPIRVRSTYSNDKGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 VV------VGSIKDVPMEDPILIGVAH--DRSEAKVTI-VGLPDIPGYAAKVFRAVARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286 RROHRHGAAERLOGRGRODRHHLHLLPQTSGPPPWKNWTRSE-----TRSASTQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---------NAGISVDFFNITPSEIVYTVAGNKTETAQRILM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 VQKFGGTSVKDDKGRKLALGHIKEAISEGYKVVVVVSAMGRKGDPYATDSLLGLLYGDQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 RLQTALEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
R Subtilist; BG10784; dapG.

R InterPro; IPR001048; Aa Kinase.

DR InterPro; IPR001341; Aspārtate kinase.

DR InterPro; IPR00556; aspiral Aspārtate kinase.

DR IGRPAM; IGR00656; aspiral Aspartate kinase.

DR IGRPAM; IGR00657; asp kinases; 1.

DR TGRPAM; IGR00657; asp kinases; 1.

RW Transferase; Kinase; Diaminopimelate biosynthesis;

V. Sine biosynthesis; Complete proteome.

1 A04 ASPARTOKINASE I ALPHA SUBUNIT.

ASPARTOKINASE I BETA SUBUNIT.

ASPARTOKINASE I BETA SUBUNIT.

ASPARTOKINASE I BETA SUBUNIT.

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ASPARTOKINASE I BETA SUBUNIT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a Seore 532; DB 1; Length 404; Similarity 36.5%; Pred. No. 3e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaea; Euryarchaeota; Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable aspartokinase (EC 2.7.2.4) (Aspartate kinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---YDDHI----GKVSLIGAGMRSHPGVTATFCEALA 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        328 DMGYDPMVTRNCAKVSAVGAGIMGVPGVTSKIVSALS 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Q57991;
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AK METTA AK METTA AL OSTS MAN OSTS MAN OSTS MAN OSTS MAN OSTS MAN OSTS MAN OSTS MET AN OSTS MET AN OSTS MET AN OSTS MAN OSTS MET AN OSTS MAN OSTS MAN OSTS MAN OSTS MAN OSTS MAN OSTS MAN OSTS MAN OVER MEN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER MAN OVER M
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Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C., "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.";
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22.4%; Score 492; DB 1; Length 473;
Best Local Similarity 27.2%; Pred. No. 2.3e-27;
Matches 129; Conservative 92; Mismatches 126; Indels 128; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGREAMS; TIGRO0656; asp kin monofn; 1.
TIGREAMS; TIGRO0657; asp kinases; 1.
PROSITE; PSO0324; ASPARTOKINASE; 1.
Transferase; Kinase; Threonine biosynthesis; Complete proteome.
SEQUENCE 473 AA; 51392 MW; 811C6E0F4B66EC5F CRC64;
                                                                                                                       Science 273:1058-1073(1996).
-!- CATALYTIC ACTIVITY: ATP + L-aspartate = ADP + 4-phospho-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001048; Aa kinase.
InterPro; IPR002912; ACT.
InterPro; IPR005260; Asp kin monofn.
InterPro; IPR001341; Aspartate_kinase.
Pfam; PF00696; aakinase; 1.
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Search completed: November 21, 2003, 16:04:16 Job time : 5.99955 secs

GenCore verBion 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd. in search, using sw model
version - 2003 model
GenCore (c) 1993 using sw
GenCore version Copyright (c) 1993 - 2003 OM protein - protein search, using sw model

November 21, 2003, 15:56:56; Search time 20.8635 Seconds (without alignments) 5244.295 Million cell updates/sec Run on:

US-09-688-672A-4 2193 1 VQXYGGSSVADAERIRRVAE......SAATRRPRCTRGRDGRWACQ 424 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 830525 seqs, 258052604 residues Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Q9cb77 mycobacteri Q8kq29 streptomyce Q9rq25 amycolatops Q93c57 crynebacte Q9ac57 crynebacte Q9ac55 corynebacte Q9ac5 corynebacte Q9ac5 streptomyce Q9qq5 streptomyce Q8qq5 streptomyce Q8qq5 streptomyce Q8ty strigmatella P74569 synechocyst Q8fb65 leptospira Q8cluO5 methylobaci Q8dhwO synechococ Q8dhwO synechococ Q8dhwO synechococ Q8dhwO synechococ Q8dhwO synechococ Q8dhwO synechococ Q8dhwO synechococ Q8dhwO synechococ	Vogoyo DiriuoDacce Q9jtn3 neisseria m
SUMMARIES	Q9CB77 Q8KQ29 Q8KQ29 Q93C55 Q93C55 Q9AX17 Q9XX17 Q9XX16 Q9XX16 Q9XX16 Q9XY16 Q8F865 Q8DHWQ Q8DHWQ	Qecera Qectiva
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Result No.	, 11111111 112441147	16

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09JYN6 09K8B0 09FHT4 09SHT6 09WZ17 08Y073 08Y073 08Y7N9 08Y7N9 08Y7N9 08Y7N9 08Y197 09BC91 09BC91 09BC91 09BC91 09BC91 09BC91 09BC91 09BC91 09BC91	Q8DC48 Q99U91 Q99EV36 Q8EV36 Q8CSM8 Q98CSM9 Q98CQT0 Q92ER9 Q92GF9 Q8Y765
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ALIGNMENTS

	421 AA.		sequence update)	annotation update)				Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,	ycobacterium.							T., Churcher C., Harris D.,		Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,	Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,	ndream M.A., Rutherford K.M.,	ds M., Skelton J., Squares R.,	tehead S., Woodward J.R.,		illus.";												4A3BA44D1CEEFE06 CRC64;
	PRT; 4			Last annot				tinobacter	riaceae; M						khill J.,	nier T., C	D., Chill	oy S., Fel	ls K., Lac	M.A., Raja	Simon S., Simmonds M.,	or K., Whi		eprosy bac		;		se.		Aspartate_kinase.			ases; 1.	ASE; 1.		
	PRELIMINARY;	. 17,	. 17,	(TrEMBLrel. 21,			leprae.	inobacteria; Ac	Corynebacterineae, Mycobacteriaceae, Mycobacterium	:65		N.A.		MEDLINE=21128732; PubMed=11234002;	glmeier K., Par	P.R., Honore N., Garnier	asham D., Brown	Devlin K., Duth	ornsby T., Jage	iver K., Quail	eger K., Simon	S., Stevens K., Taylor K., Whitehead		decay in the l	Nature 409:1007-1011(2001).	5; CAC31839.1;	23;	IPR001048; Aa kinase	002912; ACT.	IPR001341; Asparta	PF00696; aakinase; 1.	PF01842; ACT; 2.	R00657; asp kin	PROSITE; PS00324; ASPARTOKINASE;	ete proteome.	421 AA; 44663 MW;
LT 1	9CB77;			01-JUN-2002 (J	Aspartokinase.	ASK OR ML2323.	Mycobacterium leprae.	Bacteria; Acti	Corynebacterir	NCBI TaxID=1769;	[1]	SEQUENCE FROM N.A.	STRAIN=IN;	MEDLINE=211287	Cole S.T., Eig	Wheeler P.R.,	Mungall K., Ba	Davies R.M., I	Holroyd S., Ho	Murphy L., Oli	Rutter S., Seeger K.,	Squares S., St	Barrell B.G.;	"Massive gene	Nature 409:100	EMBL; AL58392	Leproma; ML2323;	InterPro; IPR(InterPro; IPR	Pfam; PF00696	Pfam; PF01842	TIGRFAMS; TIG	PROSITE; PS000	Kinase; Complete proteome.	SEQUENCE 42
RESULT Q9CB77	ID AC	PT	D.	TO	DE	O.S.	SO	8	0	ŏ	RN	RP	RC	RX	RA	RA	RA	RA	RA	RA	RA	RA	RA	RT	RL	DR	DR	DR	DR	DR	DR	DR	DR	DR	ΚW	ŎS

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61 ELDMLITAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296 RLO-----GRGRODRHHLHLLPQTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLIGAG
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      Length 421;
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Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.
                                                                   60; Indels
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         DB 2;
      Score 1272.5; DB Pred. No. 7.5e-78;
                                                                   51; Mismatches
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TIGREPAMS; TIGRO0657; asp. kinases; 1.
TIGREPAMS; TIGRO0656; asp. kin monofn; 1.
PROSITE; PS00324; ASPARTOKINĀSE; 1.
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InterPro; IPR005260; Asp kin monofn.
InterPro; IPR001057; Glu_Skinase.
58.0%;
66.1%;
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Pfam; PF01842; ACT; 2.
                                                                   Conservative
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SEQUENCE 421 AA;
                                      l Similarity
257; Conserv
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      Query Match
                                   Local
                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 IKDVPMEDPILTGVAHDRSEAKVTIVGIPDIPGYAAKVFRAVA------DADVNIDM 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296 VLQNVSKVEDGKTDITFTCSRDSGPIAVAKLGSLRDEIGFTQLLYDDHIGKVSLIGAGMR 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RVVHNARKLDTVTFFEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYADKPGTVIVGS 244
                                                                                                                                                          9
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                                                                                                                                                    1 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR
                                                                                                                                                                                                                                                                                                                                                                                                                                      125 LDEGRIVLVAGFQGVSQDTRDITTLGRGGSDTTALAMAAALGADVCEIYTDVDGIFSADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               296 RLQGRGRQDRHHLHL---LPQTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLIGAGMR
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                                                                                             17; Gaps
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"Isolation and characterization of the aspartokinase and aspartate
"Isolation dehydrogenase genes from cephamycin C-producer
Streptomyces clavuligerus.";
Thesis (2002), University of Middle East Technical University, Ank
                                   Length 421;
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Streptomycineae; Streptomycetaceae; Streptomyces.
NCBL_TaxID=1901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Aspartate kinase alpha subunit (EC 2.7.2.4) (Aspartokinase)
                         ; Score 1545.5; DB 16; Lengt; Pred. No. 3e-96; 18; Mismatches 43; Indels
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-- SABARTATE.
-- SIMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY.
INTERPRO; IPRO01048; Aa_kinase.
INTERPRO; IPRO01341; AGT.
INTERPRO; IPRO01341; ASPARTATE kinase.
INTERPRO; IPRO01341; ASPARTATE kinase.
INTERPRO; IPRO01341; ASPARTATE kinase.
INTERPRO; IPRO01351; AU_SKinase.
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TIGRPAMS; TIGRO0657; asp_kinases; 1.
TIGRPAMS; TIGRO0656; asp_kin_monofn; 1.
PROSITE; PSO0124; ASPARTOKINASE; 1.
Kinase; Transferase
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                             70.5%;
80.4%;
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01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
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Pfam; PF01842; ACT; 2.
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                      Query Match
Best Local Similarity 80.4
Matches 319; Conservative
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61 BLDMLLTAGERISNALVAWAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTFGRLQTA 120
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                                                      120
                                                                                                             LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADF 180
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                                                                       09
                            64
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Thesis (2000), Department of Area of Microbiology, University of Leon,
                                                        ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA
                                                                                                                                        125 LDEGKICIVAGFQGVNKETRDVTTLGRGGSDTTAVALAAALNADVCEIYSDVDGVYTADP
                                                                                                                                                                                   HGAAERLQGRGRQD-RHHLHLL--PQTSGPPPWKNWTRSETRSASTQLLYDDH1GKVSLI
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                RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
 VOKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPR
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-!- CATÀLYTIC ACTIVITY: ATP + L-ASPARTATE = ADP + 4-PHOSPHO-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.
NCBI_TaxID=1913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MR-2003 (TrEMBLrel. 23, Last annotation update)
Aspartokinase alpha subunit (BC 2.7.2.4) (Aspartate kinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56.0%; Score 1228.5; DB 2; Length
64.3%; Pred. No. 7e-75;
live 52; Mismatches 66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 AA; 44141 MW; 802FBE02D01B7F95 CRC64;
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                                                                                                                                                                                                                                                                                                   RLQG-----RGRQDRHHLHLLPQTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLIGAG 350
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                                                                                   64
                                                                                                                                                                                                                                             RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                         1 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR
                                                                                                                                                                    LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCE1YTDVDG1FSADP
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                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MRR-2003 (TrEMBLrel. 23, Last annotation update)
Feedback-resistant aspartokinase Lysc alpha subunit (EC 2.7.2.4)
                            21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.2%; Score 1232.5; DB 2; Length 421; llarity 64.3%; Pred. No. 3.7e-75; Conservative 55; Mismatches 58; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corynebacterium crenatum.", Submitted (AUG-2001) to the BMBL/GenBank/DDBJ databases.
  Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=168810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu Y., Ding J., Wang J.; "Cloning and sequence analysis of aspartokinase genes from
                            61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 AA; 44738 MW; 473A19409C0215E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASPARTATE.
-!- SIMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY.
EMBL; AF4140684; AALON807.1; -.
INTERPRO: IPR001048; Aa Kinase.
INTERPRO: IPR001341; ASPARTATE Kinase.
INTERPRO: IPR001341; ASPARTATE Kinase.
PERM: PF00696; askinase; I.
PENO6842; ACT; 2.
  DB 2;
57.8%; Score 1267.5; DB 65.3%; Pred. No. 1.6e-77; ive 53; Mismatches 61
                                                                                                                                                                                                                                                                                                                                                                                               MRSHPGVTATFCEALAAVGVNIELISTSE 379
                                                                                                                                                                                                                                                                                                                                                                                                             MRSHPGVTATFCEALAEAGVNIEIINTSE 382
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TIGRFAMS; TIGRO0656; asp_kin_monofn; 1.
PROSITE: PSO0324; ASPARTÖKINĀSE; 1.
Kinase; Transferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterium crenatum.
                             254; Conservative
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                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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01-DEC-2001 (
01-DEC-2001 (
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Matches 252;
Query Match
Best Local S
Matches 254
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290
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       184
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                                                    RIVENARKLDIVIFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                             291 HGAAERLQGRGRQD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SITALIN-A3(2) / M145;
MIDLINE-21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Thomson N., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Marren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome sequence of the model actinomycete Streptomyces coelicolor {\rm A3}\,(2)\,.\,,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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STRAIN=A31(2);
James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                              241 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                        348 GAGMRSHPGVTATFCEALAAVGVNIELISTSE 379
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EMBL, AL939117; CAB45482.1; -.

InterPro; IPR001049; Aa Kinase.

InterPro; IPR001341; ASPartate kinase.

InterPro; IPR001341; Aspartate kinase.
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ASK OR SC03615 OR SC66T3.26C.
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Submitted (JUN-1999) t
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                                                                                                                                                                                                                                                                  296 RLQ-----GRGRQDRHHLHLLPQTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLIGAG 350
                                                                                                                                                                                                                                                                                                                                                              296 VLQNVSNTSSGRID--ITFILSKANGPKAVASLEKIKEELGFSSVLYDDHVGKVSLVGAG 353
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65 EMDMLITAGDGISNALVAMAISAQGAQAWSFTGSQAGVVTTAVHGNARIIDVTPSRVSER 124
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                                               LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP
                                                                        125 LEQGYVALVAGFQGVAQDTKDITTLGRGGSDTTAVALAAALNADVCEIYSDVDGVYSADP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corynebacterium_crenatum.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + L-ASPARTATE = ADP + 4-PHOSPHO-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.8%; Score 1224.5; DB 2; Length 421; 64.0%; Pred. No. 1.3e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
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"Cloning and sequence analysis of aspartokinase genes from
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 13, Last annotation update)
Aspartokinase LysC alpha subunit (EC 2.7.2.4) (Aspartate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         354 MRSHPGVTATFCEALCKVGVNIEIINTSE 382
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InterPro; IPR001048; Aa kinase.
InterPro; IPR001341; ACT.
InterPro; IPR001341; Aspartate kinase.
InterPro; IPR005560; Asp_kin_monofn.
Pfam; PF00696; aakinase; I.
Pfam; PF01842; ACT; 2.
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Best Local Similarity
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STGLTDIS-----FTLPKAEGRKAIDALERAKGSIGFESLRYDDQIAKISLVGAGMKT 357
ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 120
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                    RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                             241 IK-DVPMEDPILIGVAHDRSEAKVIIVGLPDIPGYAAKVFRAVARRR-----RQHRHGA
                                                            LEEGRVVLVAGFOGVSQDTKDVTTLGRGSDTTAVAMAAALGADVCEIYTDVDGIFSADP
                                                                                                                                                                                                          294 AERLOGRGRODRHHLHLILPQTSGPPPWKWWTRSETRSASTQLLYDDHIGKVSLIGAGMRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDINE=21110452; PubMed=11182319; Silakowski B., Nordsiek G., Kunze B., Blocker H., Muller R.; Silakowski B., Nordsiek G., Kunze B., Blocker H., Muller R.; Novel features in a combined polyketide synthase/non-ribosomal peptide synthetase: the myxalamid biosynthetic gene cluster of temyxobacterium Stigmatella aurantiaca Sgals."; Chem. Biol. 8:59-69(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 13, Last annotation update)
Putative aspatrokinase (EC 2.7.2.4) (Aspartate kinase).
Stigmatella aurantiaca.
Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales; Cystobacterinee; Cystobacteriae; Cystobacteriae; Cystobacteriae; Cystobacteriae; Missella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 434;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46023 MW; D400C1992D888B56 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- SIMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY.
EMBL, AF319998, AAK57182.1; -
INTERPO; IPR001048; Aa kinase.
INTERPO; IPR00213, AcT.
INTERPO; IPR001341; ASPARTATE kinase.
INTERPO; IPR001341; ASPARTATE kinase.
INTERPO; IPR001057; Glu_5kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.4%; Score 821; DB 2;
44.3%; Pred. No. 2.2e-47;
iive 79; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00696; aakinase; 1.
Pfam; PF01842; ACT; 2.
PRINTS; PR00474; GLU5KINASE.
TIGRPAMS; TIGR00657; asp_kinases; 1.
TIGRPAMS; TIGR00656; asp_kinases; 1.
PROSTPMS; TIGR00656; asp_Kin_monofn; 1.
Rinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                   358 NPGVTAGFFEALSDAGVNIELISTSE 383
                                                                                                                                                                                                                                                                                                                      354 HPGVTATFCEALAAVGVNIELISTSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 44.3 es 178; Conservative
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Matches
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                                                                                                                                                                                                                                       ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 120
                                                                                                                                                                                                                                                           ELDMLLTAGERISMALLAMAIKNIGHEAQSFTGSQAGVITDSVHNKARIIDVTPGRIRTS 124
                                                                                                                                                                                                                                                                                                         LEEGRVVLVAGFOGVSODIKDVIILGRGGSDITAVAMAAALGADVCEIYIDVDGIFSADP 180
                                                                                                                                                                                                                                                                                                                        291
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                                                                                                                                                                                           5 VQKYGGSSVADAEGIKRVAKRIVEAKKNGNQVVAVVSAMGDTIDELIDLAEQVSPIPAGR
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                                                                                                                                                                          1 VOKYGGSSVADAERIRRVAERIVATKKQGNDVVVVSAMGDTTDDLLDLAQQVCPAPPR
                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Amplification of the ask-asd operon in aminoethoxyvinylglycine-
producing Streptomyces sp. NRR 5331 results in stimulation of
aminoethoxyvinylglycine production.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                            16;
                                                                                                             425;
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Bacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBL_TaxID=159599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81; Indels
                                                                                                            Query Match 52.0%; Score 1141; DB 16; Length Best Local Similarity 61.6%; Pred. No. 5.6e-69; Matches 239; Conservative 54; Mismatches 79; Indels
                                                                Complete protecme. 
E 425 AA; 44779 MW; 4A61177D9D128D15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  423 AA; 44581 MW; 6DA2938627D9366A CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             423
 Pfam, PF01842; ACT; 2. TIGRPAMS; TIGRO0657; asp. kinases; 1. TIGRPAMS; TIGRO0656; asp. kin monofn; 1. PROSITE; PS00324; ASPARTOKINĀSB; 1.
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01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
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STRAIN=NRRL 5331;
Cuadrado Y.;
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Best Local Simil
Matches 233; C
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244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 -EDKIMEKLKVSGVTAKNDQARITIAGVPDKPGLAAGLFGELSSKHILVDMIVQSSPHNG 302
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                                                                                                                                                                                                                                                                                                                                                                                                            358 IAIAGAGMIGRPGIAAKMFKTLADVGVNIEMISTSEVKVSCVIDQRDADRAIAALSN 414
                                                                                                                                                                                                                                                                                                                                                                            344 VSLIGAGMRSHPGVTATFCEALAAVGVNIELISTSE------DQR--SRCCAATPN 391
                                                                            PRIVRNARKLDTVTFBEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVG
                                                                                                         185 PRLVPEAQLMAEITCDEMLELASLGAKVIHPRAVEIARNYGIPLVVRSSWSDEPGTKVVA
                                                                                                                                                                           240 SIKDVPMEDPILT-----GVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRR----
                                                                                                                                                                                                                                                                             ---RQHRHGAAERLQGRGRQDRHHLHLLPQTSGPPPWKNWTRSETRSASTQLLYDDHIGK
                                                                                                                                                                                                                                                                                                                             301 LIIQSIHDGNSNDIAFTVVKDLLNTABAVTSAIAPALRSYPEADQBA---BIIVEKGIAK
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Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.6%; Score 803; DB 16; Length 405; 45.2%; Pred. No. 3.2e-46; Live 77; Mismatches 113; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE011255; AAN47892.1; -.
Kinase; Transferase; Complete proteome.
SROHENCE 405 AA; 43059 MW; DE30E782AD0CD6D9 CRC64;
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Last sequence update)
Last annotation update)
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LYSC OR LA0693.
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                                                                               RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS 240
                                                                                                                                                                              200 NMVPAARKLERIAYEEMLELASVGAKVIQIRSVEFAMKYKVPLWVKSSFIDDPGTLVCE- 258
                                                                                                                                                                                                                                                                          318 RIDVIFIVGRAD-----LIKA------KDVVKKIAKSVKAEGVEIDDQVSKVSIVGVGM 365
                                               LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 180
                                                                                                                                                                                                                                                241 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARR------RRQHRHG 292
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EQDVVVATGEQVSIGLVALAIQTQKRKAVSFLGHQVRITTDSTFSKARIKSIDAERIVDA 140
                                                                                                                                                                                                                                                                                                                                               AABRLQGRGRQDRHHLHLLPQTSGPPPWKNWTRSETRSASTQ-LLYDDHIGKVSLIGAGM 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RSHPGVTATFCEALAAVGVNIELISTSEDQRSRCCAATPNWT 393
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SEQUENCE 600 AA, 63533 MW; B30B7101E9FC4D46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroccoccales; Synechocystis.
NCBI TaxID=1148;
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Last annotation update)
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TIGRFAMS; TIGR00656; asp_kin_monofn; 1.
PROSITE; PS00324; ASPARTOKINĀSE; 1.
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InterPro, IPR001048; Aa kinase.
InterPro, IPR002912; ACT
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Pfam; PF01842; ACT; 4.
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SEQUENCE FROM N.A.
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Tabata S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                 Motoyama H., Anazawa H.; "Analysis of the nucleotide sequence of lysC of Methylobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                             43;
                                                                                                               Methylobacillus glycogenes.
Bacteria, Proteobacteria, Betaproteobacteria, Methylophilales,
Methylophilaccae, Methylobacillus.
NCBI_TaxID=406,
                                                                                                                                                                                                                      glycogenes.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + L-ASPARTATE = ADP + 4-PHOSPHO-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 408;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
36.4%; Score /ye.s; Lc., L.,
Best Local Similarity 41.7%; Pred. No. 6.5e-46;
Matches 168; Conservative 78; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       341 IGKVSLIGAGMRSHPGVTATFCEALAAVGVNIELISTSEDQRS 383
                                                                                                                                                                                                                                                                                                                                                                                                               44328 MW; 3894F2315A6EBD75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             342 TAKVSVVGVGMRSHVGIVSQMFRTLAEEGINIQMISTSEIQIS
                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY EMBL; AB038354; BAB84686.1; -.
                                                                  01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Aspartate kinase (EC 2.7.2.4) (Aspartokinase).
                                 408 AA
                                                                                                                                                                                                                                                                                        Interpro; IPR001048; Aa Kinase.
Interpro; IPR00212; ACT.
Interpro; IPR001341; Acpartate_kinase.
Interpro; IPR001341; Aspartate_kinase.
Interpro; IPR00656; Asparin_monofn.
Pfam; PF00696; Act; 2.
TIGRPAMS; TIGR00657; asp_kinases; 1.
TIGRPAMS; TIGR00656; asp_kin monofn; 1.
Kinase; Transferase.
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01-JUN-2002 (
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                                Q8RU02
         RESULT 12
Q8RU02
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RESULT 13 Q8DHW0 ID Q8

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                                                                                                                                                                                                                                               Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokaka C., Kohara M., Matsumoto M., Matsumo A., Nakazaki N., Shimpo S., Sugimoto M., Tabeuchi C., Yamada M., Tabata S., "Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1."; mophilic cyanobacterium DNA Res. 9:12:130(2002).

EMBL, AP005375, BAC09385.1; -...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 599;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
35.9%; Score 786.5; DB 16; Length
Best Local Similarity 45.7%; Pred. No. 7e-45;
Matches 184; Conservative 67; Mismatches 129; Indels
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                                                                                                   Synechococcus elongatus (Thermosynechococcus elongatus).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBL_TaxID=32046;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      346 LIGAGMRSHPGVTATFCEALAAVGVNIELISTSEDQRSRCCAA
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Kaneko T., Nakamura Y., Wolk C.P.,
                                                                                                                                                                                                           STRAIN=BP-1;
MEDLINE=22225144; PubMed=12240834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anabaena sp. (strain PCC 7120)
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233,
23,
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238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 QSIH-----SHONSIDAFTVTTPILKRAEAVAAAIAPSLRSP-----SHPKSDEAE 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 120
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Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki M., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaana sp. strain PCC 7120.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.4%; Score 776.5; DB 16; Length 606; 43.2%; Pred. No. 3.3e-44; ive 74; Mismatches 115; Indels 41;
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SEQUENCE FROM N.A.
STRAINENCC 2705;
WEDLINE=22294977; PubMed=12381787;
SCHBIL M.A., Karmirantzou M., Shel B., Vilanova D., Berger B., Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M., Pridmore R.D., Arigoni F.;
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Bacteria, Actinobacteria, Actinobacteridae, Bifidobacteriales,
Blidobacteriaceae; Bifidobacterium.
NCBI_TaxID=216816;
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Last annotation update)
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TIGRFAMS; TIGR00656; asp_kin monofn; 1.
PROSITE; PS00324; ASPARTOKINASE; 1.
                                                                                                                                                                                                       EMBL; AP003593; BAB75343.1; -.
InterPro; IPR001648; Aa kinase.
InterPro; IPR001341; AcT
InterPro; IPR001341; Aspartate_kinase.
InterPro; IPR005260; Asp kin_monofn.
Pfam; PF00696; aAkinase; 1.
Pfam; PF00696; AcT; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            606 AA;
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les 175; Conserv
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AC 08G6Y6;
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DF ASPATOI
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61 ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 180
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                                          to the human gastrointestinal tract.";
Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
EMBL. AE014669; AAN24323.1;
SKinase; Complete proteome.
SEQUENCE 254 AA; 27041 MW; 28D9F48C68822225 CRC64;
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64.3%; Pred. No. 1.7e-44;
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Matches 153; Conservative
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Sequence Sequence Sequence 20601. A Sequence 1953, A Sequence 3979, Appli Sequence 30698, A Sequence 2, Appli Sequence 5687, Appli S

27463, A 31388, A 2, Appli 6, Appli 6, Appli 2, Appli

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APPLICANT: Skeiky; Yasir A.W.
APPLICANT: Skeiky; Yasir A.W.
APPLICANT: Skeiky; Yasir A.W.
APPLICANT: Skeiky; Yasir A.W.
APPLICANT: Campos-Neco, Antonio
APPLICANT: Campos-Neco, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Washing. Daniel B. B.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
STATE: Washington
CONTRY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER: IBM PC Compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: BAREATION IN Release #1.0, Version #1.30
COMPUTER: IBM PC Compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CLASSIFICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
TELEPHONE: (206) 682-6931
TELEPHONE: (206) 682-6931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 324; DB 3; Length 66; larity 100.0%; Pred. No. 2.3e-37; Conservative 0; Mismatches 0; Indels
                 US-09-046-086-2
US-09-524-643-2
US-09-252-991A-31388
US-08-336-4088-2
US-08-36-4088-2
US-08-36-115-6
US-08-252-991A-30601
US-09-252-991A-19533
US-09-134-010-399-2
US-09-134-010-399-3
US-09-134-010-399-3
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US-09-107-535-2
US-09-107-535-2
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US-09-252-991A-30698
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US-09-107-535-2
                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 77, Application US/08818112
Patent No. 6290969
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 66; Conserv
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US-08-818-112-77
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Sequence 77, Appl Sequence 78, Appl Sequence 78, Appl Sequence 78, Appl Sequence 209, App Sequence 219, App Sequence 7, Appl Sequence 7, Appl Sequence 7, Appl Sequence 7, Appl Sequence 176, App Sequence 176, App Sequence 24373, App Sequence 24373, App Sequence 24373, App Sequence 24373, App Sequence 24373, App Sequence 24373, App Sequence 24373, App Sequence 24373, App Sequence 27169, App Sequence 27169, App Sequence 27169, App Sequence 27169, App Sequence 27169, App Sequence 5, Appli
                                                                                                                                 November 21, 2003, 15:58:31; Search time 1.39184 Seconds (without alignments) 2006.354 Million cell updates/sec
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1 VIDIIGTSPTSWEQAAAEAV.......KITYRIKLEVSFKMRPAQPR 66
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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                 GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-09-05-556-78

US-09-072-596-78

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US-09-072-591A-21917

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US-09-072-591A-25318

US-09-031-392-7

US-09-031-392-7

US-09-031-392-7

US-09-031-392-7

US-09-031-352-9

US-09-071-035-174

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US-09-071-035-174

US-09-071-035-176

US-09-172-423-1

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US-09-252-991A-16702
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Maximum Match 100%
Listing first 45 summaries
                                                                                            protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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US-09-072-596-78
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                                          1 VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM 60
VIDIIGTSPISWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM 60
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 78, Application US/08818111

Patent No. 6338852

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Olllon, Davin C.
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Transcript Connection Consequence Applicant: Vedvick, Thomas S.
APPLICANT: Transcript Consequence Applicant: Vedvick, Thomas S.
APPLICANT: Transcript Consequence Application Consequence Application Consequence Application Consequence Application Consequence Application Consequence Application Consequence Application Consequence Application Consequence Application Consequence Application Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Consequence Conseq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-09-056-556-77
US-09-056-556-77
Sequence 77, Application US/09056556
Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 78:
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Best Local Similarity 100.0
Matches 66; Conservative
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STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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US-08-818-111-78
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TUBERCULOSIS
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APPLICANT: Skeiky, Yasir A.W.

PEPLICANT: Dillon, Davin C.

IIIIE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED AND BERKY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INCORNATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Kaymond
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael G.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Hendrickson, Ronald C.
ATITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 324; DB 4; Length 66; Best Local Similarity 100.0%; Pred. No. 2.3e-37; Matches 66; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                 COUNTRY: Sealcre
COUNTRY: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER: ELADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION NUMBER: 21,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELEFACOM (206) 682-6031
INPORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 78, Application US/09072596
; Patent No. 6458366
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CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDITM TYPE: Floppy disk
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ADDRESSEE: SEED and
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                                                                                                                                                                             1 VIDIIGTSPISWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM
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                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Shilon, Davin C.
APPLICANT: Campos-Weto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Thomas S.
APPLICANT: Lodes, Michael B.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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                                                                          100.0%; Score 324, DB 4, Length 802, 100.0%; Pred. No. 5.9e-36; ive 0; Mismatches 0; Indels
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COUNTRY: USA
ZIP: 98104-7092
COMPUTER: USA
COMPUTER: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Parentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                          09, Application US/09072596
6458366
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NAME: MAKI, David J.
REGISTRATION UNMBER: 31,392
REFRENCK/DOCKET NUMBER: 2101;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAK: (206) 632-6031
INFORMATION FOR SEQ ID NO: 209:
SEQUENCE CHARACTERISTICS:
LENGTH: 802 mmino acids
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Best Local Similarity 100..
...hes 66; Conservative
                                                                                                    Best Local Similarity 100.
Matches 66; Conservative
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       ; TOPOLOGY: linear
US-09-056-556-214
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US-09-072-596-209
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US-09-072-596-209
                                                                                  Query Match
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Patent No. 6350456

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Read, Steven G.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Dillon, Davin C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 324; DB 4; Length 66; Best Local Similarity 100.0%; Pred. No. 2.3e-37; Matches 66; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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STATE: Washing.
COUNTRY: USA

ZIP: 98104-7092

ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION NUMBER: 31,392
ATTORNEY/AGENT INFORMATION:
MAME: Maki, David J.
REGISTAATION NUMBER: 31,392
REBERNCE/DOCKET NUMBER: 210121.457
FELECOMMUNICATION INFORMATION:
COOKET NUMBER: 210121.457
FELECOMMUNICATION INFORMATION:
COOKET NUMBER: 210121.457

FELECOMMUNICATION INFORMATION:
COOKET NUMBER: 210121.457

FELECOMMUNICATION INFORMATION:
COOKET NUMBER: 210121.457

FELECOMMUNICATION OF 214:
CROSSIBLE COOKET NUMBER: 210121.457

FELECOMMUNICATION OF 214:
CROSSIBLE COOKET NUMBER: 210121.457

FELECOMMUNICATION OF 214:
CROSSIBLE COOKET NUMBER: 210121.457
                                      CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596

FILING DATE: 05-MAY-1998

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392

REGISTRATION NUMBER: 31,392

REGISTRATION NUMBER: 31,392

REGISTRATION INFORMATION:
TELEPHONE: (206) 622-4900

TELEPHONE: (206) 622-4900

TELEFAX: (206) 622-4900

TELEFAX: (206) 622-6031

INFORMATION FOR SEQ ID NO: 78: SEQUENCE CHARACTERISTICS:
LEMOGTH: 66 amino acids

LYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 6300
CITY: Seattle
The: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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US-09-056-556-214
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US-09-072-596-78
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Sequence 25318, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 WVDFIDTQGTFCEQAELETAQALFHAQEVHNDAQVLHVLKRKFAGGSTENSPLGERLEVD 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VIDIIGTSPTSWEQA---AAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVS 57
                                                                                                                                                                                                                                                                                                                                                                                                     2 IDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM 60
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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US-09-16
Sequence 16, Application US/09300909
Sequence 16, Application US/09300909
Sequence 16, Application US/09300909
Sequence 16, Application US/09300909
Sequence 16, Application US/09300909
Sequence 16, Application US/09300909
Sequence 17 TILE OF INVENTION: PREPARATION OF HUMAN PAPILLOMAVIRUS E1 HAVING
TITLE OF INVENTION: HELICASE ACTIVITY AND METHOD THEREFOR
NUMBER OF SEQUENCES: 27
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 657;
                                                                                                                                                                                                                                                                                                             21.3%; Score 69; DB 4; Length 92; 25.4%; Pred. No. 0.038;
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                                                                                                                                                                                                                                                                                                                                                      27; Indels
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SOFTWARE PATENTIAN PATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/300,909
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/083,942
FILING DATE: 01-MAY-1998
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
; CURRENT APPLICATION NUMBER: US/09/252,991A; CURRENT FILING DATE: 1999-02-18; PRIOR APPLICATION NUMBER: US 60/074,788; PRIOR FILING DATE: 1998-02-18; PRIOR APPLICATION NUMBER: US 60/094,190; PRIOR FILING DATE: 1998-07-27; NUMBER OF SEQ ID NOS: 33142; SEQ ID NO 21917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 61.5; DI
Pred. No. 5.3;
                                                                                                                                                                                                                                                                                                                                                      17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                  TYPE: PRT; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.0%;
29.2%;
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Best Local Similarity 25.48
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Best Local Similarity 29.24
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-09-300-909-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: six
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :: |
107 TELSP 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
US-09-252-991A-25318
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BACEL NO. 6551795
CENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                          TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VIDIIGTSPISWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·;
                                                                                                                                                                           APPLICANT: Reed, Steven G.
APPLICANT: Reed, Yasir A.W.
APPLICANT: Skirky, Yasir A.W.
APPLICANT: Campos Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Lodes, Michael R.
APPLICANT: Lodes, Michael G.
APPLICANT: Renaid C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATER: IBM PC compatible
COMPATER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLESSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 324; DB 4; 1
100.0%; Pred. No. 5.9e-36;
iive 0, Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                   Sequence 346, Application US/09072596
Patent No. 6458366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 346:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 802 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RPAQPR 66
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            RPAQPR 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
US-09-252-991A-21917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                    US-09-072-596-346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-072-596-346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Matches
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임 ò 엄

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TOPOLOGY:
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                                                                                   RESULT 12
US-09-299-549-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-610-417-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 VGLAĞVNPDGQGDRLEBABQRAQLVVBDQRVALGAASGGBQHRGVDQGVBVDQVLBQ 226
                                                                                                                                                                                                                                                                                                                                                                                                                  -----RVIEQDMAVDSAGKITYR 51
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                                                                                                                                                                                                                                                                                                                Query Match
17.9%; Score 58; DB 4; Length 446;
Best Local Similarity 24.7%; Pred. No. 9.7;
Matches 18; Conservative 14; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 17.7%; Score 57.5; DB 2; Length 5 Best Local Similarity 43.1%; Pred. No. 13; Matches 22; Conservative 9; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tartaglia, Louis A.
APPLICANT: Weng, Xu.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING GLUTEX AND USES THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
CCUNTRY: USA
ZIP: 02110-2804
ZIP: 02110-2804
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: IBM COMPATIBLE
COMPUTER: TBM COMPATIBLE
COMPUTER: TBM COMPATIBLE
COMPUTER: TBM COMPATIBLE
COMPUTER: TBM COMPATIBLE
COMPATING SYSTEM: Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/031,392
FILING DATE: 26-FEB-1998
ATTORNEY/AGNT INFORMATION:
NAME: Mekilejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFRENCE/DOCKET NUMBER: 07334/072001
TELECOMMUNICATION INFORMATION:
TELECHONE: 617/542-5770
TELECHONE: 617/542-5770
TELECHONE: 011542-5770
TELECHONE: 011542-5770
TELECHONE: 011542-5770
TELECHONE: 011542-5770
TELEPAX: 6117/542-8906
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF 252 ID NOS: 33142
SEQ ID NO 25318
LENGTH: 446
TYPE: PRT
CRGANIGM: Pseudomonas aeruginosa
US-09-252-991A-25318
                                                                                                                                                                                                                                                                                                                                                                                                             2 IDIIGTSPTSWEQAAAEAVQRARDSVDDIRVA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/09031392
Patent No. 5942398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 500 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-031-392-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 ARIGATVDRRGDO 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 IKLEVSFKMRPAQ 64
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US-09-031-392-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: 1
STATE:
                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
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Gaps
227 EAAAKKALQTLRGWDSVDR-EVAEIRQEDEAEKAAGFISV-LKL---FRMR 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 EQAAAEAVQRAR--DSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3; Length 500;
                                                                                                               Sequence 7, Application US/09299549

Patent No. 6136547

GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.

APPLICANT: Weng, Xun

TITLE OF INVENTION: GLUTEX AND USES THEREOF

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 25 Franklin Street

CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Tartaglia, Louis A.
Meng, Xun
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
GLUTEX AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Mindows95
SOFTWARE: FastSEC for Windows Version 2.0
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,549
FILING DATE: 26-APR-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/031,392
FILING DATE: 26-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Melklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
17.7%; Score 57.5; D
Best Local Similarity 43.1%; Pred. No. 13;
Matches 22; Conservative 9; Mismatches
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CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07334/072002
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Patent No. 6346374
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                500 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein US-09-299-549-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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Query Match
Best Local Similarity
US-09-328-352-8072
                                                                                                                                                                                                                                                      SEQ ID NO 8072
LENGTH: 900
                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT:
MARC J. RUDenfield et al.
APPLICANT:
MARC J. RUDenfield et al.
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PLILING DATE: 1999-02-18
PRIOR PLILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-7
NUMBER OF SEQ ID NOS: 33142
NUMBER OF SEQ ID NOS: 33142
LENGTH: 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      227 EAAAKKALQTLRGWDSVDR-EVAEIRQEDEAEKAAGFISV-LKL---FRMR 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20; Indels 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 17.7%; Score 57.5; DB 4; Length 500; Best Local Similarity 43.1%; Pred. No. 13; Matches 22; Conservative 9; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 633;
                                MEDIUM TYPE: Diskette
CONBUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FESSES for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/610,417
FILING DATE: 05-Jul-2000
PRION APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/299,549
FILING DATE: UNKnown:
ATTONEY/AGENT INFORMATION:
NAME: Welklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/072002
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELEEX: 200154
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHRACHTERISTICS:
SEQUENCE CHRACHTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 17.7%; Score 57.5; DE Similarity 31.7%; Pred. No. 18; 20; Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-09-252-991A-26229
; Sequence 26229, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 500 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26229
  COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 GKI 48
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317 GAV 319

RESULT 15

; Sequence 8072, Application US/09328352
; Patent No. 6563958
; GENERAL INFORMATION:
; APPLICANT'S GAZY L. Breton et al.
; TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTOS9-0378
; CURRENT APPLICANTION NUMBER: US/09/328,352
; CURRENT PILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 8072
; LENGTH: 900
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
; US-09-328-352-8072
; CORSENTA MATCH
Best Local Similarity 31.7%; Pred. No. 28;
Matches 19; Conservative 9; Mismatches 21; Indels 11; Gaps 2;
Matches 19; Conservative 9; Mismatches 21; Indels 11; Gaps 2;

Qy 13 EQARABACWALUTEORAKATLDAMRAH--QCDSAAQSAPKARAVVKKRGGGTVKPA 179

Search Completed: November 21, 2003, 16:11:38
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Mycobacterium anti Mycobacterium tube M. tuberculosis fu M. tuberculosis fus M. tuberculosis fus Antigenic fusion p M. tuberculosis fo Drosophila melanog Human papillomavir Human papillomavir

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Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant; skin testing; M.tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis antigen TbRa3.
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ABP57388
AAR21516
AAY40501
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AAY39224
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ABU05888
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AAB39229
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95US-0523436.
95US-0533634.
96US-0620874.
96US-0659683.
 AAW32433 standard; Protein;
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Twardzik DR, Vedvick TH;
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(CORI-) CORIXA
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22-SEP-1995;
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           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                            1107863 segs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
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AAW32365
AAW81668
AAW64305
AAX39107
AAX3970
AAE29718
AAE17582
AAW81746
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Gapop 10.0 , Gapext 0.5
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324
1 VIDIIGTSPTSWEQAABAV.
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Maximum DB seq length: 200000000
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Human cytoskeleton Arabidopsis thalia Plant SDF encoded Human mddt protein Human transient re

Human secreted pro Human cancer assoc Drosophila melanog Fruit fly E93 prog Gene 2 human secre

Human ovarian anti

Human Canlon prote Human cation chann

Human transporter

Human BION1 protei

Polyfunctional pro A. thaliana yaeL p

Skeiky YAW;

Score

Result Š. Cotton (+)-delta-c M. tuberculosis an Streptomyces virid Sucrose-specific p

Drosophila melanog Salmonella typhi c Human ORF313 prote

(or

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A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or modifications). The present sequence represents a M.tuberculosis antigen, TSAS3. The bresent sequence represents a M.tuberculosis antigen, TSAS3. The hamunogenic polypeptide can be used to diagnose antibodies in frection by forming complexes with specific antibodies in the sample. Fragments of DNA encoding the immunogenic polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen, especially monoclonal antibodies or equivalent polyclonal antibodies, are also used for diagnosis.
                                                                                                                                                                                                                                                                                                                                                         AAW81668 standard; Protein; 66 AA.
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96US-0730510.
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Best Local Similarity 100.
Matches 66, Conservative
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                                   New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are useful in vaccines for prevention or treatment of tuberculosis, also
                                                                                                        A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (is variant differing only in conservative substitutions and/or modifications). The present sequence represents a M tuberculosis antigen, TDRa3. The immunogenic protein, and fusion proteins containing one or more of the proteins or one of the proteins ESAT-6, are useful in vaccines, preferably when formulated with a M. tuberculosis (for treatment or prevention).
                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New immunogenic polypeptide(s) from soluble M. tuberculosis antigens - useful for diagnosis of M. tuberculosis infection
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                                                                                                                                                                                                                                                   Query Match
100.0%; Score 324; DB 18; Length 66;
Best Local Similarity 100.0%; Pred. No. 1e-35;
Matches 66; Conservative 0; Mismatches 0; Indels 0
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                                                                                   Example 3; Page 113; 168pp; English.
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95US-0523435.
95US-0532136.
96US-0620280.
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Twardzik DR, Vedvick TH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis
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N-PSDB; AAT91412.
1997-192903/17.
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          N-PSDB; AAT91475
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                                                            for diagnosis
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22-SEP-1995;
22-MAR-1996;
05-JUN-1996;
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                                                                           Gaps
                                                                           ..
   Length
                                                                           Indels
100.0%; Score 324; DB 18;
100.0%; Pred. No. 1e-35;
ive 0; Mismatches 0;
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Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;

    4. tuberculosis immunogenic polypeptide TbRa3.

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WO9942076-A2
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18-FEB-1998;
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                                                            1 VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM
                                              1 VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated Mycobacterium tuberculosis polypeptides and DNA - used to develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis
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  DB 19; Length 66;
                         Indels
                                                                                                                                                                                                                                                                          Tuberculosis; infection; diagnosis; antigen; TbRa3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dillon DC, Houghton R, Lodes MJ; y YAW, Twardzik DR, Vedvick TS;
100.0%; Score 324; DB 19;
100.0%; Pred. No. 1e-35;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                   Mycobacterium tuberculosis antigen TbRa3.
                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis strain H37Ra.
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                                                                                                                                                                              AAW64305 standard; Protein; 66 AA.
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96US-0729622.
                                                                                                                                                                                                                            (first entry)
            Similarity 100.
66; Conservative
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Reed SG, Skeiky YAW,
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Best Local Similarity
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N-PSDB; AAV44353.
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9
                                   1 VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM 60
1 VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antigens from Mycobacterium tuberculosis useful in diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection; immune response; skin test.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Houghton R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M. tuberculosis antigen TbRa3 amino acid seguence.
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Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Page 107; 299pp; English.
                                                                                                                                                                                                                                                                                                                                  AA.
                                                                                                                                                                                                                                                                                                                               AAY39107 standard; Protein; 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US03268.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAZ19263.
                                                                                                                  61 RPAOPR
                                                                                                                                                                            61 RPAOPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RPAOPR
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The invention relates to a recombinant nucleic acid molecule encoding a least like in polypeptide. The recombinant nucleic acid comprises a heterologous polymentedide. The recombinant nucleic acid comprises a heterologous polymucleotide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polymucleotide sequence encoding a polypeptide or its fragment. The Leishmania polymucleotide is selected from TSA, LeIF, MIS, and 6H polymucleotides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polynucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is
                                                                                                                                                                                                                                                                                                                    New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 324; DB 23; Length 66; 100.0%; Pred. No. 1e-35; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 107-108; 155pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium species TbRa3 protein.
                                                                                                                                                                                                                         Guderian J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ä.
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                                                                                                 13-MAR-2002; 2002WO-US08223.
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                                                                                                                                       13-MAR-2001; 2001US-275837P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                       Skeiky Y, Brannon M,
                                                                                                                                                                                                                                                            WPI; 2002-759844/82
                                                                                                                                                                                (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RPAQPR 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium sp.
                                                                                                                                                                                                                                                                                 N-PSDB; AAD47095
                   WO200272792-A2
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                                                        19-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VIDIIGTSPISWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                       Antigen; diagnosis; detection; infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaccine; immunity; diagnostic agent; gene therapy; TbRa3 antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide comprising antigenic portions of M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 20; Length 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Houghton R;
Z, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis TbRa3 antigenic protein.

    M. tuberculosis recombinant antigen protein TbRa3.

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100.0%; Pred. No. 1e-35;
ive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Campos-Neto A, Dillon DC, Hendrickson RC, H.
Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Page 151; 323pp; English
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                                                        AAY38970 standard; Protein; 66 AA.
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98US-0024753.
                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US03265
                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORI-) CORIXA CORP.
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18-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                 26-AUG-1999.
                                                                                                 AAY38970;
                                                                                                                                                                                                                                               vaccine;
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New

RESULT 7 AAE29718

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1 VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM
                                                                                                                                                                                                                                                                Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the fusion protein TbF-2 which is composed eliminogenic polypeptides from Mycobacterium tuberculosis (MT). This protein is used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tuberculosis; infection; diagnosis; 38 kDa antigen; TbRa3; DPEP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dillon DC, Houghton R, Lodes MJ; YAW, Twardzik DR, Vedvick TS;
                                                                                                                                         Campos-Neto A, Dillon DC, Houghton R, Lodes MJ;
Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 324; DB 19;
100.0%; Pred. No. 2.4e-34;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium antigen TbF2 protein fusion.
                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 208-211; 230pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW64379 standard; Protein; 802 AA.
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96US-0729622.
                                        .97US-0818112.
96US-0730510.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66; Conservative
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Reed SG, Skeiky YAW,
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                                                                                                     (CORI-) CORIXA CORP.
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N-PSDB; AAV55801.
                                                                                                                                                                                                        WPI; 1998-261042/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                802 AA;
                                                                                                                                                                                                                           N-PSDB; AAV64567
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                                        13-MAR-1997;
11-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-0CT-1997;
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11-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          임
                                                                                                                                                                                                                                                                                                                 The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with tuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. Sequences of the invention and prevention of Mycobacterium infection. The fusion proteins and the polynucleotides are useful as diagnosis, treatment and prevention of Mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or cell-mediated immunity against M: tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as immunogens to generate or alicit a protective immune response in a patient and for raising anti-M. tuberculosis antibodies in a non-human immal. Sequences of the invention are also used as vaccines. MTB32A fusion proteins of the invention are also used as vaccines. MTB32A fusion proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VIDIIGTSPISWEQAAAZAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKW 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                    Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in a subject -
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                                                                                                                                                                                                                                                                                   Claim 9; Page 123-124; 136pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M. tuberculosis fusion protein TbF-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW81746 standard; Protein; 802 AA
                                                                                                     Alderson M;
20-JUN-2000; 2000US-0597796
01-FEB-2001; 2001US-265737P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.00
These 66; Conservative
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Mycobacterium tuberculosis.
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                                                                                                                                         WPI; 2002-147798/19.
N-PSDB; AAD28353.
                                                            (CORI-) CORIXA CORP
                                                                                                     Reed S,
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                                                                                                     Skeiky Y,
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9 VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM 68
                                                                                                       This polypeptide comprises a fusion protein, designated TbF-2, composed of Mycobacterium tuberculosis antigens TbR31 (see AAW64295), 38 kDa antigen (see AAW64364), TD38-1 (see AAW64321) and DPEP (see AAW64322). It was produced by PCR amplification (see AAW44450-57) of the appropriate antigen DNA sequences, cloning into an expression vector, and expression in E. coli. TbF-2 can be used for serodiagnosis of tuberculosis. The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAW64291-W64379) comprising antigens, or fusion proteins, DNA sequences encoding such polypeptides, recombinant expression vectors and host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VIDIIGTSPISWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New fusion proteins useful for diagnosis, prevention and treatment of tuberculosis -
           New isolated Mycobacterium tuberculosis polypeptides and DNA - used to develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tuberculosis, antigen, fusion protein, TbF-2, TbRa3, 38kD; Tb38-1, DPEP, diagnosis, therapy, vaccine, immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents a recombinant Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 324; DB 19; Length 802; 100.0%; Pred. No. 2.4e-34; .ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis antigen fusion protein TbF-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Campos-Neto A;
                                                                             Example 7; Page 223-226; 250pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY32063 standard; Protein; 802 AA.
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98US-0223040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
hes 66; Conservative
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                                                                                                                                                                                                                                                                                                                                      802 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-OCT-1999
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1 VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's, DNAs encoding them, derived fusion proteins other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to
tetra-antigen fusion protein, termed TDF-2, composed of the antigens TDRa3, 39kD, TD38-1 and DDEP. The fusion protein is expressed in host cells using a vector carrying apolymucleotide (see AAZ20198) comprising the 4 coding sequences. The invention provides fusion proteins (see AAX3059-71) containing at least 2 M tuberculosis antigens. The new fusion proteins and polymucleotides encoding them are useful as vaccines for preventing tuberculosis (claimed) for diagnosis (via in vitro assays or intradermal skin tests for detection of anti-M, tuberculosis antibodies), monitoring of effective immunogens than mixtures of the individual protein
                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis, M. tuberculosis, antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection; immune response; skin test.
                                                                                                                                                                                                                                                                                     Length 802;
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R, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M. tuberculosis fusion protein TbF-6 amino acid sequence.
                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 324; DB 20;
Best Local Similarity 100.0%; Pred. No. 2.4e-34;
Matches 66; Conservative 0; Mismatches 0;
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Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 37; Page 271-273; 299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX39224 standard; Protein; 802 AA.
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98US-0025197.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-NOV-1999 (first entry)
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N-PSDB; AAZ19457.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RPAQPR 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 RPAQPR 74
                                                                                                                                                                                                                                                802 AA;
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                                                                                                                                                                                                               components.
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AAY39224
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The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's. DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion tuberculosis-immune subjects. AAZ19249 to AAZ19460 and AAX39083 to AAX39225 are used in the exemplification of the present invention.
                                                                                                                                                                                                                     9 VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKW
                                                                                                                                                                                              VIDIIGTSPTSWEQAAABAVQRARDSVDDIRVARVIEQDWAVDSAGKITYRIKLEVSFKM
                                                                                                                                                                 Gaps
M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T, B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AAZ1949 to AAZ19460 and AAX39083 to AAX39225 are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antigens from Mycobacterium tuberculosis useful in diagnostic
skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection; immune response; skin test.
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                                                                                                                                 Length 802;

    M. tuberculosis fusion protein TbF-2 amino acid sequence.

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                                                                                                                                                                 Indels
                                                                                                                                100.0%; Score 324; DB 20; 100.0%; Pred. No. 2.4e-34;
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Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                               AAY39176 standard; Protein; 802 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis.
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                                                                                                                                                                 66; Conservative
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                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                61 RPAQPR 66
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                                                                                                  802 AA;
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18-FEB-1998;
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                                                                      9 VIDIIGTSPTSWEQAAABAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel recombinant antigens and their encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 VIDIIGTSPTSWEQAAABAVQRARDSVDDIRVARVIEQDWAVDSAGKITYRIKLEVSFKW
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                                                 1 VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                          Gaps
                                                                                                                                                                                                                                                                                                 Antigen; diagnosis; detection; infection; antibody; immunisation; vaccine; immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptide comprising antigenic portions of M. tuberculosis
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Length 802;
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                          Indels
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100.0%; Pred. No. 2.4e-34;
ive 0; Mismatches 0;
100.0%; Score 324; DB 20; 100.0%; Pred. No. 2.4e-34;
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YAW, Twardzik DR,
                          0; Mismatches
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                                                                                                                                                                                                                                                                            M tuberculosis fusion protein TbF-6.
                                                                                                                                                                                                AAY39081 standard; Protein; 802 AA
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Lodes MJ, Reed SG, Skeiky
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                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                  (first entry)
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                           Conservative
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Best Local Similarity
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               Similarity
                                                                                                       61 RPAQPR 66
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N-PSDB; AAZ19245
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                                                                                                                                                                                                                                                   05-NOV-1999
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Matches
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This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                                                                                                                                              Antigen; diagnosis; detection; infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptide comprising antigenic portions of M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 324; DB 20; Length 802; Best Local Similarity 100.0%; Pred. No. 2.4e-34; Matches 66; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                    Houghton R;
R, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                    Campos-Neto A, Dillon DC, Hendrickson RC, Ho
Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 10; Page 251-253; 323pp; English.
                                                                                                                M. tuberculosis fusion protein TbF-2.
                            AAY39033 standard; Protein; 802 AA.
                                                                                                                                                                                                                                                                                                          98US-0072596.
                                                                                                                                                                                                                                                                                99WO-US03265
                                                                                                                                                                                        Mycobacterium tuberculosis
                                                                                  05-NOV-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-527416/44.
N-PSDB; AAZ19156.
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                                                                                                                                                             vaccine; immunity.
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                                                                                                                                                                                                                    WO9942118-A2
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                                                                                                                                                                                                                                                                                                          05-MAY-1998;
18-FEB-1998;
                                                                                                                                                                                                                                                  26-AUG-1999.
                                                        AAY39033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
RESULT 15
              AAY39033
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9 VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM 68

61 RPAQPR 66 RPAQPR 74

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Search completed: November 21, 2003, 16:03:12 Job time : 4.99592 secs

1 VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM

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Sequence 77, Appl Sequence 78, Appl Sequence 37, Appl Sequence 10, Appl Sequence 214, Appl Sequence 214, Appl Sequence 346, Appl Sequence 63, Appl Sequence 63, Appl Sequence 63, Appl Sequence 63, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl
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Sequence 2, Appli
Sequence 539, App
                                                                                                   November 21, 2003, 16:08:22 ; Search time 2.57415 Seconds (without alignments) 4680.740 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                               324
1 VIDIIGTSPTSWEQAAAEAV.......KITYRIKLEVSFKMRPAQPR 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_MEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/NEM_PUB_PEP:*
5: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
. GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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2 US-10-193-002-78
2 US-09-2872A-37
2 US-09-2873-214
2 US-10-084-843-214
2 US-10-193-002-346
2 US-10-193-002-346
2 US-10-193-002-346
2 US-10-193-002-346
3 US-10-184-60-10
5 US-10-16-225A-63
5 US-10-16-225A-63
6 US-10-16-225A-63
6 US-10-067-534-13952
8 US-10-0867-534-13952
6 US-10-0867-534-13952
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                                                                                                                                                                                                                                                                                                    666188 segs, 182559486 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length DB
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                                                                                                                                                                            Title:
Perfect score:
                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq
Maximum DB seq
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                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                          Run on:
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equence 8,	0-153-219-	12	d.	œ.	54.5	45	
Sequence 6, Appli	-10	15	1143	16.8	54.5	44	
equence 4,	0-153-219-	15	\circ	Ġ.	54.5	43	
equence 120	-10-156-761-	15	-	ė	54.5	42	
4,	19-801-574-44	σ	CA.	۲.	52	41	
equence 161	-10-097-340-16	15	œ	Ľ.	55	40	
equence 148	-10-156-761-	15	œ	۲.	55	99	
eguence 6,	-10-136-841-6	15	α	7.	55.5	38	
equence 5,	-10-120-145-	13	П	۲.	55.5	3.7	
edneuce e'	-09-826-581-	10	œ	۲.	55.5	36	
equence 2,	-10-278-536-	16	Ø	۲.	55.5	35	
quence 1, 1	09-851-682A-	σ	4	۲.	56	34	
12	-10-306-905-1	12	. 515	7	56	33	
equence 283	-10-029-386-2	13	O)	7	56	32	
equence 40,	-09-866-582-4	10	ᅥ		56.5	31	
equence 64,	-10-198-070-64	15	N		57	30	
equence 113	-10-156-761-	15	ശ		57.5	29	
equence 7,	-09-981-947A-	10	0		57.5	28	
equence 3,	-10-178-791-	15	m		58	27	
equence 1,	-10-178-791-1	13	3		53	26	
equence 72,	-10-198-070-7	15	ထ		28	25	
equence 63,	-10-198-070-6	15	α		58	24	
equence 108	10-198-070-1	15	_		58	23	
equence 23,	-10-210-152-2	12	\sim		S 8	22	
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equence 97,	-10-198-070-97	15	m		58	20	
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quence 1264	19-925-301-12	σ	σ'n.		58.5	18	
11,	-10-016-76	14	N		59	17	
26,	-09-905-176-2	10			59	16	

ALIGNMENTS

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REBULT 1

US-10-084-843-77

US-10-084-843-77

Sequence 77, Application US/10084843

Sequence 77, Application US/10084843

Publication No. US20030143243A1

GENERAL INFORMATION:
Skeiky, Yasir A.W.
Dillon, Davin G.
Campos Neco, Autonic
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hondfickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS

NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREE: Washington
CONPUTER: Washington
CONPUTER: Hashington
COMPUTER: IBM PC compatible
OFFRAING SYSTEM
MEDILCATION NUMBER: US/10/084,843

FILING DATE: SF-Feb-2002

CLASSIFICATION NUMBER: US/10/084,843

FILING DATE: SF-Feb-2002

ATTORNEY/AGENT INPERMATION:
NAME: Maki, IDAVIG J.

NAME: Maki, IDAVIG J.

NAME: Maki, IDAVIG J.
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Sequence 37, Application US/10098732A

Publication No. US20030175294A1

Publication No. US20030175294A1

GENERAL INFORMATION:

APPLICANT: Skeiky, Yasir

APPLICANT: Skeiky, Yasir

APPLICANT: Greixa Corporation

TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a

TITLE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION: Leishmania Antigen

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TITLE OF INVENTION: Leishmania Antigen

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TITLE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION: Leishmania Antigen

FILE REFERENCE: 0104058-012010US

CURRENT APPLICATION NUMBER: US 60/275,837

PRIOR APPLICATION UNMER: US 60/275,837

NUMBER OF SEQ ID NOS: 80

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Sheiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-00902003
CURRENT APPLICATION NUMBER: US/09/287,849
                                                                                                                                                                                                                                                                        1 VIDIIGTSPTSWEQAAABAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM 60
                                                                                                                                                                                                                                                                                                         1 VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM 60
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                                                                                                                                                                         Length 66;
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                                                                                                                                                                 100.0%; Score 324; DB 12;
100.0%; Pred. No. 1.7e-35;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 324; DB 12; Best Local Similarity 100.0%; Pred. No. 1.7e-35; Matches 66; Conservative 0; Mismatches 0;
                                                                TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQUENCE DESCRIPTION: SEQ ID NO: 78:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/09287849
Patent No. US20020009459A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
                                         STRANDEDNESS: single
                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 66; Conservative
             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
COTHER INFORMATION: TDRA3
US-10-098-732A-37
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US-09-287-849-10
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Lodes, Michael J.
Hendrickson, Ronald C.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                               Length 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
OPERATING SYSTEM: PC-DOS/WS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FLING DATE: 10-Jul-2002
CLASSIFICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STEEFS: 620 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 324; DB 12; Best Local Similarity 100.0%; Pred. No. 1.7e-35; Matches 66; Conservative 0; Mismatches 0;
RECISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHAX: (206) 682-6031
                                                                                                                                                                                                                                            ; TOPOLOGY: linear ; SEQUENCE DESCRIPTION: SEQ ID NO: 77: US-10-084-843-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence Supplication No. Constitution No. Constitution Security States A.W. Skeiky, Yasir A.W. Skeiky, Yasir A.W. Dillon, Davin C. Campos-Neto, Antonia Houghton, Raymond Vedvick, Thomas S. Vedvick, Thomas S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
US-10-193-002-78
; Sequence 78, Application US/10193002
; Publication No. US20030135026A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 66 amino acids
                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RPAQPR 66
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Gaps

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1 VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM
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Lodes, Michael J.
Hendrickson, Ronald C.
HITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
                                                                                                                                                                                                                                                                                                                     Length 802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PETALIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION - UNknown>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 324; DB 12; Best Local Similarity 100.0%; Pred. No. 3.8e-34; Matches 66; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
            REFERENCE/DOCKET NUMBER: 210121.411C9
                                                                                                                                                LENGTH: 802 amino acids
TYPE: amino acid
STRANDENESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 214:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 351, Application US/10084843 Publication No. US20030143243A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 351:
SEQUENCE CHARACTERISTICS:
LENGTH: 802 amino acids
TYPE: amino acid
                                                                          INFORMATION FOR SEQ ID NO: 214: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RPAQPR 66
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                                                                                                                                                                                                                                                                        US-10-084-843-214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence:tetra-fusion US-09-287-849-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .<u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 802;
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Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNO'
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: <unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 100.0%; Score 324; DB 9; 1 Similarity 100.0%; Pred. No. 3.8e-34; 66; Conservative 0; Mismatches 0:
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FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
CURRENT FILING DATE: 1999-04-07

PRIOR APPLICATION NUMBER: US 09/818,112

PRIOR FILING DATE: 1997-03-13

PRIOR PILING DATE: 1997-03-13

PRIOR PILING DATE: 1997-10-01

PRIOR PILING DATE: 1997-10-01

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-04-07

PRIOR FILING DATE: 1998-04-07

PRIOR FILING DATE: 1998-04-07

PRIOR PILING DATE: 1998-12-30

NUMBER OF SEQ ID NOS: 46

SOFTWARE: PATCHTIN Ver. 2.1

LENGTH: 802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 214, Application US/10084843
Publication No. US20030143243A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 66; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RPAQPR 66
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JS-10-193-002-346
99
Matches
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Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 324; DB 12; Length 802; 100.0%; Pred. No. 3.8e-34;
                                                                                                                                                                                                                               Length 802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIF: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORM:
MEDIUM TYPE: FLORM:
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                   Score 324; DB 12;
Pred. No. 3.8e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                              Mismatches
                        TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 351:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: SINGAR SEQUENCE DESCRIPTION: SEQ ID NO: 209: US-10-193-002-209
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Publication No. US20030135026A1
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NAME: Maki, David J.
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MATION FOR SEQ ID NO: 209:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
                                                                                                                                                                                                                                   100.0%;
100.0%;
STRANDEDNESS: single
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STATE: Washington
                                                                                                                                                                                                                                                                                                                  66; Conservative
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Best Local Similarity
Matches 66; Conserv
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Best Logal Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
US-10-193-002-209
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                                              1 VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM
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Skeiky, Yasir A.N.

Dillon, Davin C.

Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.

Twardzik, Daniel R.

Lodes, Michael J.

Hendrickson, Ronald C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 324; DB 12; Best Local Similarity 100.0%; Pred. No. 3.8e-34; Matches 66; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-0ul-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION UNBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 346:
US-10-193-002-346
                                                                                                                                                                                                                                                                                                               Sequence 346, Application US/10193002 Publication No. US20030135026A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (206) 622-4900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Maki, David J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ropology: linear
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                             61 RPAQPR 66
                                                                                                                                                                                           69 RPAQPR 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
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; IENGTH: 342
; TYPE: PRT
ORGANISM: Rickettsia prowazekii
US-10-166-225A-63
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272 SG 273
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                                         1 VIDIIGTSPTSWEQAAABAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence:tetra-fusion US-10-359-460-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

100.0%; Score 324; DB 12; Length 802;
Best Local Similarity 100.0%; Pred. No. 3.8e-34;
Matches 66; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-166-225A-63
US-10-166-225A-63
Sequence 63, Application US/10166225A
Publication No. US20030148416A1
GENERAL INFORMATION:
APPLICANT: BRETZEL, Werner
APPLICANT: HUMBELIN, Markus
APPLICANT: HUMBELIN, Markus
APPLICANT: LOFEZ-ULIBERRI, Rual
APPLICANT: YELISEEV, Alexel A.
TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
FILE REPERENCE: C38438/121966
CURRENT FILEGO DATE: 2002-06-05
UMBER OF SCO ID NOS: 197
SOFTWARE: Patentin version 3.1
SEQ ID NO 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
|||||||
RPAQPR 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RPAQPR 66
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COMPANY RICHEST STREETERS PROWATER!

QUETY MARCH

Dest Local Similarity 23.6; Score 63.5; DB 22; Length 342;

Best Local Similarity 23.6; Score 63.5; DB 22; Length 342;

Best Local Similarity 23.6; Score 63.5; DB 22; Length 342;

Dest Local Similarity 23.6; Score 63.5; DB 22; Length 342;

Dest Local Similarity 23.6; Score 63.5; DB 22; Length 342;

Dest Local Similarity 23.6; Score 63.5; DB 22; Length 342;

Dest Local Similarity 23.6; DB 22; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23; DB 23
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(+) -Delta-Cadinene-8-Hydroxylase Gene from Cotton
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US-10-080-170-539

US-10-080-170-539

Sequence 539, Application US/10080170

Publication No. US20030129601A1

GENERAL INFORMATION:

APPLICANT: COLE, S. T.

TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR

TITLE OF INVENTION: IDEMTIFYING TRAGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR

TITLE OF INVENTION: USBWIFFYING TRACETS FOR THE DIAGNOSIS, PROPHYLAXIS OR

TITLE OF INVENTION: 18APLICATION UNBER: 08/10/080,170

CURRENT FILING DATE: 2002-06-10

PRIOR APPLICATION NUMBER: 60/270,123

FILE REFERENCE: SEQ ID NOS: 652

WUMBER OF SEQ ID NOS: 652

SOFTWARE: Patentin Ver. 2.1
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                Gaps
                                                                                          8 SPISWEQAAAEAVQRARDSVDDIRVARVIEQDMA-VDSAGKITYRIKLEVSFKMRP 62
                                                                                                                                            25 SPMSW-----IERIKSNITPTRKASIPEGVWTKCDSCGQVLYRAELERNLEVCP 73
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18.5%; Score 60; DB 14; Length 535;
Best Local Similarity 28.2%; Pred. No. 23;
Matches 22; Conservative 15; Mismatches 23; Indels
                20; Indels
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                12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Chem. Xiao.ya haranga APPLICANT: Chem. Xiao.ya APPLICANT: Luo, Ping APPLICANT: Luo, Ping APPLICANT: Luo, Ping APPLICANT: Luo, Ping Chem. TITLE OF INVENTION: CDNA Clone of (+)-Delta FILE REFERENCE: 006602-113
CURRENT APPLICATION NUMBER: US/10/067,534
CURRENT FILING DATE: 2002-02-07
PRIOR APPLICATION NUMBER: US 60/267,160
PRIOR FILING DATE: 2001-02-07
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
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ilarity 43.3%; Pred. No.
Conservative 7; Mismatc
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ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                              ; Sequence 2, Application US/10067534; Publication No. US20020187538A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Essenberg, Margaret K. APPLICANT: Chen, Xiao-Ya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          380 RYLDAAVKETFRLHPPMP 397
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ORGANISM: Gossypium arboreum
                16; Conservative
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Best Local Similarity
Matches 13; Conserv
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APPLICANT: Gusyatiner, Mikhail M
APPLICANT: Rostova, Yulia G
APPLICANT: Rostova, Yulia G
APPLICANT: Rostova, Yulia G
APPLICANT: Sampolskaya, Tatyana A
TITLE OF INVENTION: New Mutant Carbamoylphosphate
TITLE OF INVENTION: Compounds Derived from Carbamoylphosphate
TITLE OF INVENTION: Compounds Derived from Carbamoylphosphate
CURRENT APPLICATION NUMBER: US/10/210,115
PRIOR APPLICATION NUMBER: RU 2001-121697
PRIOR APPLICATION NUMBER: RU 2001-121697
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.1
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APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Xu, H. Howard
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
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Best Local Similarity 29.0%; Pred. No. 35;
Matches 18; Conservative 18; Mismatches
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
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SOTTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13952
LENGTH: 330
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Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Hacelbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.8%;
28.6%;
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ORGANISM: Escherichia coli
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ORGANISM: Salmonella typhi
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LENGTH: 10'
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Compugen Ltd.
GenCore version
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OM protein - protein search, using sw model

November 21, 2003, 15:57:31; Search time 1.37687 Seconds (without alignments) 4609.825 Million cell updates/sec Run on:

324 1 VIDIIGTSPTSWEQAAAEAV......KITYRIKLEVSFKWRPAQPR US-09-688-672A-6 Perfect score: Sequence: Title:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283308 Total number of hits satisfying chosen parameters:

283308 segs, 96168682 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	ote	hypothetical prote	_		carbamoy1-phosphat	opqď-	transcription regu	hypothetical prote		flagellin [importe	protein kinase - s	cobM protein - Pse	El protein - human	beta-glucosidase (tumor supressor pr	hypothetical prote	myosin-RhoGAP prot	carbamoy1-phosphat	hypothetical prote	cell division prot	hypothetical prote	ABC transporter (A	probable Helix-tur	c	14	۲	A acetyl	ä
SOUTHWANDS	QI	7083			D95850			AE1822	C71704	H97792	AD3528	849313	H36145	W1WL18	S08243	SYECCP	T13797	H84227	T31099	AE0510	\$23604	AF2652	C97434	H69803	C70867	A43554	93	269	H291	o O
	DB																										~			
	Length	71	77	71	69	1073	1073	96	342	342	282	1094	253	657	947	1073	1477	94	2626	1075	181	246	267	396	1624	458	620	959	393	393
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A39127	S15193	T13283	D86468	H70785	T08523	832177	T03461	F84225	A23662	T46858	F86185	G02864	A36629	F84946	D87564
C)	(1)	N	N	N	N	7	0	7	Н	N	7	0	N	0	(7)
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9	9	59	58.5	58.5	58.5	58.5	58.5	58	28	57.5	57.5	57.5	57.5	57.5	57
30	31	32	33	34	35	36	37		39	40	41	42	43	44	45

ALIGNMENTS

F70833								
probable	protein	tansport	protein	- Myc	probable protein tansport protein - Mycobacterium tuberculosis (strain	tubercu	losis	strain
C;Species: Mycobacterium tuberculosis	:: Mycoba	acterium (tuberculo	sis				
. O. O. O.	7-T111-1	THEFT WEE	Tran and	200	C.Date. 17-11,1-1998 #semience revision 17-,11,1-1998 #fext Change 22-Oct	#tpxt	abueda	22 - Ogt

RESULT

n H37RV)

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: P70833
S;Cole S. T. Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S., Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome s A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Residues: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-71 colb.
A;Cross_references: GB:AL021931; GB:AL123456; NID:g3261526; PIDN:CAA17385.1; PID:e1252494
A;Experimental source: strain H37Rv
C;Genetics:

.. O 9 0; Gaps Query Match 100.0%; Score 324; DB 2; Length 71; Best Local Similarity 100.0%; Pred. No. 5e-30; Matches 66; Conservative 0; Mismatches 0; Indels

6 VIDIIGTSPTSWEQAAABAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM 1 VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM 61 RPAQPR 66 66 RPAQPR 71 셤 ઠે D. ò

65

RESULT

Description of the protein Ung1446h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: E84298
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor Jung, K.H.; Alam, M.; Freitas, T. 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Listle: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MuID:20504483; PMID:11016950
A;Reference number: Preliminary
A;Reference under: Preliminary
A;Residues: 1-77 <STO>

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20.2%;
30.6%;
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A, Status: preliminary
A, Molecule type: DNA
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                                                        A; Genome: plasmid
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C; Species: Sinorhizoblum meliloti
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C; Species: Sinorhizoblum meliloti
C; Species: Sinorhizoblum meliloti
R; Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl., Sea Guence of the 1,683-kbp SymB megaplasmid from the N2-fixing endc
A; Title: The complete sequence of the 1,683-kbp PNID: 11481431
A; Status: preliminary
A; Molecule type: DNA
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A; Molecule type: DNA
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K.; Lim,
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A/Accession: B83641
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         GB:AE004437; NID:g10580943; PIDN:AAG19753.1; GSPDB:GN00138
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Best Local Similarity 31.1%; Pred. No. 0.00013;
Matches 19; Conservative 22; Mismatches 20;
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C,Genetics:
A,Gene: VNG1446H
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carbamoyl-phosphate synthase large subunit [imported] - Escherichia coli (strain O157:H7, C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: 18-Ual-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: 199633
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genom A;Reference number: A99629; MUID:21156231; PMID:11258796
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A;Cross-references: GB:AE005174; NID:g12512719; PIDN:AAG54335.1; GSPDB:GN00145; UWGP:Z00:
A;Experimental source: strain 0157:H7, substrain EDL933
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A;Nolecule type: DNA
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Rosidues: 1-1073 «HAX>
A;Cross-references: GB:BA000007; PIDN:BAB33459.1; PID:g13359492; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: EC80036
C;Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain; biotin of C;Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain;
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: C85484
Perna, NT.; Flunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
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A)Gene: carB
C;Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain; biotin
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Length
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                                                                                                                 17; Mismatches
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Pred. No. 27;
Score 66;
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20.4%;
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Best Local Similarity 30.6%;
Matches 19; Conservative 1
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2

Gaps

19; Indels

Mismatches

17;

19; Conservative

Matches

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C.Species: Brucella meliteness
C.Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C.Accession: AD328
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C;Species: Dictyostelium discoideum
C;Species: Dictyostelium discoideum
C;Species: Dictyostelium discoideum
C;Accession: S52076; S49313
R;Wetterauer, B.W.; Hamker, U.; von Haeseler, A.; MacWilliams, H.K.; Simon, M.N.; Veron, Biochim: Biophys. Acta 1265, 97-101, 1995
A;Title. A protein kinase from Dictyostelium discoideum with an unusual acidic repeat dom A;Reference number: S52076; MUID:95161460; PMID:7857991
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Pred. No. 15;
6; Mismatches 18; Indels
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25.8%; Pred. No. 13;
ive 13; Mismatches
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Best Local Similarity 36.8
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SG 273
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A;Cross-references: GB:AJ235271; GB:AJ235269; NID:g3868717; PIDN:CAA14909.1; PID:g386100
A;Experimental source: strain Madrid E
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19.6%; Score 63.5; DB 2; Length 342;
Best Local Similarity 25.8%; Pred. No. 13;
Matches 16; Conservative 14; Mismatches 13; Indels 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: carotenoid biosynthesis protein homolog
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Best Local Similarity 26.7%
Matches 16; Conservative
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SY 718
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SG 273
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A,Cross-references: GB:XO5015; NID:g60975; PIDN:CAA28666.1; PID:g60978 C;Superfamily: papillomavirus El protein C;Keywords: early protein
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es 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 TELSP 111
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Cispecies: human papillomavirus type 18
Cispecies: human papillomavirus type 18
Cipate: 30-89-1987 #sequence_revision 30-8ep-1987 #text_change 16-Jul-1999
Cipacession: C26465, C26251
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C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C;Reywords: ATP
F;20-281/Domain: protein kinase homology «KIN»
F;28-36/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Pseudomonass procession 30-Nov-1990 #text_change 24-Sep-1999 (C;Species: Pseudomonass procession: H3645 sp. 1900 #sequence_revision 30-Nov-1990 #text_change 24-Sep-1999 (C;Date: 30-Nov-1990 #sequence_revision 30-Nov-1990 #text_change 24-Sep-1999 (C;Couzet, 0.; Cameron, B.; Cauchois, L.; Rigault, S.; Rouyez, M.C.; Blanche, F.; Thibau Bacteriol. 172, 5980-5990, 1990 (A;Title: Genetic and sequence analysis of an 8.7-kilobase Pseudomonas denitrificans frag A;Reference number: A36145; MUID:91008976; PMID:2211521 (A;Morecule type: DNA A;Residues: 1-253 <CR: A;Molecule type: DNA A;Residues: 1-253 <CR: A;Molecule type: DNA A;Residues: 1-253 <CR: A;Molecule type: DNA A;Residues: 1-253 <CR: A;Molecule type: DNA A;Residues: 1-253 <CR: A;Molecule type: DNA A;Residues: 1-253 <CR: A;Molecule type: DNA A;Residues: 1-253 <CR: A;Molecule type: DNA A;Residues: 1-253 <CR: A;Molecule type: DNA A;Residues: 1-253 <CR: A;Molecule type: DNA A;Residues as Pseudomonas denitrificans C;Superfamily: precorrin-3 methylase
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A,Molecule type: DNA
A,Residues: 1-74 <CSE2
A,FORDidues: 1-74 <CSE2
A,FORDidues: 1-74 <CSE2
A,CORDIGUES: 1-74 <CSE2
A,CORDIGUES: 1-74 <CSE2
A,CORDIGUES: 1-74 <CSE2
A,CORDIGUES: 1-74 <CSE2
B,COLDIGUES: 2-74 <CSE2
A,FORDIGUES: 2-74 <CSE2
A,FORDIGUES: 2-74 <CSE2
A,FORDIGUES: 2-74 <CSE2
A,ACCESSION: C26251
A,ACCESSION: C26251
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A,Accession: S52076
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-1094 <WE2>
A,Cross-references: BMBL:Z37981; NID:g551445; PIDN:CAA86053.1; PID:g551446
C,Genetics:
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Best Local Similarity 30.0%
Matches 15; Conservative
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C;Species: Pseudomonas sp.
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A Residues: 1-657 <COL>
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A/Molecule type: DNA
A/Residues: 1-1073 < YUR.
A/Rolecule type: DNA
A/Residues: 1-1073 < YUR.
A/Ross-references: EMBL: D10483; NID:g216434; PIDN:BAA01311.1; PID:g216460
A/Ross-references: EMBL: D10483; NID:g216434; PIDN:BAA01311.1; PID:g216460
A/Riblatener, F.R.: Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col.
A/Riblatener, F.R.: Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col.
A/Rible: The complete genome sequence of Escherichia coli K-12.
A/Rocsession: A64724
A/Rocsession: A64724
A/Rotaus: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
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Proc. Natl. Acad. Sci. U.S.A. 80, 4629-4633, 1983
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Proc. Natl. Acad. Sci. U.S.A. 80, 4629-4633, 1983
Proc. Natl. The carse gene of Escherichia coli: a duplicated gene coding for the large subuni A.Reference number: A01198
A.Accession: A01198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
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C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 15-Oct-1999
C;Accession: $08243
                                                                                                                                                                                                                                                1 VIDIIGTSPISWEQA---AAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVS
                                                                                                                              Gaps
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Nucleic Acids Res. 18, 671, 1990
Nucleic Acids Res. 18, 671, 1990
Nucleic Acids Res. 18, 671, 1990
Arithe: DNA sequence of a beta-glucosidase from Ruminococcus albus.
A;Reference number: S08243
A;Recession: S08243
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-947 < OMM>
A;Residues: 1-947 < OMM>
A;Cxoss-references: EMBL:X15415; NID:g45967; PIDN:CAA33461.1; PID:g45968
C;Reywords: glycosidase; hydrolase; polysaccharide degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64
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Length 657;
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DB 1;
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19.0%; Score 61.5; D 29.2%; Pred. No. 44; ive 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . Match
Local Similarity 33.3%; Pred. No. 66;
les 18; Conservative 11; Mismatches
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A; Residues: 1-1073 < RELAT>
A; Cross-references: GB:ABC00113; GB:U00096; NID:g2367095; PIDN:AAC73144.1; PID:g1786216;
A; Experimental source: strain K-12, substrain MG1655
C; Genetics:
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Best Local Similarity 29.0%; Pred. No. 76;
Matches 18; Conservative 18; Mismatches 19; Indels
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Search completed: November 21, 2003, 16:09:52 Job time : 2.37687 secs

57 SF 58 |: 717 SY 718 This Page Blank (uspto)

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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 21, 2003, 15:51:11; Search time 0.778231 Seconds (without alignments) 3988.226 Million cell updates/sec Run on:

US-09-688-672A-6 Title: Perfect score: Sequence:

324 1 VIDIIGTSPTSWEQAAAEAV......KITYRIKLEVSFKWRPAQPR 66 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

127863 seqs, 47026705 residues Searched:

127863

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

					SUMMARIES		
ายคลา		% O.1617					
NO.	Score	Match	Length	DB	DI	Description	
	5.	20.2	1072		Ĭ	· w	scherichia
7	63.5	ο,	342		IDI2_RICCN		
٣	m	19.6	342				ttsia
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10	ö	18.7	351		IDIZ RHILO	Q98915 rhizobium	bium l
11	60.5	18.7	0		CARB_SALTI	Q82917 salmo	nella
12	ö	18.7	1074		CARB_SALTY	P14846 salmo	nella
13	9	œ	321		K6PF_PASMU	Q9cph2 paste	pasteurella
14	9.	18.4	45		DESM_XENLA	P23239 xenopus	us lae
15	59.5	œ	ຜ		SYL AERPE		eropyrum p
16	6	ω.	98		E4L2 MOUSE		mus musculu
17	59	æ	50		SCRY_SALTY		salmonella
18	58.5	18.1	36		COBT_MYCTU		mycobacteri
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20	S S	7	97		TRP4 MOUSE		musculu
21	58	7	97		TRP4_HUMAN		homo sapien
22	58	7.	76		TRP4_RAT		rattus norv
23	9	7.	86		TRP4_BOVIN		bos taurus
24	58	7.	157		MYSH_ACACA		acanthamoeb
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26	57.5	•	Ñ				homo sapien
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31	56		1.		2	_	nosarc
32	56	17.3	515	Н	팀	P43861 haemo	phil
33	26		u,		ASPH_BOVIN	Q28056 bos t	aurus

Q8fpg8 corynebacte Q8fnp5 corynebacte	P35593 escherichia Q9ugi9 homo sapien P08236 homo sapien	P13332 bacteriopha O35451 mus musculu	P46700 mycobacteri P48612 drosophila	P71017 bacillus su P21134 aphanocapsa	Oghmt9 halobacteri
1 RBFA COREF	1 NIKU ECOLI 1 AAKI HUMAN 1 BGLR HUMAN	1 VG18 BPT4 1 AT6B MOUSE	1 THT2 MYCLE 1 PELO DROME	1 GBSB_BACSU 1 CRII_APHSP	1 UVRB_HALN1
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ALIGNMENTS

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                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformeatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
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promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate. Tetramer of heterodimers (alpha, beta) 4 (By similarity). SIMILARITY: BELONGS TO THE CARB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Gaps
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
1sopentenyl-diphosphate dalta-isomerase (EC 5.3.3.2) (IPP isomerase)
(Isopentenyl pyrophosphate isomerase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS, PRODOS, CESASE.

FIGRO1369; CPSASE.

PROSITE; PSO0865; CPSASE.1; 2.

PROSITE; PSO0867; CPSASE.2; 2.

Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat; Arginine biosynthesis; Complete proteome.

Alt. binding; Manganese; Complete proteome.

INIT MET 0. CARBOXYPHOSPATE SYNTHETIC DOWAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
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MANGANESE 3 (BY SIMILARITY).
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17; Mismatches 19; Indels
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EMBL; AE015040; AAM41696.1; ---
EMBL; AE015040; AAM41696.1; ---
EMBL; AE015040; AAM41696.1; ---
EMBL; D90633; D90633.

HAMAP; MF 01210; ---
InterPro; IPR006275; CarA L glu.
InterPro; IPR00649; CPase L D2.
InterPro; IPR006480; CPase L D3.
InterPro; IPR006480; CPase L D3.
InterPro; IPR006481; CPase L D3.
InterPro; IPR00481; CPase L D3.
InterPro; IPR00481; CPase L D3.
InterPro; IPR00481; CPase L D3.
InterPro; IPR00481; CPase L D3.
InterPro; IPR00481; CPase L D3.
InterPro; IPR00481; CPase L D3.
InterPro; IPR00481; MGS. IIRe
Ffam; PF02789; CPSase L D3; 1.
Pfam; PF02789; CPSase L D3; 1.
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1072 AA;
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SY 717
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AC Q924M7;
DT 28-FEB-2003
DT 28-FEB-2003
DT 28-FEB-2003
DT 28-FEB-2003
DT 28-FEB-2003
DT 28-FEB-2003
DE (Isopentenyl-
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16-OCT-2001 (Rel. 40, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
Isopentenyl-diphosphate delta-isomerase (EC 5.3.3.2) (IPP isomerase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --- FUNCTION: Catalyzes the 1,3-allylic rearrangement of the homoallylic substrate isopentenyl (IPP) to its allylic isomer, dimethylallyl diphosphate (DMAPP) (By similarity).
--- CATALYTIC ACTIVITY: Isopentenyl diphosphate = dimethylallyl
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STRAIN=Madrid E;
MDDLINE=99039499; PubMed=9823893;
Andersson 3.G.E., Zomorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
Eriksson A.-S., Winkler H.H., Kurland C.G.;
                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Malish 7;
MEDILINE=21442074; PubMed=11557893;
Ogata H., Addic S., Renesto-Addiffren P., Fournier P.-E., Barbe Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
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Rickettsia conorii.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=781;
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FNI OR RP452.
Rickettsia prowazekii.
Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiaceae; Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Rickettsiaceae, Ric
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- COFACTOR: FWN and NADPH (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the IPP isomerase type 2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR, H97792, H97792.
Hambly WF 00354; -; FNN enzyme.
InterPro, IPR003009, FNN enzyme.
Isomerase, Isoprene biosynthesis; Flavoprotein; FMN; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         342 AA; 37336 MW; D346003CCD99B7A3 CRC64;
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SEQUENCE 342 AA;
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                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
                      Nature 396:133-140(1998).

-!- FUNCTION: CATALYZES THE 1.3-ALLYLIC REARRANGEMENT OF THE HOMOALLYLIC SUBSTRATE ISOPENTENYL (IPP) TO ITS ALLYLIC ISOMER, DIMETHYLALLYL DIPHOSPRATE (DMAPP) (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: Isopentenyl diphosphate = dimethylallyl
genome sequence of Rickettsia prowazekii and the origin of
                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
                                                                                                                                                                                                                                                                                                                                                                                                   / Match 19.6%; Score 63.5; DB 1; Length 342; Local Similarity 25.8%; Pred. No. 11; hes 16; Conservative 14; Mismatches 13; Indels 19
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-: CATALVITY: 3-(5-oxo-4,5-dihydro-3-H-imidazol-4-y1)propanoate = urocanate + H(2)O.
-: COFACTOR: NAD (By similarity)
-: COFACTOR: NAD (By similarity)
-: PATHWAY: Histidine degradation; second step.
-: SIMILARITY: BELONGS TO THE UROCANASE FAMILY.
                                                                                                           COFACTOR: FWN AND NADPH (BY SIMILARITY).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to the IPP isomerase type 2 family.
                                                                                                                                                                                                                                                                                                                HAWAP, MF 00354; -; 1.
InterPro; IPR003009; FMN enzyme.
Isomerase; Isoprene biosynthesis; Flavoprotein; FMN; NADP;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2000 (Urocanase hydratese (EC 4.2.1.49) (Urocanase)
[Imidazolonepropionate hydrolase)
                                                                                                                                                                                                                                                                                                                                                                         342 AA; 37363 MW; FE452A843CA1B950 CRC64;
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                                                                                                                                                                                                                                                                                   EMBL; AJ235271; CAA14909.1; -.
PIR; C71704; C71704.
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SG 273
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J. Bacteriol. 175:7430-7440(1993).
-!- FUNCTION: METHYLTRANSFERAS.
-!- FUNCTION: METHYLTRANSFERAS.
-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + precorrin-4 = S-adenosyl-L-homocysteine + precorrin 5.
-!- PATHWAY: Cobalamin biosynthesis.
-!- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS SUMT, CYSG, CBIF/COBM AND CBIL/COBI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94042219; PubMed=8226690; Debussche L., Thibaut D., Cameron B., Crouzet J., Blanche F.J.; "Biosynthesis of the corrin macrocycle of coenzyme B12 in Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas denitrificans.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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J. Bacteriol. 172:5980-5990(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Precorrin-4 Cll-methyltransferase (EC 2.1.1.133) (Precorrin-3 methylase)
                                                                                                                                                                                                                                                                                                            Length 731;
                                                                                               Pfam; PF01175; Urocanase; 1.
Probom; PD025423; Urocanase; 1.
Probom; PS01233; UROCANASE; 1.
HYDOChetical protein; Histidine metabolism; Lyase; NAD.
SEQUENCE 731 AA; 81523 NW; 891EF61C9A604E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           687 GVTRRSWSGNAKAQEAIQRAEKQVDGLRVTLPVEAD 722
                                                                                                                                                                                                                                                                                                                                                                                                                                           6 GISPISW--EQAAAEAVQRARDSVDDIRVARVIEQD 39
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                                                                                                                                                                                                                                                                                                            19.4%; Score 63; 41.7%; Pred. No.
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InterPro; IPR000178; Cor/por Metransf.
InterPro; IPR003043; Uropor Metransf.
Pfam; PF00590; TP methylase; 1.
TIGRFMS; TIGR01465; cobM cbiF; 1.
PROSITE; PS00839; SUMT_1; 1.
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MEDLINE=91008976; PubMed=2211521;
EMBL, AL132952; CAB61139.1; -. WormPep; Y51H4A.7; CE22333. InterPro; IPR000193; Urocanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M59301; AAA25801.1; -.
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 41.7
Matches 15; Conservative
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P15885;
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Schneider Gaedicke A., Schwarz E.;
"Different human cervical carcinoma cell lines show similar transcription patterns of human papillomavirus type 18 early genes.";
EMBO J. 5:2285-2292(1986).
-! - FUNCTION: ATP-DEPENDENT DNA HELICASE REQUIRED FOR INITIATION OF VIRAL DNA REPLICATION OF PROTEIN: THE E1-E2 COMPLEX BINDS TO THE REPLICATION ORIGIN WHICH CONTAINS BINDING SITES FOR BOTH PROTEINS.
                                                                                                                                                               Gaps
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                                                                                                                                                            7 ;
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"Nucleotide sequences of cDNAs for human papillomavirus type 18
PROSITE; PS00840; SUMT_2; 1.
Cobalamin blosynthesis; Porphyrin blosynthesis; Transferase;
Methyltransferase
SEQUENCE 253 AA; 26862 MW; 50F5E6F5F67FF733 CRC64;
                                                                                                                   Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inagaki Y., Tsunokawa Y., Takebe N., Nawa H., Nakanishi S.,
Terada M., Sugimura T.;
                                                                                                                 ; Score 61.5; DB 1; Length 2; Pred. No. 13; 14; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human papillomavirus type 18.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           657 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (1) SEQUENCE FROM N.A. MEDLINE=87283882; PubMed=3039146; Cole S.T., Danos O.; Cole S.T., Commence and comparate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-528 FROM N.A. MEDLINE=88188247; PubMed=2833614;
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MEDLINE=87053870; Pubmed=3023067;
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EMBL; M20225; AAA99516.1; -.
EMBL; M205799; AAA46948.1; -.
PIR; C26165; W1W118.
InterPro; IPR001177; Papillom_E1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Virol. 62:1640-1646(1988).
                                                                                                                 19.0%;
                                                                                                                                                            21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                       Best Local Similarity
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NCBI_TaxID=10582;
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P06789;
                                                                                                                   Query Match
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191418
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                                                                                                                                                                                                                                                                                              Gaps
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Pfam; PF00519; E1; 1.
Pfam; PF00524; E1 N; 1.
Brarly protein; DNA replication; Helicase; ATF-binding; DNA-binding; Nuclear protein.
Nuclear protein.
ATP (POTENTIAL).
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28-FBB-2003 (Rel. 41, Last annotation update)
28-FBB-2003 (Rel. 41, Last annotation update)
Beta-glucosidase (BC 3.2.1.21) (Gentiobiase) (Cellobiase) (Beta-D-glucoside glucohydrolase).

Ruminococcus albus.

Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 EQAAABAVQRARDSVDDIRVARV -- IBQDMAVDSAGKITYRIKLEVSFKMRPAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohmiya K., Takaho M., Shimizu S.;
"DNA sequence of a beta-glucosidase from Ruminococcus albus.";
Nucleic Acids Res. 18:671-671(1990)
-!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing be glucose residues with release of beta-D-glucose.
-!- PATHWAY: Cellulose degradation.
-!- SATHWAY: Celluloss TO PAMILY 3 OF GLYCOSYL HYDROLASES.
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                                                                                                                                                                                                                                                                                           14; Mismatches 29; Indels
                                                                                                                                                                                                                                     Length
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7; C43B8CDD9D60A115 CRC64;
                                                                                                                                             94 T -> K (IN REF. 2).
73736 MW; B18E68BCE1DB330A CRC64;
                                                                                                                                                                                                                                     DB 1;
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InterPro; IPR001772; Glyco hydro_3C.
Pfam; PF00933; Glyco hydro_3; 1.
Pfam; PF01915; Glyco hydro_3; 1.
PRNYS; PR00133; GLHYDRIASE3—
PROSITE; PS00775; GLYCOSYL HYDROL F3; 1.
Hydrolase; Glycosidase; Cellulose degradation.
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; Pred. No. 47;
11; Mismatches
                                                                                                                                                                                                                                 19.0%; Score 61.5; I 29.2%; Pred. No. 33;
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MEDLINE=90175009; PubMed=2106673;
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18; Conservative
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                                                                                                                                                                        657 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 FKMRP 62
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MEDLINE-84248072; PubMed-6330744;
Plette J., Whundya H., Lusty C.J., Cunin R., Weyens G., Crabeel M., Charlier D.R.M., Glansdorff N., Pletard A.;
"DNA sequence of the carA gene and the control region of carAB: tandem promoters, respectively controlled by arginine and the pyrimidines, regulate the synthesis of carbamoyl-phosphate synthetase in Bscherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                 MEDLINE=84248073; PubMed=6377309;
Bouvier J., Patte J.-C., Stragier P.;
"Multiple regulatory signals in the control region of the Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97317071; PubMed=9174345;
Thoden J.B., Holden H.M., Wesenberg G., Raushel F.M., Rayment I.;
"Structure of carbamoyl phosphate synthetase: a journey of 96 A from
Substrate to product.";
Biochemistry 36:6305-6316(1997).
                                                                                                                                                                                                                                           Nyunoya H., Lusty C.J.;
"The carB gene of Escherichia coli: a duplicated gene coding for the large subunit of carbamoyl-phosphate synthetase.";
Proc. Natl. Acad. Sci. U.S.A. 80:4629-4633(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92334977; PubMed=1630901;
Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N.,
Yura T., Mizobuchi K., Nakata A.;
"Systematic sequencing of the Escherichia coli genome: analysis of the 0-2.4 min region.";
Nucleic Acids Res. 20:3305-3308(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE FROM N.A.
STRAIDSALZ / MG165A.
STRAIDSALZ / MG167; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98301363; PubMed=9636022;
Moden J.B., Miran S.G., Phillips J.C., Howard A.J., Raushel F.M.,
Holden H.M.;
"Carbamoyl phosphate synthetase: caught in the act of glutamine
                                                                  21-UUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Carbamcyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamcyl-phosphate synthetase ammonia chain).
CARB OR PYRA OR B0033.
                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 81:4134-4138(1984).
                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 81:4139-4143(1984).
                                              PRT; 1072 AA.
                                                                                                                                                                                                        SEQUENCE FROM N.A., AND SEQUENCE OF 1-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
                                                                                                                                                                                                                               MEDLINE=83273669; PubMed=6308632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-6 FROM N.A.
                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                             Escherichia coli
                                                                                                                                                                                NCBI_TaxID=562;
                                              CARB ECOLI
P00968;
                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=K12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phosphate synthetase.";
J. BAOL. Chem. 274:22502-22507(1999).

-!- CATALYTY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + phosphate + L-glutamate + carbamoyl phosphate.
-!- CATALYTY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + phosphate + L-glutamate + carbamoyl phosphate.
-!- PATHWAY: Binds 3 manganese ions per subunit.
-!- PATHWAY: Arginine biosynthesis.
-!- PATHWAY: Pyrimidine biosynthesis;
-!- PATHWAY: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by promotes the hydrolysis of glutamine to ammonia, which is used by Tetramer of heterodimers (alpha, beta)4.
-!- SIMILARITY: BELONGS TO THE CARB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIINE=20056035; PubMed=10597438;
Thoden J.B., Huang X., Raushel F.M., Holden H.M.;
"The small subunit of carbamoyl phosphate synthetase: snapshots along
                                                                MEDLINE=9190825; PubMed=10089390; Thoden J.B., Raushel F.M., Benning M.M., Rayment I., Holden H.M.; "The structure of carbamoyl phosphate synthetase determined to 2.1-A resolution.";
                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
MEDLINE=99155207; PubMed=10029528;
Thoden J.B., Wesenberg G., Raushel F.M., Holden H.M.;
"Carbamoyl phosphate synthetase: closure of the B-domain as a result of nucleotide binding.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
The Spinits of inosine monophosphate to Escherichia coli carbamoyl "The binding of inosine monophosphate to Escherichia coli carbamoyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE=20056035; Pubmed=10587438;
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ECOGENE; E510135; carB.
HAMAP; MF.01210; .; 1.
InterPro; IPR006475; CarA L.glu.
InterPro; IPR005479; CPase_L.D.
InterPro; IPR005483; CPase_L.D.
InterPro; IPR005481; CPase_L.D.
InterPro; IPR005481; CPase_L.D.
InterPro; IPR005481; CPase_L.D.
InterPro; IPR005481; CPase_L.D.
InterPro; IPR005481; CPase_L.D.
InterPro; IPR005481; CPase_L.D.
InterPro; IPR00480; CPSase_L.Chai, 2.
Pfam; PF00289; CPSase_L.Chai, 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the reaction pathway.";
Biochemistry 38:16158-16166(1999).
                                                                                                                                                                                                                                                                 Acta Crystallogr. D 55:8-24(1999).
Biochemistry 37:8825-8831(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochemistry 38:2347-2357(1999)
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PDB; LJDB; 17-JUN-98.
PDB; LA9X; 21-OCT-98.
PDB; LBXR; 20-APR-99.
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1C30; 10-DEC-99.
1C30; 10-DEC-99.
1CS0; 10-DEC-99.
1KEE; 21-DEC-01.
1MGV; 13-NOV-02.
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                             CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
ALLOSTERIC DOMAIN.
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MANGANESE 1.
MANGANESE 2.
MANGANESE 3.
MANGANESE 3.
                                                 (POTENTIAL).
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29.0%; Pred. No. 53;
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PF02787; CPSase L D3; 1.
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RESULT 9

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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II, Brassicales, Brassicaceae, Brassica.
NCBI_TaxID=3712;
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SEQUENCE FROM N.A.

MEDLINE=21082930; PubMed=11214968;

Matanabe T., Nakamura Y., Sato S., Agamizu E., Kato T., Sasamoto S.,

Matanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,

Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,

Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,

Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                             οĘ
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Gossen K.K., Fatavic V., Taylor D.C.;
Mucleotide sequence of a cDNA from microspore derived embryos of
"Nucleotide sequence of a cDNA from microspore derived s7:";
Brassica oleracea is homologous to 40S ribosomal protein S7:";
(In) Plant Gene Register PGR99-096.
-! SIMILARITY: BELONGS TO THE S7E FAMILY OF REDSCOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23; Indels 12;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
18-FEB-2003 (Rel. 41, Last annotation update)
18-FEB-2003 (Rel. 41, Last sequence response (Rel. 41, Last sequence response (Rel. 41, Last sequence Rel. 5.3.3.2) (IPP in (Isopentenyl pyrophosphate isomerase).
FNI OR MIR6371.
FNI OR MIR6371.
Bacteria: Proteobacteria; Alphaproteobacteria; Rhizobiales; Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
19. Score 61; DB 1; Length 191;
Best Local Similarity 23.1%; Pred. No. 11;
Matches 15; Conservative 15; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22154 MW; 175A2D794210077C CRC64;
                                                                              Last sequence update)
Last annotation update)
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191 AA
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InterPro, IPR000554; Ribosomal S7E.
Pfam; PF01251, Ribosomal S7F; 1.
ProDom; PD006276; Ribosomal S7E; 1.
PROSITE; PS00948; RIBOSOMAL_S7E; FALSE_NEG.
                                                                                                                                                                                      Brassica oleracea (Cauliflower).
                                                    Created)
                                                                     28-FEB-2003 (Rel. 41, Last
28-FEB-2003 (Rel. 41, Last
40S ribosomal protein 87.
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STANDARD;
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28-FEB-2003 (Rel. 41,
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SEQUENCE 191 AA;
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68 RLRKA 72
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SEQUENCE
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CARB SALTY
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STRANIE-172 / Arcc 700931;
MEDLINE-22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J. Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Kroph A., Larsen T.S., Leacher S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                   DNA Res. 7:331-338 (2000).
-!- FUNCTION: Catalyzes the 1,3-allylic rearrangement of the homoallylic substrate isopentenyl (IPP) to its allylic isomer, dimethylallyl diphosphate (DMAPP) (By similarity).
-!- CATALYTIC ACTIVITY: Isopentenyl diphosphate = dimethylallyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Carbamcyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamcyl-phosphate synthetase ammonia chain).
CARB OR STY0077 OR T0068.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Próteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.7%; Score 60.5; DB 1; Length 351; 53.6%; Pred. No. 23; cive 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    HAMAP; MF_00354; -; 1.
InterPro; IPR003009; FMN_enzyme.
Isomerase; Isoprene biosynthesis; Flavoprotein; FMN; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351 AA; 36531 MW; 680D504F53E588A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1074 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        217 VIDVAGAGGTSW--AAVEG-ERARDAAD 241
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                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AP003009; BAB52681.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   llarity 53.6%;
Conservative
                 Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
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Matches 15; Conserv
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J. Bacteriol. 185:2330-2337(2003).

-!- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + possible to the phosphate + L-glutamate + carbamoyl phosphate.

-!- COFACTOR: Binds 3 manganese ions per subunit (By similarity).
-!- PATHWAY: Arginine biosynthesis.
-!- PATHWAY: Pyrimidine biosynthesis, first step.
-!- PATHWAY: Pyrimidine biosynthesis, the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By
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OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
ALLOSTERIC DOMAIN.
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DOMAIN 403 1 402 CARBANDYL PHOSPHATE SYNTHETIC DOMAIN.

DOMAIN 403 935 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
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InterPro: IPR006479; CPase L D2.
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InterPro: IPR005481; CPase L D3.
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Pfam; PF02187; CPase L D3; 1.
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                                                                                                                                                                                                                                                                                                                              MEDINE=8829100; PubMed=2843375;

A Kilstrup M., Lu C.D., Abdelal A., Neuhard J.;

Invalentide sequence of the carA gene and regulation of the carAB
operon in Salmonella typhimurium.";

Eur. J. Biochem. 176.421-429(1988).

- CATALITIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP +
Dhosphate + L-glutamine + carbamoyl phosphate.

- COFACTOR: Binds 3 manganese ions per subunit (By similarity).

- PATHWAY: Pyrimidine biosynthesis.

- PATHWAY: Pyrimidine biosynthesis;

- SUBUNIT: Composed of two chains; the small (or glutamine) chain
promotes the hydrolysis of glutamine to ammonia, which is used by
the large (or ammonia) chain to synthesize carbamoyl phosphate.
                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
MEDLINE=21534948; PubMed=11677609;
MCCIelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                     6.3.5.5) (Carbamoyl.
                                                                 Bacteria; Próteobacteria; Gammaproteobacteria; Enterobacteriales
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TIGREAMS; TIGRO1369; CPSaseII_lrg; 1.
PROSITE; PSO0866; CPSASE_1; 2.
PROSITE; PSO0867; CPSASE_2; 2.
Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
                                                                                                                                    Lu C.D., Walthall D.A., Abdelal A.T.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
            28-FEB-2003 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC
(Rel. 41, Last sequence update) (Rel. 41, Last annotation updat
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                                                                              Enterobacteriaceae; Salmonella.
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                                                       Salmonella typhimurium.
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STRAIN=LT2;
                                                                                         NCBI_TaxID=602;
                                              STM0067
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MEDLINE=21145866; PubMed=11248100;
May B.J., Zhang Q., Li L.I., Paustian M.L., Whittam T.S., Kapur "Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
-!- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-fructose 1,6-bisphosphate
-!- PATHWAY: Key concrol step of glycolysis.
-!- PATHWAY: Key concrol step of glycolysis.
-!- SIMILARITY: Belongs to the phosphoffructokinase family.
ATP-binding; Manganese; Complete proteome.

INIT MET 0 0 BY SIMILARITY.

DOMAIN 1 402 CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (BY SIMILARITY)
SIMILARITY).
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Pasteurellaceae; Pasteurella.
NCBL_TaxID=747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 1074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
6-phosphofructokinase (EC 2.7.1.11) (Phosphofructokinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY).
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MANGANESE 1 (BY SWANGANESE 2 (BY SWANGANESE 2 (BY SWANGANESE 3 (BY SWANGANESE 3 (BY SWANGANESE 3 (BY SYANGANESE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               321 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 60.5;
Pred. No. 68
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HAWAP; MF 00339; -; 1.
Interpro; JPR000023; Ppfruckinase.
Pfam; PF00365; PFK; 1.
PRINTS; PR00476; PHPRCTKINASE.
ProDom; PD000707; Ppfruckinase; 1.
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28-FEB-2003 (Rel. 41, Last seq
28-FEB-2003 (Rel. 41, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18; Conservative
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PFKA OR PM0069.
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302
284
298
300
828
840
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716 SY 717
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Q9CPH2;
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SEQUENCE
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SO
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                                                                                                                                                                                                                 3 DIIGTSPT----SWEQAAABAVQRARDSVDDIRVARVIE-----QDMAVDS--AGKITY 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDINE-2806128; Herrmann H., Fouquet B., Franke W.W.; Herrmann H., Fouquet B., Franke W.W.; Expression of intermediate filament proteins during development of Xenopus laevis. II. Identification and molecular characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Development 105:299-307(1989).

-!- FUNCTION: DESMIN ARE CLASS-III INTERMEDIATE FILAMENTS FOUND IN MUSCLE CELLS.

NETWORK CONNECTING MYOFIBRILS TO EACH OTHER AND TO THE PLASMA MEMBRANE FROM THE PERIPHERY OF THE Z-LINE STRUCTURES.

-!- SUBUNIT: Homopolymer.

-!- SUBCELLULAR LOCATION: Cytoplasmic.

-!- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                Local Similarity 29.4%; Pred. No. 23; ones 20; Conservative 11; Mismatches 25; Indels 12;
                                                                                       Score 60; DB 1; Length 321;
PROSITE; PS00433; PHOSPHOFRUCTOKINASE; 1.
Kinase; Transferase; Glycolysis; Complete proteome.
SEQUENCE 321 AA; 35025 MW; 4871609FECCAC91D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00038; filament; 1.
Pfam; PF00038; filament head; 1.
PROSITE; PS00226; IF; 1.
Intermediate filament; Colled coil; Muscle protein.
DOMAIN 1 96 HEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                          458 AA:
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TAIL.
COIL 1A.
LINKER 1.
COIL 1B.
LINKER 12.
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LINKER 2.
COIL 2B.
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InterPro; IPR006821; Filament_head.
InterPro; IPR001664; IF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X16842; CAA34740.1; -.
                                                                                          18.5%;
29.4%;
                                                                                                                                                                                                                                                                                                                     191 IVASEVEF 198
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NCBL_TaxID=8355;
                                                                                                                                                                                                                                                                         51 RIKLEVSF 58
                                                                                                                                                                                                                                                                                                                                                                                                                                     DESM XENLA
P23239;
                                                                                          Query Match
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99310339; PubMed=10382966;
A Kawarabayasi Y., Hino Y., Horkkawa H., Yamazaki S., Haikawa Y.,
A Kawarabayasi Y., Hino Y., Horkkawa H., Yamazaki S., Haikawa Y.,
Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
A Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
A Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
A Yamazaki J., Kushida N., Oguchi H., Anki K.-I., Kubota K.,
A Nakamura Y., Nomura N., Sako, Y., Kikuchi H.,
A "Complete genome sequence of an aerobic hyper-thermophilic crenaronome Aeropyrum pernix Kl.";
D NA Res. 6:83-101(1999).
C CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP + diphosphate + L-leucyl-tRNA(Leu).
C -i- SUBCELLULAR LOCATION: Cytoplasmic.
C -i- SUBCELLULAR LOCATION: Cytoplasmic.
C -i- SUBLIARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                         PIR; H72699; H72699.

HAMMP; MF 00049; -; 1.
InterPro; IPR004493; Leu-tRNA-syntla.
InterPro; IPR004412; LRNA-synt.la.
InterPro; IPR001412; LRNA-synt.la.
InterPro; IPR00131; LRNA-synt.la.
ITGRPAMS; TIGR00395; leuß arch; 1.
ITGRPAMS; TIGR00395; leuß arch; I.
Aminoacyl-tRNA synthétase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                         6 GTSPTSWEQAAAEAVQRARDSVDDI--RVARV-IEQDMAVDSAGKITYRIKLEVSFK 59
                                                                                                                                                                                                                                                                                                                                                                                                   SYL AERPE STANDARD; PRT; 959 AA.

99YD97,
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeurS).
LEUS OR APE1015.
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                                                                                                                                             ä.
                                                                              18.4%; Score 59.5; DB 1; Length 458; larity 31.6%; Pred. No. 38; Conservative 11; Mismatches 25; Indels
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Pred. No. 78;
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Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
Desulfurococcaceae; Aeropyrum.
NCBI_TaxID=56636;
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ATP (BY SIMILARITY).
1, 985CB5168728F7AB CRC64;
                            E96167E1D8FDEB74 CRC64;
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STUTTER
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342 S'
52802 MW;
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Best Local Similarity 27.9%;
Matches 17; Conservative
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641
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640 6
959 AA;
                         458 AA;
                                                                                     Query Match
Best Local Similarity
Matches 18; Conserv
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BINDING
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833 VLSLIGGADTLVVTVAAEWKYRAVEAVRRARERGASMKEALREAFKVEGVDKREAARLVQ 892

38 0 38

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893 Q 893

Search completed: November 21, 2003, 16:04:17 Job time : 1.77823 secs

Title: Perfect score:

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Sequence:

Scoring table:

Searched:

Minimum DB Maximum DB

Database :

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Q8ydms brucella me
Q8fus2 brucella su
Q8fus2 brucella su
Q8fus1 legionella
Q23915 dictyosteli
Q921v3 rhizobium n
Q8624 human papil
Q8f134 drosophila
Q8f1nj1 drosophila
Q8fnj2 drosophila
Q8fnj2 drosophila
Q8fg14 corynebacte
Q9fg10 drosophila
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Q8j0z4 cryptococcu
Q8j122 cryptococcu
Q9rcz5 streptomyce
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Q8kpt8 synechococc
Q8jl22 virus phich
O52068 brucella ab
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MEDLINE=9829597; PubMed=9634230;

A Gordon S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,

A Gordon S.V., Eiglmeler K., Gas S., Barry C.E. III, Tekaia F.,

Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

A Badcock K., Farwell T., Gentles S., Hamlin N., Holroyd S.,

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Oliver S., Seeger K., Skelton S., Squares S., Squares R.,

Sulton J.E., Taylor K., Whitehead S., Barrell B.G.;

T Deciphering the biology of Mycobacterium tuberculosis from the

Complete genome sequence.";

Nature 333:537-544(1998).
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SEC OR RV0379 OR MTV036.14.
Mycobacterium tuberculosis.
Bacteria, Actinobacteria, Actinobacteriah, Actinobacteriah, Actinobacteriah, Actinobacteriah, Actinobacteriahes, Corynebacterium.
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100.0%; Score 324; DB 16; Length 71;
Best Local Similarity 100.0%; Pred. No. 1.5e-29;
Matches 66; Conservative 0; Mismatches 0; Indels
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Q8KCXQ
Q8KDYZ
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Q8FUS
Q9REFI
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                                                                                                                  NCBI_TaxID=1773;
 SEQUENCE
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1 VIDIIGTSPTSWEQAAAEAV......KITYRIKLEVSFKMRPAQPR
              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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61 PAQP 64
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   6 VIDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM 65
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 04, Last annotation update)
01-JUL-1997 (TrEMBLrel. 04, Last annotation update)
Hypothetical 7.2 kDa protein (Fragment).
Mycobacterium tuberculosis.
Bacteria, Actinobacteria, Actinobacteriades, Actinomycetales, Corynebacterinee, Mycobacterinee, Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.5%; Score 319; DB 2; Length 116; 98.5%; Pred. No. 1e-28; Live 0; Mismatches 1; Indels
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STRAIN-TB patient sputum #NTI64719;
Rao A.R., Vijaya S.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, U85467; AABS8554.1; -.
Hypothetical protein.
NON_TER
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                                                                                                                                                                                                                                                                                                                                                   01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 04, Last annotation update)
Hypothetical 12.7 kDa protein (Fragment).
Mycobacterium tuberculosis.
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Matches 65; Conservative
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                                                                      RPAOPR 66
                                                                                                                               66 RPAOPR 71
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Matches
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                                                                                                                                        Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 110;
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Pred. No. 2e_08;
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                                                                                                                                                                                                                    STRAIN=NTI 64719;
Satchidanandam V., Rama Rao A., Hegde S.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF001302; AABS4028.1; -.
                                                                                                                                                                                                                                                                                                                                                                 110 110 110 110 AA; 11903 MW; A21AB7D99A7B4F54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VIDIIGTSPISWEQAAAEAVQRARDSVDDIRVARVIEQDMAV 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 VIDIIGTSPTSWEQAAAEAVQXARDSVHDIRVARVIEQDMAV 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96 AA; 10298 MW; ZE5B14CB1D1E445C CRC64;
                                    01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 04, Last annotation update)
Hypothetical 11.9 kDa protein (Fragment).
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 04, Last annotation update)
Hypothetical 10.3 kDa protein (Fragment)
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VIDIIGTSPISWEQAAAEAVQRARDSVDDIRVARVI 36
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 190; DB 2;
Pred. No. 4.8e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 2e-08;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                58 6%; Scor. No. 4.0.
95.2%; Pred. No. 4.0.
... 0; Mismatches
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110 AA
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01-JUL-1997 (TrEMBLrel. 04, Created)
PRT;
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86.1%;
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NCBI_TaxID=1097;
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                                                                                Q8KAD4
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          RESULT 8
Q8KAD4
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                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDILINE-20504483; PubMed=11016950;

Ng W.V. Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukla-H.D., Lasky S.P., Maliga N.S., Thorsson V., Sbrogna J.,
Swartzell S., Weir D., Hall J., Dahl T.A., Welli R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., Jussana S.,
"Genome sequence of Halbbacterium species NRC-1.",
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
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STRAIN=MB4 / JCM 11007;

STRAIN=21992816; PubMed=11997336;

BaO Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J., Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling J. Tan H., Chen R., Wang J., Yu J., Yang H.;

Tan H., Chen R., Wang J., Yu J., Yang H.;

Genome Res. 12:689-700(2002)

EMBL, AD013092; AAM24542.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 31.2%; Score 101; DB 17; Length 77; Local Similarity 31.1%; Pred. No. 0.00044; les 19; Conservative 22; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 28.4%; Score 92; DB 16; Length 110; Best Local Similarity 28.8%; Pred. No. 0.0071; Matches 17; Conservative 17; Mismatches 25; Indels
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Bacteria, Firmicutes, Clostridia, Thermoanaerobacteriales,
Thermoanaerobacteriaceae, Thermoanaerobacter.
                                                                                                                                   Halobacterium sp. (strain NRC-1).
Archaea; Buryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
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SEQUENCE 110 AA; 11862 MW; 43C0606A4B05F6DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 AA; 8378 MW; C3C359B65E8A8306 CRC64;
01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) Vng1446h.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QBRAA6;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein TTE1318.
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                                                                                                                                                                                                                                          NCBI_TaxID=64091;
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2 IDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITY-RIKLEVSFKM 60
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 2. DISM 12025;

MEDLINE=22103685; PubMed=1203901;

A Bisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,

Bisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,

A Dodson R.J., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H.,

A Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,

A Hickey E.K., Peterson J.P., Durkin A.S., Kolonay J.L., Yang F.,

A Hickey E.K., Peterson J.P., Hansen C.L., Craven M.B., Radune D.,

Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,

Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.,

The complete genome sequence of Chlorobium tepidum TLS, a

Photosynthetic, anaerobic, green-sulfur bacterium.",

Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
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STRAIN-ATCC 15692 / PAO1;
STRAIN-ATCC 15692 / PAO1;
STRAIN-ATCC 15692 / PAO1;
STRAIN-ATCC 15692 / PAO1;
STRAIN-ATCC 15692 / PAO1;
STRAIN-ATCC 15692 / PADMEd=10984043;
STRAIN-ATCC C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Waarrener P., Hickey M.J., Brinkman F.S.L., Hufhagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Golter D.T., Folger R.R., Kas A., Lazbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pseudomonadaceae, Pseudomonas.
                                                                                                                                                                                                                                      Chlorobium tepidum. '
Bacteria; Chlorobi; Chlorobiales; Chlorobiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypotherical protein, Complete proteome.
SEQUENCE 70 AA; 7922 MW; 8C662B18D044F153 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e proteome.
5925D78BE2709A5E CRC64;
                                                              01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein CT2229.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
Hypothetical protein PA0038.
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Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.5%; Score 76; DB 16
30.0%; Pred. No. 0.28;
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EMBL; AE004443; AAG03428.1;
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nes 18; Conservative
PRELIMINARY;
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Best Local Similarity
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Nature 415:497-502(2002)
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Rest Local Similarity
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Best Local Similarity
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66 RLEOAE 71
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Q962B3
ID Q962B
AC Q962B
DT 01-DE
DT 01-DE
DT Amino
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                                                                                                           10 IELVGSSKTSIEDAINNALAEAAKSIQHLEWFEVVDTRGHIENGAVGHYQVTLKVGFRI 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P., Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J., Golding B., Puehler A., Thernandez-Lucas I., Becker A., Cowie A., Gouzy J., Golding B., Puehler A., The complete sequence of the 1,683-kb psymB megaplasmid from the N2-fixing endosymbiont Sinorhizoblum meliloti.", Proc. Natl. Acad. Sci. U.S.A. 98:9889-9834 (2001).

PMDL, ALG03642; CAC494681.; Complete proteome. SEQUENCE 69 AA; 7792 MW; FS3FBF80AE62C07D CRC64;
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                                                                    2 IDIIGTSPTSWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSFKM
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Ralstoniaceae; Ralstonia.
NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical procein RB0068.
RB0068 OR SMB20068.
Rhizobium meliloti (Sinorhizobium meliloti).
Blasmid 29/ymB (megaplasmid 2).
Bacteria; Proceobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium.
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Pred. No. 3.8;
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tive 17; Mismatches 14; Indels
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
11-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein RSp1175.
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Ralstonia solanacearum (Pseudomonas solanacearum).
       27;
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       Mismatches
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MEDLINE=21681879; PubMed=11823852;
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   17;
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Best Local Similarity 27.9%
Matches 19, Conservative
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       Conservative
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60 VMKVGFRI 67
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092X94
AC 092X9
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DT 01-DE
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Q8XQP6
       Matches
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A WOOD I.S., Castano-Merediz B.F., Dyer J., Shirazi-Beechey S.P.;

Wordiner regulator-Merediz B.F., Dyer J., Shirazi-Beechey S.P.;

Submitted (AUG-2001) to the EMBL/Genank/DDBJ databases.

-!- SHBCELDULAR LOCATION: INTEGRAL MENBRANE PROTEIN (BY SIMILARITY)

-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.

REMBL; AJ315928; CAC86564.1; -..

RICEPPO: IPR00105; HTHARAC.

RICEPPO: IPR001058; SUBA transporter.

RICEPPO: IPR001863; SUBA transporter.

RICEPPO: IPR001863; SUBA transporter.

REPPO: IPR001863; SUBA transporter.

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REPPO: IPR001863; SUBA TRANSPORT.
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                                                                                                                                                                                                          Score 65; DB 16; Length 83;
Pred. No. 6.1;
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PROSITE; PS00217; SUGAR_TRANSPORT_2;
SUGAR_TRANSPORT_2.
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EMBL; AL646083; CAD18326.1; -. Plasmid; Hypothetical protein; Complete proteome. SEQUENCE 83 AA; 9140 MW; 1EAAD51D4FA4871A CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Aminopeptidase N (EC 3.4.11.2).
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Last annotation update)
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40.0%; Pred. No. 56;
:ive 10; Mismatches
                                                                                                                                                                                                                                                                                                                     20; Mismatches
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PROSITE; PSO0041; HTH_ARAC_FAMILY_1; 1.
PROSITE; PS50850; MFS; 1.
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28.8%;
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SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicoverpa armigera (Cotton bollworm).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
Noctuidae; Heliothinae; Helicoverpa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X MEDLINE=21595285; PubMed=11759840; MEDLINE=21595285; PubMed=11759840; MEDLINE=21595285; PubMed=11759840; Marianeko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Kaneko T., Nakamura Y., Wolk C.P., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsumo A., Muraki A., Nakazaki M., Silmpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.; Sugimoto M., Takazawa M., Yamada M., Tabata S., Sugimoto M., Takazawa M., Yamada M., Tabata S., Sugimoto M., Takazawa M., Yamada M., Rawida M., Tabata S., Sugimoto M., Takazawa M., Yamada M., Rawida M., Tabata S., Sugimoto M., Takazawa M., Yamada M., Rawida M., Tabata S., Sugimoto M., Takazawa M., Yamada M., Rawida M., Tabata S., Sugimoto M., Takazawa M., Yamada M., Rawida M., Yamada M., Yamada M., Yamada M., Rawida M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.9%; Score 64.5; DB 5; Length 1030; 30.4%; Pred. No. 1.3e+02; Live 14; Mismatches 17; Indels 1.
                                                                                                                                                                   Angelucci C., Akhuret R.J., East P.;
Helicoverpa armigera aminopeptidase N gene APN2.";
Submitted (UNN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY038608; AAR85539.1; -.
R MEROPS; M01.013; -.
R InterPro; IPR001930; Ala peptase.
R InterPro; IPR0010525; Zn MTpeptdse.
R Pfam, PF01433; Peptidase M1; 1.
R PRINTS; PR00756; AlaDIPTASE.
R PROSITE; PS00142; ZINC_PROTEASE; 1.
Aminopeptidase; Hydrolase.
SEQUENCE 1030 AA; 114505 MW; 258A43E74EFBFCA7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 SWEQAAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEV 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.8%; Score 64; DB 16; Length 96; 26.7%; Pred. No. 9.4; tive 10; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 AA; 10897 MW; AC89D93E3B06C901 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 AA.
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Best Local Similarity
Local 16; Conserve
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SEQUENCE 96 AA;
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Q8Z0H1;
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Q75741;
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206 AA

PRT;

PRELIMINARY;

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18 ERMRRAEPAADKVRAVSRVLEKHGAITSSNTAANNVDCAMLEAQEEEEVSFPVRPQVP 75
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Mariani R., Kairchhoff F., Greenough T.C., Sullivan J.L.,
Desrosiers R.C., Skowronski J.;
"High frequency of defective nef alleles in a long-term survivor with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
19.8%; Score 64; DB 15; Length 206;
Best Local Similarity 31.0%; Pred. No. 23;
Matches 18; Conservative 12; Mismatches 18; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 EAVORARDSVDDIR-VARVIBODMAVDSAGKITYRI------KLEVSFKMRPAQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nonprogressive HIV-1 infection.";
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: NEF HAS GIPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES. IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 206 AA; 23974 MW; 12410737A86F8F25 CRC64;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Nef (Negative factor) (F-protein) (27 kDa protein)
                                                                                                                                                                                          Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U61813; AAB04732.1; -.
INESP; PO946; IEFN.
InterPro; IPR001559; HIV_Nef.
Pfam; PF00469; F-protein; 1.
Probom; PD000031; HIV_Nef; 1.
AIDS; GTP-binding; Lipoprotein; Myristate.
NON_TER
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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		eA º			SUMMARIES	
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
। । त ।	466	100.0	95	138	AAW32444	Mycobacterium tube
2	466	100.0	95	18	AAW32376	Mycobacterium tube
m	466	100.0	95	13	AAW81747	M. tuberculosis im
4	466	100.0	95	13	AAW64321	Mycobacterium tube
S	466	100.0	95	20	AAY32097	Mycobacterium tube
9	466	100.0	95	20	AAY39118	M. tuberculosis an
7	466	100.0	95	20	AAY38981	M. tuberculosis re
00	466	100.0	95	23	AAE29717	Mycobacterium tube
σ	466	100.0	95	23	AAE17581	Mycobacterium spec

Campos-neto A, Dillon DC, Houghton R, Reed SG, Skeiky YAW; Twardzik DR, Vedvick TH;

(CORI-) CORIXA CORP.

M. tuberculosis in Mycobacterium tube	cuberculosi	. tuberculosis		Mycobacterium tube	M. tuberculosis an	Mycobacterium tube	Antigenic fusion p	ų O	Mycobacterium anti	tub	M. tuberculosis fu	losis f	sis f	cuberculos	ſΩ	S	. tuberculos	sacterium	Mycobacterium tube	M. tuberculosis im	Mycobacterium tub	M. tuberculosis an	M. tuberculosis re	M. tuberculosis LH	culosis	culosis	M. tuberculosis LH	erium t	tuberculosi	M. tuberculosis an	erium tub	osis i	w	
7.7	913	99	521	984	598	960	459	4	137	306	922	Γ	908	3	AAU74592	8	2	Ŋ	8	70	134	3	399	9	20	36	7.1	16	9	AAY39128	3245	3169	AAY39126	
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4. 4. 6.6 6.0	466	9	v	ø	9	9	9	9	9	9	9	466	9	9	9	φ	ω	σ	σ	392	9	9	σ	ч	0	~	3	0	2	7	2	3	(
0 H	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	50	30	31	32	33	34	32	98	37	38	<u>რ</u>	40	41	42	43	44	

ALIGNMENTS

Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant; skin testing; M.tuberculosis. Mycobacterium tuberculosis antigen Tb38-1. AAW32444 standard; Protein; 95 AA. 96US-0680574. 95US-0523436. 95US-0533634. 96US-0620874. 96WO-US14674 Mycobacterium tuberculosis. (first entry) WO9709428-A2 30-AUG-1996; 01-SEP-1995; 22-SEP-1995; 22-MAR-1996; 05-JUN-1996; 12-JUL-1996; 09-JAN-1998 13-MAR-1997 AAW32444;

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AAW81747;
                                                                                                                                                                      Н
                                                                                                                Sequence
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                                                                                                                                                                                                                                                          TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 60
                                                                                                                                                                                                                                       1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
                                                                                                                                                                                                                    Gaps
                                                                                 A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, Tb38-1. The immunogenic protein, and fusion proteins containing one or more of the proteins or one of the proteins BSAT-6, are useful in vaccines, preferably when formulated with a mon-specific adjuvant, to induce an immune response against M.tuberculosis (for treatment or prevention).
                           New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are useful in vaccines for prevention or treatment of tuberculosis, also for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                        immunogen; vaccine; tuberculosis; non specific adjuvant;
                                                                                                                                                                                                                    .,
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                                                                                                                                                                                                  100.0%; Score 466; DB 18; Length 95; 100.0%; Pred. No. 2.1e-43; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                             KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95
                                                                                                                                                                                                                                                                                              KQELDEISTNIRQAGVQYSRADBEQQQALSSQMGF 95
                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculósis antigen Tb38-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Campos-neto A, Dillon DC, Houghton R,
Twardzik DR, Vedvick TH;
                                                               English
                                                                                                                                                                                                                                                                                                                                              AAW32376 standard; Protein; 95
                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%;
Marches 95; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                 testing; M.tuberculosis.
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95US-0523435.
95US-0532136.
96US-0650280.
                                                               Example 3; Page 124; 168pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96WO-US14675.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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N-PSDB; AAT91445.
WPI; 1997-192903/17.
N-PSDB; AAT91509.
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                                                                                                                                                                                 95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-JUL-1996;
01-SEP-1995;
22-SEP-1995;
22-MAR-1996;
05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9709429-A2
                                                                                                                                                                                                                                                                                                                                                                                   13-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-AUG-1996;
                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                         Antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                   skin
                                                                                                                                                                                                                                                                                                                             RESULT
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w immunogenic polypeptide(s) from soluble M. tuberculosis antigens useful for diagnosis of M. tuberculosis infection

Example 3; Page 136; 190pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB; vaccine; pharmaceutical; infection; diagnosis.
A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen. This immunogenic polypeptide can be used to diagnose M.tuberculosis infection by forming complexes with specific antibodies in the sample. Fragments of DNA encoding the immunogenic polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen, especially monoclonal antibodies or equivalent polyclonal antibodies, are also used for diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunogenic Mycobacterium tuberculosis polypeptide(s) and {\rm DNA.-} used to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 466; DB 18;
100.0%; Pred. No. 2.1e-43;
ive 0; Mismatches 0;
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Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW81747 standard; Protein; 95 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0818112.
96US-0730510.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 95; Conservative
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N-PSDB; AAV64491.
                                                                                                                                                                                                                                                                                                                                                                    95 AA;
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TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 60
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Tb38-1. The invention provides fusion proteins (see AAY32059-71)
containing at least 2 M. tuberculosis antigens such as Tb38-1, e.g.
Tb7-2 (see AAY32063) and a Tb49-Tb38-1 fusion. The new fusion
proteins are useful as vaccines for preventing tuberculosis
(claimed), for diagnosis (via in vitro assays or intradermal skin tests for detection of anti-M. tuberculosis antibodies), monitoring of disease progression, and treatment of tuberculosis. They are more effective immunogens than mixtures of the individual protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New fusion proteins useful for diagnosis, prevention and treatment tuberculosis -
                                                                                                                                                                                                                                                                                                                                                                  Tuberculosis, antigen, fusion protein; Tb38-1; diagnosis; therapy;
                                                                                                 KOELDEISTNIROAGVOYSRADEEOOOALSSOMGF
                                                             KOELDEISTNIRGAGVOYSRADEEOQOALSSOMGF
                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis antigen Tb38-1.
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                                                                                                                                                                                                   AAY32097 standard; Protein; 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 4D; 83pp; English.
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98US-0223040.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                   17-JAN-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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les 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                       vaccine; immunogen.
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                                                                                                                                                                                                                                           AAY32097;
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                                                                                                                                 1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is an antigenic portion of Mycobacterium tuberculosis antigen TD38-1. A DNA sequence (see AAV44384) coding for antigen TD38-1 was isolated from a M. tuberculosis strain H37Rv expression library using sera from patients having pulmonary or pleural tuberculosis. The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAW6421-W64379) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonucleotide probes and primers, for the diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated Mycobacterium tuberculosis polypeptides and DNA - used to develop products for the detection of M. tuberculosis infection
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Best Local Similarity 100.0%; Pred. No. 2.16-43;
Matches 95; Conservative 0; Mismatches 0; Indels
                   Length 95;
                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tuberculosis; infection; diagnosis; antigen; Tb38-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis antigen Tb38-1 peptide.
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Twardzik DR, Vedvick TS;
                   100.0%; Score 466; DB 19;
100.0%; Pred. No. 2.1e-43;
ive 0; Mismatches 0;
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                                                                                                                                                                                                     KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF
                                                                                                                                                                           61 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF
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                                                                                                                                                                                                                                                                                                                       A.
                                                                                                                                                                                                                                                                                                                     AAW64321 standard; Peptide; 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosis of tuberculosis
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96US-0729622.
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              Query Match
Best Local Similarity 100.
Matches 95; Conservative
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Reed SG, Skeiky YAW,
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                                                                                         1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGGWRGAAGTAAQAAVVRFQEAANKQ
                                  Gaps
                                   .,
Length 95;
                                  Indels
100.0%; Score 466; DB 20;
100.0%; Pred. No. 2.1e-43;
tive 0; Mismatches 0;
                                                                                                                                    95
                                                                                                                                                                   61 KOELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95
                                                                                                                                    61 KOELDEISTNIRQAGVOYSRADEEQQQALSSQMGF
                                                                                                                                                                                                                                   AAY39118
ID AAY39118 standard, Protein; 95
XX
                                                                                                                                                                                                                RESULT 6
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Gaps

0

1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 60

us-09-688-672a-10.rag

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Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Skeiky Y, Brannon M,
                                                                                                                   (CORI-) CORIXA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200272792-A2.
                                                                                                                                        Campos-Neto A,
                      WO9942118-A2
                                                               17-FEB-1999;
                                                                                     05-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-SEP-2002
                                           26-AUG-1999
                                                                                                                                                  Lodes MJ,
                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE29717;
                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE2971
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                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                    The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's, DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion tuberculosis—immune subjects. AAX192949 to AAX19460 and AAX39033 to AAX39225 are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TDAATLAĢĒAGNFĒRISGDLKTQIDĢVĒSTĀGSLĢGĢWRGAAGTĀAĢĀAVVRFĢĒAANKQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                   New antigens from Mycobacterium tuberculosis useful in diagnostic
skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antigen; diagnosis; detection; infection; antibody; immunisation; vaccine; immunity.
                                                              Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection; immune response; skin test.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 95;
                                                                                                                                                                                                                                                 Houghton R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                             M. tuberculosis antigen Tb38-1 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M. tuberculosis recombinant antigen protein Tb38-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 466; DB 20; 100.0%; Pred. No. 2.1e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KOELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95
                                                                                                                                                                                                                                                Dillon DC, Hendrickson RC, Hc
SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                    Example 3; Page 113; 299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY38981 standard; Protein; 95
                                                                                                                                                                                             98US-0072967.
                                                                                                                                                                         99WO-US03268.
                                                                                                                                                                                                       98US-0025197.
                                                                                                           Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                             (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                 WPI; 1999-527409/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95 AA;
                                                                                                                                                                                                                                                 Campos-Neto A,
Lodes MJ, Reed
                                                                                                                                WO9942076-A2
                                                                                                                                                                         17-FEB-1999;
                                                                                                                                                                                             05-MAY-1998;
                                                                                                                                                                                                        18-FEB-1998;
                       05-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-NOV-1999
                                                                                                                                                    26-AUG-1999
                                                                                                                                                                                                                                                            Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY38981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TDAATLAQBAGNFBRISGDLKTQIDQVBSTAGSLQGQWRGAAGTAAQAAVVRFQBAANKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaccine; immunity; diagnostic agent; gene therapy; Tb38-1 antigen;
                                                                                                                                                                                                                                                                                                                                                             New polypeptide comprising antigenic portions of M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                            Houghton R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis Tb38-1 antigenic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 466; DB 20;
100.0%; Pred. No. 2.1e-43;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KOELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95
                                                                                                                                                                                            Hendrickson RC, Ho
YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF
                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Page 159; 323pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guderian J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE29717 standard; Protein; 95
                                                                                                                                                                                                                       Skeiky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-MAR-2002; 2002WO-US08223
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99WO-US03265
                                                     98US-0072596
                                                                                98US-0024753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis.
                                                                                                                                                                                            A, Dillon DC,
Reed SG, Skeiky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95; Conservative
                                                                                                                                         CORP.
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                                                                                                                                                                                                                                                                                   WPI; 1999-527416/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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07-OCT-1997;
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11-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW81706;
                          Claim 9;
                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                 The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polynucleotide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a polypeptide or its fragment. The Leishmania polynucleotide is selected from TSA, Leff, MIS, and 6H polynucleotides. Sequences of the invention are useful as vaccines to eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polynucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is My tuberculosis TD38-1 antigenic protein. TD38-1 is also referred to
                                                                                                                                                                                                                                                                                                                                                                         1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRCAAGTAAQAAVVRFQEAANKQ 60
                                                                                                                                                                                                                                                                                                                                                                                         New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polymucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fusion protein; antigen; serological sensitivity; immune response; tuberculosis; infection; vaccine; Tb38-1; Mtb11; 38-1 protein.
                                                                                                                                                                                                                                                                                                                                                    .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in
                                                                                                                                                                                                                                                                                                                            Length 95;
                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium species Tb38-1 (Mtb11; 38-1) protein.
                                                                                                                                                                                                                                                                                                                           100.0%; Score 466; DB 23;
100.0%; Pred. No. 2.1e-43;
ive 0; Mismatches 0;
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ც
                                                                                                                                                                                                                                                                                                                                                                                                                         KOELDEISTNIRQAGVOYSRADEEQQQALSSOMGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                KOELDEISTNIRQAGVOYSRADEEQQQALSSOMGF
                                                                                           Disclosure; Page 107; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alderson M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE17581 standard; Protein; 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JUN-2001; 2001WO-US19959
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01-FEB-2001; 2001US-265737P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-14,7798/19.
N-PSDB; AAD28352.
WPI; 2002-759844/82
N-PSDB; AAD47094.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Skeiky Y, Reed S,
                                                                                                                                                                                                                                                                                                    95 AA;
                                                                                                                                                                                                                                                                             MTb11 or 38-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200198460-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE17581;
                                                                                                                                                                                                                                                                                                     Seguence
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                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
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The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nuclectides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with tuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention are useful for eliciting an immune response in a mammal, e.g., human, immunised with BCG. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the polynucleotides are useful as diagnostic tools in patients infected with Mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the immunogens to generate or elicit a protective immune response in a patient and for raising anti-M. tuberculosis and non-manning patient and for raising anti-M. tuberculosis antibodies in a non-human patient and for raising anti-M. tuberculosis antibodies in a non-human patient and for raising anti-M. tuberculosis antibodies in a non-human patient and for raising anti-M. tuberculosis antibodies in a non-human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for intradermal skin test. The present sequence is Mycobacterium species (DAS8-1 (Mtbl1; 38-1) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnostic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           animal. Sequences of the invention are also used as vaccines. MTB32A (usion proteins of the invention are useful as in vivo diagnostic age for intradermal skin test. The present seminance is Monochamana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DC, Houghton R, Lodes MJ;
Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 466; DB 23; Best Local Similarity 100.0%; Pred. No. 2.1e-43; Matches 95; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M. tuberculosis immunogenic polypeptide Tb38-IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF
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Page 123; 136pp; English.
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96US-0730510.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dillon DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-JAN-1999 (first entry)
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Reed SG, Skeiky YAW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-261042/23.
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kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonucleotide probes and primers, for the diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9942076-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-FEB-1998;
                                                                                                                                                                                                                                                                                                                       05-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lodes MJ,
                                                                                                                                                                                                                                                                                               AAY39136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                       Sequence
                                                                             Query Match
                                                                                           Local
                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                              RESULT 12
                                                                                                                                                                                                                                                            AAY39136
    88 X G G G
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                                                                                                                                                                                                                                                         65
                                                                                                                                                                                                                                                 This polypeptide comprises a partial sequence of Mycobacterium tuberculosis antigen Tb38-IN. It is encoded by genomic DhA isolated form a M. tuberculosis strain H37Rv genomic library using a probe derived from clone Tb38-I (see AAV44384). The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAW6429-W6479) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic
                                                                                                                                                                                                                                  TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
                                                                                                                                                                                                          Gaps
                                                                                                                      may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated Mycobacterium tuberculosis polypeptides and DNA - used to develop products for the detection of M. tuberculosis infection
  to develop products for the detection of M.\ tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
                                                                This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a me for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or be used for the diagnosis of tuberculosis.
                                                                                                                                                                                                          o,
                                                                                                                                                                                  Length 100;
                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tuberculosis; infection; diagnosis; antigen; Tb37-FL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dillon DC, Houghton R, Lodes MJ; YAW, Twardzik DR, Vedvick TS;
                                                                                                                                                                               100.0%; Score 466; DB 19;
llarity 100.0%; Pred. No. 2.2e-43;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                    KOELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100
                                                                                                                                                                                                                                                                                    95
                                                                                                                                                                                                                                                                                                                                                                                                                                                  tuberculosis antigen Tb38-IN.
                                         Example 3B; Page 138-139; 230pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Page 145; 250pp; English.
                                                                                                                                                                                                                                                                                                                                                                          AAW64339 standard; Protein; 100 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-US18214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0818111.
96US-0729622.
                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Campos-Neto A, Dillon
Reed SG, Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-251292/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP
                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 95; Conserv
                                                                                                                                                        100 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAR-1997;
11-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                           09-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-APR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                   AAW64339;
                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                  RESULT 11
AAW64339
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M. tuberculosis Ag's. DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytckine secretion by, T. B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AZI2949 to AAZI3460 and AAY39083 to AAX39225 are used in the exemplification of the present invention.
                                                                                                                                                                         9
                                                                                                                                                                                                                             TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
                                                                                                                                                                      1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antigens from Mycobacterium tuberculosis useful in diagnostic
skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection; immune response; skin test.
                                                                                                        0
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                                                 Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Houghton R;
Vedvick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M. tuberculosis antigen Tb38-IN amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 466; DB 20;
ilarity, 100.0%; Pred. No. 2.2e-43;
Conservative 0; Mismatches 0;
                                                 1100.0%; Score 466; DB 19;
1100.0%; Pred. No. 2.2e-43;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                            KOELDEISTNIROAGVOYSRADEEQOOALSSOMGF 100
                                                                                                                                                                                                                                                                                       95
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YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                       61 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF
                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Page 133-134; 299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY39136 standard; Protein; 100 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dillon DC,
SG, Skeiky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0072967.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                              95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Campos-Neto A, Dill
Lodes MJ, Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 95; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-527409/44
                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 AA;
100 AA;
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TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides the protein and coding sequences for members of the esat-6 gene family from Mycobacterium tuberculosis. Th proteins include RV0287, RV1036c, RV3346c, RV2346c, RV2554c, RV2654c, RV3090c, RV3990c, RV3905c. These can be used to produce vaccines against, and in the diagnosis of, tuberculosis (TB) infection. The present sequence is on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptide encoded by a member of the esat-6-gene family for immunizing against and diagnosis of tuberculosis
                                                                                    Tuberculosis, TB; vaccine; esat-6 gene family; Rv0287; Rv1036c; Rv1037c; Rv2346c; Rv2348c; Rv2653c; Rv2654c; Rv3020c; Rv3444c; Rv3445c; Rv3890c; Rv3891c; Rv3905c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MTBN4; tuberculosis; BCG; vaccine; infection; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 466; DB 22;
Pred. No. 2.2e-43;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 KOELDEISTNIRQAGVOYSRADEEQQQALSSQMGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis protein MTBN4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Page 65; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB19845 standard; Protein; 100
                                                 M tuberculosis Rv3874 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                       99DK-0001020.
99US-0144011.
                                                                                                                                                                                                                                                                    13-JUL-2000; 2000WO-DK00398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-MAY-2000; 2000WO-US12257
                                                                                                                                                                                                                                                                                                                                                            (STAT-) STATENS SERUM INST.
                                                                                                                                                             Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis.
                 24-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-091923/10.
                                                                                                                                                                                                                                                                                                                                                                                                 Skjot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 95; Conserv
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                                                                                                                                                                                             WO200104151-A2.
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                                                                                                                                                                                                                                                                                                       13-JUL-1999;
15-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                 Andersen P,
                                                                                                                                                                                                                                  18-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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             1 IDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 60
                                               65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGGWRGAAGTAAQAAVVRFQEAANKQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes novel recombinant antigens and their encoding
                                      6 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in biological sample by detecting antibodies which bind with the polypeptides, and received as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                                                                                                                                                                                                                                                                                                                                                           Antigen; diagnosis; detection; infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptide comprising antigenic portions of M. tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Houghton R;
                                                                                                                                                                                                                                                                                                                    M. tuberculosis recombinant antigen protein Tb38-IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 466; DB 20; Best Local Similarity 100.0%; Pred. No. 2.2e-43; Matches 95; Conservative 0; Mismatches 0;
                                                                                                         66 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100
                                                                                    9
53
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Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Page 179; 323pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB35218 standard; Protein; 100 AA
                                                                                                                                                                                                             AAY38993 standard; Protein; 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US03265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0072596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0024753
                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-527416/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9942118-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-MAY-1998;
18-FEB-1998;
                                                                                                                                                                                                                                                                                    05-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-AUG-1999
                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
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Gaps

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Length 100; Indels

22; ö 65

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one of

04-MAY-1999; 99US-0132505.

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1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 60
                                                                                                                                                                                                                                                                                                  The present sequence is that of the Mycobacterium tuberculosis MTBM protein. This is 1.0f 8 proteins, i.e. MTBM1-8 (see AAA99035-42) identified as being present in the genome of Kee AAA99035-42) identified as being present in the genome of Mycobacterium bovis. MTBM1-8 represent troom the genome of the BGG strain of Mycobacterium bovis. W. tuberculosis and BGG and, in particular, for diagnostic methods which discriminate between exposure of a subject to M. tuberculosis and vaccination with BGG. The invention features these MTBM polypeptides, functional fragments of them, DNA encoding them, vectors, transformed cells, and diagnostic, therapeutic, and methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                     Novel polypeptide encoded by open reading frames present in Mycobacterium tuberculosis genome and not by the BCG strain of M. bovis, useful as vaccine and for diagnosing tuberculosis infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. 2.2e-43;
Matches 95; Conservative 0; Mismatches 0; Indels 0
                                                        (PUBL-) PUBLIC HEALTH RES INST NEW YORK
                                                                                                                                                                                                                                                                  Claim 11; Fig 1; 35pp; English.
                                                                                                                               WPI; 2001-007153/01.
N-PSDB; AAA89038.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 AA;
                                                                                              Gennaro ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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Search completed: November 21, 2003, 16:03:12 Job time : 5.7517 secs

KOELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100 61 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95

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6 TDAATLAQEAGNFERISGDIKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 65

93, Appl 93, Appl 93, Appl 109, Appl 143, Appl 94, Appl 17, Appl 17, Appl 17, Appl 10, Appl 10, Appl 11, Appl 1

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database :

Result

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Arc, Antonio
APPLICANT: Campos-Arc, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Wadvick, Thomas S.
APPLICANT: Veardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,112
FILING DATE: 13-MAR-1997
               US-08 818-112-93
US-09-056-556-93
US-09-073-009-109
US-09-073-009-143
US-08-818-112-94
US-08-06-6758-1
US-08-818-112-94
US-08-818-4148-2
US-08-818-4148-3
PCT-US94-00224-1
US-09-116-492A-10
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US-08-121-3
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100.0%; Score 466; DB 3;
Best Local Similarity 100.0%; Pred. No. 2.1e-46;
Matches 95; Conservative 0; Mismatches 0;
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APPLICATION NO...
APPLICATION 424
FILING DATE: 13-MAR-1>>.
CLASSIFICATION: 424
ATOCNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 210121.411C6
TELECHONONICATION INFORMATION:
TELEPAN: (206) 682-6031
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH 95 amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 88, Application US/08818112
; Patent No. 6290969
; GENERAL INFORMATION:
  JS-08-818-112-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
88, Appl
88, Appl
89, Appl
110, App
1115, App
1116, App
209, App
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Sequence
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                                                                                                                                                                                                                                             466
1 TDAATLAQEAGNFERISGDL.....VQYSRADEEQQQALSSQMGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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/cgn2 6/ptcdata/1/jaa/5B_COMB.pep:*
/cgn2 6/ptcdata/1/jaa/6A COMB.pep:*
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/cgn2 6/ptcdata/1/jaa/PCTUS COMB.pep:*
/cgn2 6/ptcdata/1/jaa/PCTUS COMB.pep:*
               GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-818-112-88
US-09-818-111-89
US-09-072-596-89
US-09-072-596-89
US-08-818-112-115
US-08-918-111-1110
US-09-9156-556-115
US-09-9156-556-214
US-09-9156-556-214
US-09-9156-556-214
US-09-918-112-117
US-09-918-111-112
US-09-918-111-112
US-09-918-918-918-98
US-09-9116-492A-7
US-09-9116-492A-28
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US-09-9116-492A-28
                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                  328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                      November 21, 2003, 15:58:31
                                                                                              - protein search, using sw model
                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patents AA: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq length: 0
seq length: 2000000000
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STREET: 63
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STREET: 6:
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                              1 TDAATLAQEAGNFERISGELKTQIDQVESTAGSLQQQWRGAAGTAAQAAVVRFQEAANKQ 60
TDAATLAQBAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 60
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                                                                                                                                                                                                                                                                                                        APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yaair A.W.
APPLICANT: Skeiky, Yaair A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Twardix, Thomas S.
APPLICANT: Twardik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCHWARE PATENTIN Belease #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/08/111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTONENT/AGENT INFORMATION:
NAME: MAKI, DATIG J. 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 466; DB 4;
100.0%; Pred. No. 2.1e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95
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                                                                                                                  61 KOELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTY PARABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: I Floppy disk
COMPUTER: I BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                         ; Sequence 89, Application US/088181111; Patent No. 6338852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 95 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Seattle
STATE: Washington
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Best Local Similarity
Matches 95; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
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TOPOLOGY:
US-08-818-111-89
                                                                                                                                                                                                 RESULT 2
US-08-818-111-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
CITY: Se
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Sequence 88, Application US/09056556 Patent No. 6350456 GENERAL INFORMATION: APPLICANT: Reed, Steven G.

RESULT 3 US-09-056-556-88

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1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TILLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Daniel R.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: HENDRICKS: 350
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                         3: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                            E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 466; DB 4;
100.0%; Pred. No. 2.1e-46;
live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 89, Application US/09072596; Patent No. 6458366; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 95 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 95, Conservative
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Washington
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0;

Length 100; Indels

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1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 60
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                                                                                                                                                                                                                                                    Score 466; DB 3;
Pred. No. 2.3e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KOELDEISTNIROAGVOYSRADEEOOOALSSOMGF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95
                                                                                                                                                                                                                                                                                                                0; Mismatches
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Patent No. 6338852
GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%;
Matches 95; Conservative 0
                                                                        LENGTH: 100 amino acids TYPE: amino acid STRANDEDNESS:
                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIRANDEDNESS:
                                                                                                                                                                    linear
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                                                                                                                                                              , TOPOLOGY:
US-08-818-112-115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Seeiky, Yaair A.W.
APPLICANT: General A.W.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Howard A.W.
APPLICANT: Twardzik, Daniel R.
TILLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 63300 Columbia Center, 701 Fifth Avenue
CONTRY: USA
ZIP: 98104-7092
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Dainatin PC-DS/MS-DOS
COMPUTER: Dainatin PC-DS/MS-DOS
COMPUTER: Dainatin PC-DS/MS-DOS
COMPUTER: Dainatin PC-DS/MS-DOS
COMPUTER: Dainatin PC-DS/MS-DOS
COMPUTER: Dainatin PC-DS/MS-DOS
COMPUTER: Dainatin PC-DS/MS-DOS
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COMPUTER: Dainatin PC-DS/MS-DOS
COMPUTER: Dainatin PC-DS/MS-DOS
COMPUTER: Dainatin PC-DS/MS-DOS
COMPUTER: Dainatin PC-DS/MS-DOS
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COMPUTER: IBM.PC compatible
COMPUTER: IBM.PC compatible
SOSTWARE: PatentIN DARS.
CURRENT APPLICATION DARS:
TLING DATE: 05-MAY-1998
CLASSITCATION:
FILING DATE: 05-MAY-1998
CLASSITCATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAK; David J. 31,392
REFRENCE/POCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 95 aming acids

LONGTH: 95 aming acids
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APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATA:
FILING DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,32
REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
100.0%; Score 466; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.1e-46;
Matches 95; Conservative 0; Mismatches 0;
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Patent No. 6290969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SS: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: siz
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US-09-072-596-89
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1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
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APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neco, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Wedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SECTIONES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and PPPLY.
STREEP.
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100.0%; Score 466; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 2.3e-46;
Matches 95; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: Seattle
STREET: 6300 Columbia Center, 701 Fifth Avenue
STREET: 6300 Columbia Center, 701 Fifth Avenue
STATE: Washington
COUNTRY: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER: ISP PC Compatible
CONPUTER: ISP PC Compatible
CORPUTER: ISP PC Compatible
CORPUTER: ISP PC Compatible
CORPUTER: ISP PC Compatible
CORPUTER: ISP PC Compatible
CORPUTER: ISP PC COMPATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAXI, DAVIG J.
REGISTRATION: WINNER: 31.392
REGISTRATION WINNER: 31.392
REGISTRATION WINNER: 31.392
REGISTRATION WINNER: 31.392
REGISTRATION WINNER: 31.392
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TUBERCULOSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRPQEAANKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 214, Application US/09056556

Patent No. 6350456

GENERAL INFORMATION:

APPLICANT: Read, Steven G.

APPLICANT: Read, Yasir A.W.

APPLICANT: Dillon, Davin C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241

CORRESPONDENCE ADDRESS:

ADDRESSES: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 100;
Hendrickson, Ronald C. VENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                   COMPUTER READABLE FORM:
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONTUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PRESENT PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
                                 NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE:
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 KOELDEISTNIROAGVOYSRADEEQQQALSSOMGF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 466; DB 4; 100.0%; Pred. No. 2.3e-46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INPORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95; Conservative
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                                                                                                               CITY: Seattle
STATE: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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Matches 95; Conserv
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US-09-072-596-110
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  APPLICANT:
                                                                                                                                                       COUNTRY:
                    LITLE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
                                                                                                                                                                                                                                                                        COMPOUNDS AND METHODS FOR THE PREVENTION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 466; DB 4; Length 100; 100.0%; Pred. No. 2.3e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                   66 KÓELDEISTNIROAGVOYSRADEBOQOALSSOMGF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KOELDEISTNIRQAGVOYSRADEEQQQALSSOMGF 100
                    61 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                           RESULT 7
3.09-09-06-556-115
Sequence 115, Application US/09056556
Patent No. 6350456
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 110, Application US/09072596 Patent No. 6458366 GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael R.
                                                                                                                                                                                                          APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (206) 622-496
TELEFAR. (206) 682-6031
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 100 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and E
STREET: 6300 Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                        Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
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APPLICANT
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TUBERCULOSIS
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                                                                                                                                                    1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 60
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                                                                                                          .
0
                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 3.5e-45;
Matches 95; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : Twardzik, Daniel R.:
: Lodes, Michael J.
: Hendrickson, Ronald C.
INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
COUNTRY: USA
CONFUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURENT APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                 489 KOELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 466; DB 4;
100.0%; Pred. No. 3.5e-45;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                          95
                                                                                                                                                                                                                                                       61 KOELDEISTNIRQAGVQYSRADEEQQQALSSQMGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 KOELDEISTNIRQAGVOYSRADEEQQQALSSQMGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
TATCANEY TAPORMATION:
NAME: Maki, David 4, 31,392
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 346, Application US/09072596
Patent No. 6458366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 346:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 802 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lodes, Michael APPLICANT: Lodes, Michael APPLICANT: Hendrickson, TITLE OF INVENTION: COMPANDERS OF SEQUENCES: 350 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein US-09-072-596-346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Seattle
     US-09-072-596-209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Skeiky, Yeasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF THIE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6500 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 466; DB 4; Length 802;
Best Local Similarity 100.0%; Pred. No. 3.5e-45;
Matches 95; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 GURRENT APPLICATION DATE: US/09/072,596 FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               489 KOELDEISTNIRQAGVQYSRADBEQQQALSSQMGF 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 KOELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95
                    NAME: Naki, David J.
REGISTRATION VNDBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELEPOMENICATION INFORMATION:
TELEPANS: (206) 622-4900
TELEFAX: (206) 622-6031
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 802 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 209, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVIG J.
REGISTRATION NUMBER: 31,392
REFRENCE/DOCKET NUMBER: 2101:
TELEPHONE: (206) 622-4900
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (206) 622-490
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 802 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                         single
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CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                              ; TOPOLOGY:
US-09-056-556-214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
US-09-072-596-209
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TUBERCULOSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                  16 ISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQKQELDBISTNIRQAG 75
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Howers S.
APPLICANT: Twadzik, Thomas S.
TITLE OF INVENTION: CoMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 148
                                                                                                                                                                                                                                                                                                                           Query Match

84.1%; Score 392; DB 3; Length 80;
Best Local Similarity 100.0%; Pred. No. 5.3e-38;
Matches 80; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111 FILING DATE: 13-MAR-1997 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 13-WAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MARI, DAVIG J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKER NUMBER: 210121.417C6
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.1%; Score 392;
                                                     210121.411C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible.
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Falance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 112, Application US/08818111
Patent No. 638852
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFRENCE/DOCKET NUMBER: 2101:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 VOYSRADEEQQQALSSQMGF 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 VOYSRADBEQQQALSSONGF 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 amino acids
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                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
US-08-818-112-117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-818-111-112
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                   US-09-116-492A-5

Sequence 5, Application US/09116492A

Sequence 5, Application US/09116492A

Patent No. 6436409

APPLICANT: BERTHERLY. PRANCOIS-XAVIER

APPLICANT: BERTHERLY. PRANCOIS-XAVIER

APPLICANT: ANDRESEN, PETER

APPLICANT: PETER

APPLICANT: PETER

APPLICANT: PETER

APPLICANT: PETER

TITLE OF INVENTION: POLYNUCLEOTIDE FUNCTIONALLY CODING FOR THE LHP PROTEIN FROM MYCOE

TITLE OF INVENTION: USING THE SAME

FILE REFERENCE: 0660-0137-27X

CURRENT APPLICATION NUMBER: US/09/116,492A

CURRENT APPLICATION NUMBER: 06725,631

PRIOR PILING DATE: 1998-07-16

PRIOR FILING DATE: 1997-07-16

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PATENTIN VEFSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
VERVION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
VENTION: AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.1%; Score 462; DB 4; Length 100; 98.9%; Pred. No. 6.5e-46; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112 FILING DATE: 13-MAR-1997 CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 KOELDEISTNIROAGVOYSRADEEOOOALSSOMGF 100
                489 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ), ORGANISM: Mycobacterium tuberculosis
US-09-116-492A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 117, Application US/08818112
Patent No. 6290969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 98.99
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: COM
TITLE OF INVENTION: AND
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 5
LENGTH: 100
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-818-112-117
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
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TREAT
                                                                           16 ISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQKQELDEISTNIRQAG 75
                                                                                                                1 ISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVREQEAANKQKQELDEISTNIRQAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQKQELDEISTNIRQAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 ISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQKQELDEISTNIRQAG 75
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCES: 241
CORRESPONDENCES: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98144-7032
COMPUTER: BADDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pacentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION: APPLICATION:
                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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  100.0%; Pred. No. 5.3e-38;
tive 0; Mismatches 0; Indels
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84.1%; Score 392; DB 4; I

Best Local Similarity 100.0%; Pred. No. 5.3e-38;

Matches 80; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 62-4900
TELEFAX: (206) 68-6031
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: November 21, 2003, 16:11:38 Job time : 2.0034 secs
                                                                                                                                                                                                                                                                                                                                                 Sequence 117, Application US/09056556 Patent No. 6350456 GENERAL INFORMATION:
                                                                                                                                                                          76 VOYSRADEEQQQALSSOMGF 95
                                                                                                                                                                                                                      61 VOYSRADEEQQQALSSOMGF 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 VOYSRADEEQQQALSSQMGF 95
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Best Local Similarity 100. Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-056-556-117
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Sequence

Sequence 7, Appli Sequence 12, Appl Sequence 12, Appl Sequence 98, Appl Sequence 96, Appl Sequence 97, Appl Sequence 97, Appl Sequence 10195, Appl Sequence 10195, Appl Sequence 104, Appl Sequence 104, Appl Sequence 104, Appl Sequence 104, Appl Sequence 107, Appl Sequence 107, Appl Sequence 107, Appl Sequence 108, Appl Sequence 108, Appl Sequence 108, Appl Sequence 108, Appl Sequence 108, Appl Sequence 108, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl

Sequence 12, Appl Sequence 12, Appl

Seguence 16, Seguence 49, Sequence 12,

protein

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METHODS FOR IMMUNOTHERAPY OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
CONNYTY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BASTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-10004, 843
FILING DATE: 25-Feb-2002
CLASSIFICATION: CURROWN>
US-10-084-843-117
US-10-193-002-112
US-10-193-002-112
US-10-140-045-6
US-10-140-045-28
US-10-140-045-28
US-10-140-045-28
US-10-184-843-98
US-10-184-843-95
US-10-084-843-95

US-10-088-732A-47
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US-10-098-732A-49
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APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVIG J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 88, Application US/10084843
Publication No. US20030143243A1
GENERAL INFORMATION:
Selven G.
Selven G.
Campos-Neto, Pavin A.W.
Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Romald C.
Hendrickson, Romald C.
TITLE OF INVENTION: COMPOUNDS AND MET
      US-10-084-843-88
                                                                                                                                                                       117
100.5
100
                                                                                                                                                                                                                                  Sequence 88, Appl
Sequence 35, Appl
Sequence 115, Appl
Sequence 110, App
Sequence 639, Appl
Sequence 8, Appli
Sequence 10, Appl
Sequence 214, Appl
Sequence 214, Appl
Sequence 311, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 116, Appl
Sequence 36, Appl
Sequence 116, Appl
Sequence 116, Appl
Sequence 116, Appl
Sequence 116, Appl
Sequence 116, Appl
Sequence 116, Appl
Sequence 116, Appl
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Sequence 116, Appl
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Sequence 116, Appl
                                                                                                          November 21, 2003, 16:08:22; Search time 3.70522 Seconds (without alignments) 4680.740 Million cell updates/sec
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                                                                                                                                                                                      466
1 TDAATLAQEAGNFERISGDL.....VQYSRADEEQQQALSSQMGF
                                                                                                                                                                                                                                                                                                                                                                                                                                            Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/PCT_RBW PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_RBW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/PCT_RBW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBGOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO6_PUBGOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

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14: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

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                    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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2 US-10-193-002-89
2 US-10-098-13-115
2 US-10-084-843-115
2 US-10-084-843-115
3 US-10-193-002-110
6 US-10-185-460-8
1 US-10-359-460-8
1 US-10-359-460-8
2 US-10-359-483-351
2 US-10-193-002-396
3 US-10-1359-460-10
3 US-10-1359-460-10
5 US-10-1359-460-10
6 US-10-1359-460-10
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Maximum Match 100%
Listing first 45 summaries
                                                                               - protein search, using sw model
                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                       US-09-688-672A-10
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Perfect score:
Sequence:
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Database :

Result No.

429789011211

Searched:

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Gaps

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1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 60
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                                                                                                                                                                                                                                        1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jeffrey
APPLICANT: Guderian, Jeffrey
APPLICANT: Constructs Comprising of ITLE OF INVENTION: Leishmania Antigen
TITLE OF INVENTION: Leishmania Antigen
FILE REPERBUE: 04058-012010US
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT FILING DATE: 2003-04-29
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Campos-Neto, Antonio
Houghton, Raymond
Veducick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendzicken, Ronald C.
Hendzicken, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
                                                                                                                                           Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 95;
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                                                                                                                                           Query Match 100.0%; Score 466; DB 12; Best Local Similarity 100.0%; Pred. No. 1.9e-43; Matches 95; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 466; DB 12;
100.0%; Pred. No. 1.9e-43;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                    61 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95
                                                                                                                                                                                                                                                                                                                                                                              61 KOELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 89:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 35, Application US/10098732A Publication No. US20030175294A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 115, Application US/10084843 Publication No. US20030143243A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 100.
Matches 95; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-084-843-115
                                                                                                 US-10-193-002-89
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Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                    Length 95;
                                                                                                                                                                                                                                                                                                                                                                              Indels
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CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                               100.0%; Score 466; DB 12; 100.0%; Pred. No. 1.9e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 KOELDEISTNIRQAGVOYSRADEEQQQALSSOMGF 95
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:

RPPLICATION NUMBER: US.10/193,002

RILING DATE: 10-U11-2002

CLASSIFICATION: «UNKNOWN»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                     ; TOPOLOGY: linear ; SEQUENCE DESCRIPTION: SEQ ID NO: 88: US-10-084-843-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 89, Application US/10193002
Publication No. US20030135026A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA ZIP: 98104 7092.
COMPUTER READBLE FORM: MEDIUM TYPE: Floppy disk
                                                         INFORMATION FOR SEQ IN O. SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 95 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         682-6031
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                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 95; Conservative
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Gaps

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Sequence 639, Application US/10080170
Publication No. US20030129601A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: COLE, S.T.
TITLE OF INVENTION: IDENTFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR TITLE OF INVENTION: TRATIENT OF MYCOBACTERIOSES
FILE REFERENCE: 03495.0218
CURRENT APPLICATION NUMBER: US/10/080,170
CURRENT APPLICATION NUMBER: 60/270,123
PRIOR PILING DATE: 2001-02-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 65
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.larity 100.0%; Pred. No. 2e-43;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 466; DB 12;
100.0%; Pred. No. 2e-43;
iive 0; Mismatches 0;
                                                                                                                                          CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-011-2002
CLASSIPICATION: «Unknown»

PRIOR APPLICATION: «Unknown»

PRIOR APPLICATION NATA:
APPLICATION NUMBER: US/09/072,596
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 KOELDEISTNIROAGVOYSRADEEQOOALSSOMGF 100
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                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 110:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 110: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 100 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: <Unknown>
                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 652
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 639
LENGTH: 100
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Best Local Similarity
Matches 95; Conserv
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Dillon, Davin C.
Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Romald C.
TILLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 12; Length 100;
                                                                                                                                                                                                                                                                      COMPUTER: 128.7 4128.4
COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION NUMBER: US/10/084,843
PRIOR APPLICATION NUMBER: US/10/084,843
PRIOR APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
RAPLICATION NUMBER: US/09/072,967
FILING DATE: 10FORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 100.0%; Score 466; DB 12; Length 1 Similarity 100.0%; Pred. No. 2e-43; 95; Conservative 0; Mismatches 0; Indels
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ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                        NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 KÖELDEISTNIRQAGVOYSRADEEQQQALSSOMGF 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELECHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 115: US-10-084-843-115
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Publication No. USZ0033135026A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                          COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 115:
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STRANDEDNESS: <Unknown>
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STATE: Washington
                                                                                                                                                     STATE: Washington
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Best Local Similarity
Matches 95; Conserv
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APPLICATION NUMBER: US/09/287,849
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US-09-287-849-10
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Best Local
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APPLICANT: Skeiky Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Netc, Autonio
APPLICANT: Campos-Netc, Autonio
APPLICANT: Corixa Corporation
APPLICANT: Corixa Corporation
APPLICANT: Corixa Corporation
APPLICANT: Corixa Corporation
APPLICANT: Corixa Corporation
APPLICANT: Corixa Corporation
APPLICANT: Davis and Their Uses
FILE REFERENCE: 014058-002020S
CURRENT FILING DATE: 1999-04-03
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR APPLICATION NUMBER: US 08/025,197
PRIOR APPLICATION NUMBER: US 08/025,197
PRIOR PLILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
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Publication No. US20030147911A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Conisa Corporation
TITLE OF INVENTION: Pusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TDAATLAQBAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQBAANKQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 466; DB 9; Length 358; Best Local Similarity 100.0%; Pred. No. 9.6e-43; Matches 95; Conservative 0; Mismatches 0; Indels
66 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 358
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CURRENT APPLICATION NUMBER: US/10/359,460
CURRENT FILING DATE: 2003-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / OTHER INFORMATION: Xaa = any amino acid
US-09-287-849-8
                                                                                                                                                                                                            Sequence 8, Application US/09287849
Patent No. US20020009459A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MOD RES
LOCATION: (254)
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LENGTH: 358
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APPLICANT: Different Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Compos-Neto, Antonio
APPLICANT: Compos-Neto, Antonio
APPLICANT: Corras Corporation
TITLE OF INVENTION: End Their Uses
FILE REFERENCE: 014058-00902003
CURRENT APPLICATION NUMBER: US 08/918,112
PRIOR APPLICATION NUMBER: US 08/912,578
PRIOR FILING DATE: 1997-02-13
PRIOR FILING DATE: 1997-02-18
PRIOR PLICATION NUMBER: US 08/92,578
PRIOR PLICATION NUMBER: US 09/025,197
PRIOR PLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,37
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: PALEALLING DATE: PALEALLING DATE: PALEALLING DATE: PALEALLING DATE: PALEALLING DATE: PALEALLING DATE: PALEALLING DATE: PALEALLING DATE: PALEALLING DATE: PALEALLING DATE: PALEALLING DATE: PALEALLING DATE: PALEALLING DATE: PALEALLING DATE: PALEALLING DATE: PALEALLING DATE: PALEALLING DATE: PALEALLING DATE: PALEALLING DATE: PALEALLING DATE: PALEALLING DATE: PALEALLING DATE: PALEALLING DATE: PALEALLING DATE: PALEALLING DATE: PALEALLING DATE: PALEALLING DATE: PALEALLING DATE: PALEALLING DATE: PALEALLING DATE: PALEALLING DATE: PALEALLING DATE: PALEALLING DATE: PALEALLING DATE: PALEALLING DATE: PALEALLING DATE: PALEALING DATE: PALEALING DATE: PALEALING DATE: PALEALING DATE: PALEALING DATE: PALEALING DATE: PALEALING DATE: PALEALING DATE: PALEALING DATE: PALEALING DATE: PALEALING DATE: PALEALING DATE: PALEALING DATE: PALEALING DATE: PALEALING DATE: PALEALING DATE: PALEALING DATE: PALEALING DATE: PALEALING DATE: PALEALING DATE: PALEALING DATE: PALEALING DATE: PALEALING DATE: PALEALING DATE: PALEALING DATE: PALEALING DATE: PALEALING DATE: PALEALING DATE: PALEALING DATE: PALEALING DATE: PALEALING DATE: PALEALING DATE: PALEALING DATE: PALEALING DATE: PALEALING DATE: PALEALIN
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PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/818,112
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PALENTIN VOY: 2.1
SEQ ID NO 8
LENGTH: 358
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COTATION: (254)
COTHER INFORMATION: Xaa = any amino acid
WS-10-359-460-8
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ORGANISM: Artificial Sequence
FEATURE:
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SEQ ID NO 10
LENGTH: 802
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
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429 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVFFQEAANKQ 488
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                                                                                                                                                                                  RESULT 11
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                                                                                                                                                                                                    429 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 488
                                                                                                                                                           1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
                                                                                                                   Gaps
      , OTHER INFORMATION: Description of Artificial Sequence:tetra-fusion US-09-287-849-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Houghton, Raymond
VedYick, Thomas S.
Twatdzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
Hendrickson, Ronald C.
AND DIAGNOSIS OF TUBERCULOSIS
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                                                                       Length 802;
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MEDLUM TYPES FLOPPY
COMPUTER. EBABLE FORM:
MEDLUM TYPES FLOPPY
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION NUMBER: US/09/072,967
FILING DATE: US/08/072,967
FILING DATE: OS-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAMM: MAKI, DAYIG J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 31,392
TELECOMMUNICATION INFORMATION:
                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 466; DB 12; Best Local Similarity 100.0%; Pred. No. 2.6e-42; Matches 95; Conservative 0; Mismatches 0;
                                                                                                                 0
                                                                   Score 466; DB 9;
Pred. No. 2.6e-42;
Mismatches 0;
                                                                                                                                                                                                                                                61 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95
                                                                                                                                                                                                                                                                                        KOELDEISTNIRQAGVOYSRADEEQOQALSSOMGF
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SEQUENCE DESCRIPTION: SEQ ID NO: 214:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Campos-Neto, Antonio
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 214, Application US/10084843
Publication No. US20030143243A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 802 amino acids TYPE: amino acid
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                                                                       100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
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                                                                   Query Match
Best Local Similarity 100.
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                           RESULT 10
US-10-084-843-214
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1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 60

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Indels

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429 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQCQWRGAAGTAAQAAVVRFQEAANKQ 488
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                                                                                                                                                                                                                                                                     Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Romald C.
TILLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            701 Fifth Avenue
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                                      523
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Pred. No. 2.6e-42;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FLING DATE: 25-Feb-2002
CLASSIPICATION: CURROWN-
PRIOR APPLICATION NUMBER: US/09/072,967
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                                      489 KOELDEISTNIROAGVOYSRADEEOOOALSSOMGF
61 KOELDEISTNIRQAGVQYSRADEEQQQALSSQMGF
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 351:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 31,392
                                                                                                                         US-10-084-843-351
; Sequence 351, Application US/10084843
; Publication No. US20030143243A1
; GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
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ATTORNEY/AGENT INFORMATION:
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Skeiky, Yasir A.W.
Dillon, Davin C.
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SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.0
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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Dillon, Davin C.
Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
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Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 802;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIF: 98104-7032
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 466; DB 12;
Best Local Similarity 100.0%; Pred. No. 2.6e-42;
Matches 95; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KOELDEISTNIRQAGVOYSRADEEQQQALSSQMGF 523
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REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-U1-2002
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; SEQUENCE DESCRIPTION: SEQ ID NO: 209: US-10-193-002-209
                                                                                                                                                                                Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
                                                        Application US/10193002
5. US20030135026A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (206) 622-4900
                                                                                                                     Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Washington
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                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELEPHONE:
                                                          Sequence 209, Applicat
Publication No. US2003
GENERAL INFORMATION:
                   RESULT 12
US-10-193-002-209
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; Sequence 346, Application US/10193002; Publication No. US20030135026A1; GENERAL INFORMATION:

US-10-193-002-346

APPLICANT: Reed, Steven G. Skeiky, Yasir A.W.

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APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-009020US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
Vedvick, Thomas S.
Vedvick, Daniel R.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Romald C.
TITLE OF INVENTION: COMPUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: SOO Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 466; DB 12;
Best Local Similarity 100.0%; Pred. No. 2.6e-42;
Matches 95; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         489 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Maki, David J.

REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-WAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-011-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
, SEQUENCE DESCRIPTION: SEQ ID NO: 346:
US-10-193-002-346
                                                                                                                                                                                                                                                                                                                STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM IXPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/10359460
Publication No. US20030147911A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGIH: 802 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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66 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100
                                                                                                                                                                      Search completed: November 21, 2003, 16:38:12
Job time : 4.70522 secs
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Squence 5, Application US/10140045;
Squence 6. Application US/10140045;
Publication No. US20300928991
Squence 7. Application No. US20300928991
APPLICANT: GREWARION:
APPLICANT: ANDERSENSN, PETER 8
APPLICANT: RASMUSSEN, PETER 8
APPLICANT: RASMUSSEN, PETER 8
APPLICANT: ANDERSENSN, PETER 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Description of Artificial Sequence:tetra-fusion US-10-359-460-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .,
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99.1%; Score 462; DB 15; Length 100;
Best Local Similarity 98.9%; Pred. No. 5.5e-43;
Matches 94; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 466; DB 12; Best Local Similarity 100.0%; Pred. No. 2.6e-42; Matches 95; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  489 KOELDEISTNIROAGVOYSRADEEQQOALSSOMGF 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 KOELDEISTNIROAGVOYSRADEEQQQALSSQMGF 95
                                                  CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US/09/287,849
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-10-01
PRIOR APPLICATION NUMBER: US 09/942,578
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR PILING DATE: 1998-02-18
PRIOR PRIOR PAPLICATION NUMBER: US 09/223,040
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SSQ ID NO 10
LENGTH: 802
                  CURRENT APPLICATION NUMBER: US/10/359,460
CURRENT FILING DATE: 2003-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
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61 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95

8

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GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
             Copyright
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OM protein - protein search, using sw model

November 21, 2003, 15:57:31 ; Search time 1.98186 Seconds (without alignments) 4609.825 Million cell updates/sec Run on:

US-09-688-672A-10 466 1 TDAATLAQEAGNFERISGDL......VQYSRADEEQQQALSSQMGF 95 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		d			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
;	. 9	١.,	10		H70802	hypotherical profe
C)	173	۲.	100		T10032	othetical prot
m	•	Ö.	Φ)		T35661	chromoso
4	٥.	ď.	Н		B59103	⊢
ហ	σ	σ,	S		T38435	oil prote
9	87.5	œ,	97		E70836	transcri
7	86	18.5	103	0	B70600	hypothetical prote
œ	œ	œ.	2		T43214	rotein
ወ	•	œ,	97		G70857	able PE
	ä	۲.	Ŋ		A47334	kinesi
11	80	۲.	527		833068	n heavy
	Φ	۲.	4,		A59287	in heavy
	6	Ľ.	4		T44704	otheticai
	79.5	ζ.	4		G87116	þ
	ė.	۲.	9		A61231	ă V
	6	•	9		S21801	a V
	79	7.	50		KRSHL2	keratin type II, m
	78	Ġ	3		T42722	
	16	•	49		S05408	in, type
	9.	ġ	σ		S33124	
	~	Ġ	9		F75559	
	4.	Ġ	80		D29674	phycocyanin linker
	74.5	Ġ	80		AB1873	inke
	4.	Ġ.	ч	N	4.0	in E
	4,	ė.	4	0	00	methyl-accepting c
	74	ď.	528	~	B75310	pothe
	7	Ď.	0	N	8	r S
	m	'n	3	~	33	hypothetical prote
	٠	N	4.	Н	7	ы

RESULT 2 T10032

Appothetical protein MLCB628.13c - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Accession: T1002
R;Eiglmeier, K.; Honore, N.; Woods, S.A.; Caudron, B.; Cole, S.T.
Mol. Microbiol. 7, 197-206, 1993
A;Title: Use of an ordered cosmid library to deduce the genomic organization of Mycobact
A;Accession: T10032
A;Accession: T10032
A;Accession: T10032
A;Accession: T100 < Mycobacterium leprae
A;Accession: L100 < Mycobacterium leprae
A;Cross-references: EMBL:Y14967; NID:g2370268; PIDN:CAA75210.1; PID:g2370280

37.1%; Score 173; DB 2; Length 100;

Query Match

ferredoxin-NADP(+)	periplasmic oligop	unknown protein [1	hypothetical prote	hypothetical prote	uncharacterized sm	keratin-like prote	probable exonuclea	8.9K linker polype	keratin, type II,	biphenyl-2,3-diol	secreted 45 kd pro	general stress pro	methyl-accepting c	laminin B1k chain	protein J - Yersin
AB2321	AD1824	H96760	F96673	548385	G96905	I38025	T03465	A24691	S29094	DAPSPC	G95258	B98124	D87536	A53612	T14652
440 2	552 2	745 2	313 2	1679 2	103 2.	257 2	238 2	80 2	503 2	293 1	392 2	392 2	555 2	1170 2	492 2
15.8	15.8	15.8		15.8 1				15.6	15.5					15.3 1	
73.5	73.5	73.5	73.5	73.5	73	73	73	72.5	72	71.5	71.5	71.5	71.5	71.5	71.5
30	31	32	33	34	32	36	37	38	<u>ه</u>	40	41	42	43	44	45

ALIGNMENTS

_	RESULT 1
	H70802 .
	hypothetical protein Rv3874 - Mycobacterium tuberculosis (strain H37RV)
	C;Species: Mycobacterium tuberculosis
	C.Date: 17-011-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
	CANCENSION: Breach B. Davibhill T. Chemion B. Chuschon C. Handin B. Carlin
	Action of the property of the
	Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
	Nature 393, 537-544, 1998
	A, Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
	A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
	A.vererance inducer: A.OSOO; MOLD:9829986; FMLD:9834230 A:Accession: H70802
	A; Status: preliminary; nucleic acid sequence not shown: translation not shown
	A, Molecule type: DNA
	A;Residues: 1-100 <col/>
	A; Cross-references: GB: AL022120; GB: AL123456; NID: g3261558; PIDN: CAA17966.1; PID: g296022
	A, Experimental source: strain H37Rv
	C, Genetics:
	A;Gene: Rv3874
-	
	al Similarity 100.0%; Pred. No. 9e-36;
	Marches 95; Conservative U; Mismatches O; Indeis O; Gaps O;
••••	QY 1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAQAAVVRFQEAANKQ 60
	Db. 6 TDAATTAOEAGYFERISGELKTOIDDOVESTAGSLOGOWRGAAGTAACAAVREOEAANKO 65
	QY 61 KQELDEISTNIRQAGVQYSRADEBQQQALSSQMGF 95
	Db 66 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100

g à q

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probable transcription regulator RV0287 - Mycobacterium tuberculosis (strain H37RV) C; Species: Mycobacterium tuberculosis C; Accession: Bycobacterium tuberculosis C; Date: 17-Ual-1998 #text_change 22-Oct-1999 C; Date: 17-Ual-1998 #text_change 22-Oct-1999 C; Caccession: E70836 R; Parkhill, J; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393; S37-S44, 1998 A; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; A; Reference number: A70500; MUID:98295987; PMID:9634230 A; Accession: E70836 A; Multiple Speciminary; nucleic acid sequence not shown; translation not shown A; Residues: 1-97 cCOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Cross-references: GB:AL021930, GB:AL123456, NID:g3261524, PIDN:CAA17362.1, PID:e125247
A,Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-750 <MCD>
A;Cross-references: EMBL:AL009227; PIDN:CAA15821.1; GSPDB:GN00066; SPDB:SPAC27D7.02c
A;Experimental source: strain 972h-; cosmid c27D7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 FERISGDLKTQIDQVESTAGSLOGOWRGAAGTAAQAAVVRFQEAANKOKOELDEISTNIR 72
                                                                                                                                                                                                                                coiled coil protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T3843; Wood, V; Barrell, B.G; Rajandream, M.A.
submitted to the EMBL Data Library, December 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 QEAG--NFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQKQELD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Accession: T38435
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 90; DB 2; Pred. No. 1.4; 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Mismatches
62 MMFNILQELDKIAVELERAAVKFREADE 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELKLKLNEANKKY -----QELAIS 616
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Best Local Similarity 28.24
Matches 24; Conservative
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A;Gene: SPDB:SPAC27D7.02c
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Best Local S
Matches 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
T3561
Probable chromosome associated protein - Streptomyces coelicolor
cypedies: Streptomyces coelicolor
cypedies: Streptomyces coelicolor
cybedies: Streptomyces coelicolor
cybedies: Streptomyces coelicolor
cybedies: O5-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 02-Jun-2000
cybedies: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 02-Jun-2000
sybmitted to the EMBi Data Library, December 1998
A,Reference number: 221585
A,Recession: T35661
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Rolecule type: DNA
A,Rolecule type: DNA
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A,Rolecule type: DNA
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A, Cross-references: EMB1.AL034447; PIDN:CAA22420.1; GSPDB:GN00070; SCOEDB:SC7A1.21
A, Experimental source: strain A3 (2)
C, Genetics:
A, Gene: SCOEDB:SC7A1.21
C, Superfamily: chromosome segregation protein SMC1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 DAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTA--AQAAVVRFQEAANK 59
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A,Residues: 1-410 <OKI>
A,Cross-references: GB:AF065404; NID:g4894216; PIDN:AAD32402.1; PID:g4894314
A,Experimental source: strain Sterne
C,Genetics:
                                                                                                                                                                                  6 TEAAILIQQAAQFDQIASGLSQERNFVDSIGQSFQNTWEGQAASAALGALGAFFDEAMQDQ
                                                                                                                          1 TDAATLAQBAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
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                                              Gaps
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Best Local Similarity 29.5%; Pred. No. 0.67;
Matches 26; Conservative 14; Mismatches 27; Indels 2:
        37.9%; Pred. No. 4.4e-09;
tive 20; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                      61 KOELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95
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        Best Local Similarity 37.99
Matches 36; Conservative
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Aforemental 100857, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Comnor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature, 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70800; MUID:98295987; PMID:9634230
A;Accession: G70857
A;Accession: G70857
A;Mesidues: 1-97 COLD.
A;Asesidues: 1-97 COLD.
A;Asesidues: 1-97 COLD.
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A;Asesidues: 1-97 COLD.
A;Asesidues: 1-97 COLD.
A;Asperimental source: strain H37Ry
              A,Molecule type: mRNA
A,Residues: 733-874,'E',876-916,'S',918-1038,1040-1047,'S',1049-1283,'E',1285-1347,'E',1
A,Cross-references: EMBL:M30398; NID:g159876; PIDN:AAA29413.1; PID:g159877
C;Gene: ovt.
A,Gene: ovt.
C;Keywords: leucine zipper
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C;Date: 21.58p-1993 #sequence_revision 18-Nov-1994 #text_change 02-Feb-2001
C;Accession: A47334
R;Burns Jr., J.M.; Shreffler, W.G.; Benson, D.R.; Ghalib, H.W.; Badaro, R.; Reed, S.G.
Proc. Natl. Acad. Sci. U.S.A. 90, 775-779, 1993
A;Tille: Molecular characterization of a kinesin-related antigen of Leishmania chagasi
A;Reference number: A47334; MUID:93133867; PMID:8421715
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A, Cross-references: GB:LO7879; NID:G308884; PIDN:AAA29254.1; PID:G308885
A; Cross-references: GB:LO7879; NID:G308884; PIDN:AAA29254.1; PID:G308885
A; Experimental source: MHG/MSK/82/Ba-2,C1
A; Note: sequence extracted from NCBI backbone (NCBIN:122864, NCBIP:122865)
C; Superfamily: unassigned kinesin-related proteins; kinesin motor domain homology
                                                                                                                                                                                                                                                                                                                                   7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable PE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                      6 LAQEAGNFERISGDLKTQIDQVESTAGSLQGQ-----WRGAAGTAAQAAVV-----RFQE
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                                                                                                                                                                                                                                                      Query Match
18.5%; Score 86; DB 2;
Best Local Similarity 25.5%; Pred. No. 9.8;
Matches 25; Conservative 22; Mismatches 41
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Pred. No. 0.49;
7; Mismatches
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Best Local Similarity
Matches 29; Conserv
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hypothetical protein Rv3905c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Decies: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: B70600
R;Cole, S.T.; Brosch, R.; Perkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-54, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Accession: B70600
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Moccule type: DMA
A;Residues: 1-103 <CCL-
A;Cross-references: GB:Z94121; GB:All23456; NID:g3261736; PIDN:CAB08096.1; PID:e312272; A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | : : : | : : : EPAVQCBASGANGGWRGASGSAYGSAWELWHRGAGEVQ 69
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Best Local S:
Matches 21
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임 6 B

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G87116

Conserved hypothetical protein ML1661 [imported] - Mycobacterium leprae

C)Bace: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001

C)Accession: G97116

C;Accession: G97116

R;Cole, S.T.; Eiglimeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho

R;Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, eam, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq.

A;Title: Massive gene decay in the leprosy bacillus.

A;Reference number: A86909; MUID:21128732; PMID:11234002

A;Reference number: A86909; MUID:21128732; PMID:11234002

A;Status: preliminary

A;Molecule type: DNA

A;Ross-references: GB:AL450380; NID:g13093432; PIDN:CAC30614.1; GSPDB:GN00147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein MLCB1243:13 [imported] - Mycobacterium leprae C; Species: Mycobacterium leprae C; Species: Mycobacterium leprae C; Species: Mycobacterium leprae C; Species: Mycobacterium leprae C; Species: Mycobacterium leprae C; Species: Mycobacterium leprae C; Species: Mycobacterium leprae C; Species: Mycobacterium leprae C; Species: T44704 R; Parkhill, J; Barrell, B.G.; Rajandream, M.A. Submitted to the EMBL Data Library, May 1998 A; Reference number: Z22830 A; Reference number: Z22830 A; Reference number: Z22830 A; Reference number: Z22830 A; Residues: Dreliminary; translated from GB/EMBL/DDBJ A; Residues: 1-345 cpRx A; Residues: 1-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 cpRx A; Residues: L-345 c
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                                                  DAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 IDAATLAQEA-GNFERISGDLKTQIDQVESTAGS----LOGOWRGAAGTAAQAAVVRFQE
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C;Superfamily: Mycobacterium leprae hypothetical protein MLCB1243.13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42; Indels
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                                                                                                                                                                                                                                                                                                                                17.1%; Score 79.5; DE 27.0%; Pred. No. 3.9; Live 20; Mismatches
                                                                                                                                                                                                                                                             62 QELDEISTNIRQAGVQYSRADEEQQQALSSQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 27.0%
Matches 27; Conservative
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Matches 27; Conserv
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Wyosin heavy chain - fluke (Schistosoma mansoni) (strain Brazilian LE)
C;Species: Schistosoma mansoni
C;Sate: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 08-Sep-2000
C;Accession: AS9287
R;Weston, D.S.; Schmitz, J.; Kemp, M.; Kunz, W.
Mol. Biochem. Parasitol. 58, 16.164, 1993
A;Title: Cloning and sequence characterization of a complete myosin heavy chain cDNA frc
A;Accession: AS9287
A;Accession: AS9287
A;Accession: AS9287
A;Accession: MUD:93211444; PMID:8459827
A;Accession: MSP287
A;Accession: MSP287
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Myosin heavy chain - fluke (Schistosoma mansoni) (fragment)

Mylternate names: surface antigen, 200K

C; Species: Schistosoma mansoni
C;Date: 22-Nov-1993 #sequence_revision 06-Sep-1996 #text_change 13-Feb-1998

C;Accession: S33068

R;Soisson, L.M.A.; Masterson, C.P.; Tom, T.D.; McNally, M.T.; Lowell, G.H.; Strand, M.
J. Immunol. 149, 3612-3620, 1992

A;Title: Induction of protective immunity in mice using a 62-kDa recombinant fragment of A;Reference number: A46514; MUID:93056536; PMID:1431131

A;Accession: S33068

A;Molecule type: mRNA

A;Residues: 1-527

Mylteridues: 1-527

Mylteridues: 1-527

Mylteridues: 1-527

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                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                     Length 955;
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ilarity 22.8%; Pred. No. 33;
Conservative 21; Mismatches 44; Indels
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A;Note: the authors translated the codon CAA for residue 346 as
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: ATP; surface antigen
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                                                                                                                                                                                                     ch 17.5%; Score 81.5; DB 2; Length 9. Similarity 31.0%; Pred. No. 11; 31; Conservative 12; Mismatches 44; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 FOEAANKOKOELDEISTNIRQAGVQYSRADEEQQQALSSQ 92
C;Keywords: ATP; nucleotide binding; P-loop
F;13-398/Domain: kinesin motor domain homology <KMOT>
F;122-129/Region: nucleotide-binding motif A (P-loop)
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; Pred. No. 8;
21; Mismatches 4
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A;Cross-references: GB:L01634; PIDN:AAA29905.1
A;Experimental source: strain Brazilian LE
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                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 31; Conserval
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Matches 21; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C, Genetics:
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1799 EGTVKSKYK-ASITALEAKIAQLEEQLDNETKERQAACKQVRRTEKKLKDVLLQVDDERR 1857
                                                                                                                                                                          1858 NAEQYKDQADKASTRLKQLKRQLEEAEEEAQRANASR 1894
                                                                                                                                ----KQELDEISTNIRQAGVQYSRADEEQQQALSSQ 92
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A; Molecule type: mRNA
A; Reduces: 182-218 *BEM>
A; Cross-references: GB:L29141; NID:g457249; PIDN:AAA20904.1; PID:g531134
A; Genetics:
C; Genetics: GB:MYH9
C; Genetics: GB:MYH9
A; Gross-references: GB:L20216; OMIM:160775
A; Genetics: GB:MYH9
A; Cross-references: GB:L20216; OMIM:160775
A; Map position: 22q12.3-22q13.1
C; Superfamily: myosin heavy chain; myocin motor domain homology
C; Reywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; nucleotide binding motif A (P-loop)
F; 84-764/Domain: myosin motor domain homology coil; hydrolase;
F; 174-181/Region: actin binding #status predicted
F; 626-640/Region: actin binding #status predicted
F; 626-640/Region: actin binding #status predicted
F; 626-640/Region: actin binding #status predicted
F; 637-123/Domain: S2 #status predicted coil #status predicted
F; 837-193/Domain: S2 #status predicted coil #status predicted
F; 1278-1961/Domain: arboxyl-terminal composin #status predicted
F; 1807-1981 site: NG, NG, NG-trimethyllysine (Lys) #status predicted
F; 694,704/Active site: Cys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Accession: A61231
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Residues: 1-715 <SIM>
A, Cross-references: GB.M69180; NID:g189029; PIDN:AAA61765.1; PID:g189030
B, Cross-references: GB.M69180; NID:g189029; PIDN:AAA61765.1; PID:g189030
B, Cross-references: GB.M69180; NID:g189029; PIDN:AAA61765.1; PID:g189030
B, Sizez, C.G.; Myers, U.S.A. 87, 1164-1168; J1890
A, Title: Human nonmuscle myosin heavy chain mRNA: generation of diversity through altern
A, Reference number: A34876; MUID:90138958; PMID:1967836
                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 12-May-1994 #sequence_revision 14-Jul-1994 #text_change 19-Apr-2002
C;Date: 12-May-1994 #sequence_revision 14-Jul-1994 #text_change 19-Apr-2002
C;Accession: A6121; A34876; I52562; 161692
R;Simons, M;Wang, M;McBride, O.W.; Kawamoto, S.; Yamakawa, K.; Gdula, D.; Adelstein, Circ. Res. 69, 530-539, 1991
A;Title: Human nonmuscle myosin heavy chains are encoded by two genes located on differe A;Reference number: A61231; MUID:91316803; PMID:1860190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-52, 'EA1, 56-659,'T', 661-868,'T',870-930,'C',932-1239,'KG',1242-1337 <RES>A; Cross-references: GB: M81105; NII:g188988; PIDN:AA59888.1; PID:g553596
R; Bement, W.M.; Hasson, T.; Wirth, J.A.; Cheney, R.E.; Mooseker, M.S.
Proc. Natl. Acad. Sci. U.S.A. 91, 6549-6553, 1994
A; Title: Identification and overlapping expression of multiple unconventional myosin gen A; Reference number: A55758; MUID:94294418; PMID:8022818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Molecule type: mRNA
|Residues: 715-1961 <SAE>
|Cross-references: GBEM31013; NID:g189035; PIDN:AAA36349.1; PID:g189036
|Toothaker, L.E.; Gonzalez, D.A.; Tung, N.; Lemons, R.S.; Le Beau, M.M.; Arnaout, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lood 78, 1826-1833, 1991
Filte: Cellular myosin heavy chain in human leukocytes: isolation of 5' cDNA clones, Reference number: 152562; MUID:92003925; PMID:1912569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                         Alternate names: cellular myosin heavy chain; myosin type 9; NAMHC-A
Contains: myosin ATPase (EC 3.6.4.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71;
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SINRAQSECDRL---IENGNISYEKAIQEGIKEQQRLVSQ 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Status: preliminary; translated from GB/EMBL/DDBJ Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.1%; Score 79.5; D
llarity 21.7%; Pred. No. 37;
Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 LAQEAGNFERISGDLK---TQIDQV-----
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                                                                                                                                                                                                                            myosin heavy chain nonmuscle form A - human
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Best Local Similarity
Matches 34; Conserv
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GenCore version 5.1.6
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November 21, 2003, 15:51:11; Search time 1.12018 Seconds (without alignments) 3988.226 Million cell updates/sec US-09-688-672A-10 466 1 TDAATLAQEAGNFERISGDL......VQYSRADEEQQQALSSQMGF 95 OM protein - protein search, using sw model Title: Perfect score: Sequence: Run on:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	tion	mycobacteri	mycobacteri	mycobacteri	onchocerca	leishmania	mycobacteri	homo sapien	mus musculu	ovis aries	homo sapien	anabaena va	rattus norv	anabaena sp	anabaena sp	anabaena sp	saccharomyc	rhodobacter	mastigoclad	caenorhabdi	ovis aries	pseudomonas	homo sapien	caenorhabdi	synechococc	manduca sex	homo sapien	rhizobium s	gallus gall	galleria me	enterobacte	halobacteri	leuconostoc	mycobacteri
	Description	069739	033084	005440	P21249	P46865	9sq560	P35579	P55937	P15241	P12270	044549	062812	P07124	P21890	P58558	P40457	068032	P11396	P12845	P25691	P17297	013751	P02567	P50035	P13276	002833	P55439	P14105	P80703	P21823	Q9hhc2	010419	Q9cbs9
ro.		! ! ! ! !																																
SUMMARIES	TD	CF10 MYCTU	CF10 MYCLE	ES6D MYCTU	ANT1 ONCVO	KINL LEICH	YT27 MYCLE	MYH9 HUMAN	G160 MOUSE	K2M2 SHEEP	TPR_HUMAN	FENR ANAVA	MYH9 RAT	PYS1 ANASP	FENR ANASO	FENR ANASP	YIO9 YEAST	SBCC RHOCA	PYS1 MASLA	MYSC CAEEL	K2M3_SHEEP	BPHC_PSES1	LMB3 HUMAN	MYSD_CABEL	PYS1_SYNEL	APL3 MANSE	CK13 HUMAN	Y4FA RHISN	MYH9 CHICK	APL3 GALME	MCPD ENTAE	GRPE_HALME	MESE LEUME	YM29_MYCLE
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ok	Query Match 1	100.0	37.1	18.5	18.5	7	۲.		16.7	16.3	ů,	ś	•	Ġ	IJ	ъ.	•	15.7	15.6	15.6	15.5	15.3	15,3	15.2	15.1	15.1	15.1	15.1	15.1	15.0	15.0		14.9	14.8
	Score	466	173	86	86	81.5	79.5	79.5	78	16	92	75.5	75.5	74.5	73.5	73.5	73.5	73	72.5	72.5	72	71.5	71.5	71	70.5	70.5	70.5	70.5	70.5	70	70	69.5	69.5	69
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P48667 homo sapien P33741 halobacteri	P48668 homo sapien Q10973 mycobacteri	P12608 synechococc P21758 bos taurus	P33292 pichia past O9nqx4 homo sapien	O9bv73 homo sapien O8xqi3 salmonella	P13509 alcaligenes P06159 human parai
K2CD_HUMAN HTR1_HALN1	K2CE_HUMAN YT27_MYCTU	IRPA_SYNP7 MSRE_BOVIN	PEXS_PICPA MYSC_HUMAN	CEP2_HUMAN SYFA_SALTY	CZCC_ALCEU NCAP_PI3H4
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384 535	563 245	356 453	576	327	417 515
14.8	14.8	14.7	14.7	14.7	14.6 14.6
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3.4 3.5	36	8 O M M	4.4 4.1	4. 4. 2. 8.	4 4 5

ALIGNMENTS

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requires a license agreement (See http://www.isb-sib.ch/announce/
                                                          EMBL; ALS83917; CAC29558.1; -. PIR; T10032; T10032.
Leproma; ML0050; -.
                                                                                                                                   99 AA; 10833 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis.
                                            EMBL; Y14967; CAA75210.1;
                                                                                                                                                                                            36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                               Similarity
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                                                                                                        Complete proteome.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                              5 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 64
                                                                                                                                                                                                                                                                                                                                                                             1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Stutter S., Seeger K., Simmonds M., Selton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eiglmeier K., Garnier T., De Rossi E., Fsihi H., Cole S.T.,
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                 Length 99;
                                                                                                                                                                                                                                                                                                                 100.0%; Score 466; DB 1; Length 9
100.0%; Pred. No. 5.3e-36;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                    99 AA; 10663 MW; EBCAE6A996C5489D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         KOELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 99
                                                                                                                                                                                                                                                                                                                                                                                                                                       61 KOELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Massive gene decay in the leprosy bacillus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
MLOOSO OR MLCB628.13C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 409:1007-1011(2001).
-!- SIMILARITY: BELONGS TO THE ESAT6 FAMILY.
   SIMILARITY: BELONGS TO THE ESAT6 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21128732; PubMed=11234002;
                                                                                                                                                 EMBL, AF004671, AAC83445.1; -.
EMBL, AL022120, CAA17966.1; -.
EMBL, AE001190, AAK48366.1; -.
EMBL, AF418854, AAL14999.1; -.
                                                                                                                                                                                               PIR, H70802; H70802.
TIGR, MT3988. -.
Tuberculist; Rv3874; -.
Antigen, Complete proteome.
INIT_MET
                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
Les 95; Conservative
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Barrell B.G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 TEAAILTÓQAAQFDQIASGLSQERNFVDSIGQSFQNTWEGQAASAALGALGRFDEAMQDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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STRAIN=CDC 1551 / Oshkosh;
Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann W.D., Alland D., Eisen J.A., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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Corynebacterineae, Mycobacteriaceae, Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                       37.1%; Score 173; DB 1; Length 99; 37.9%; Pred. No. 2.3e-09; iive 20; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      laboratory strains.";
Submitted (AFR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE ESAT6 FAMILY.
                                                                                                                                                                                                                                                                                               BY SIMILARITY.
859B484F7EFE5A8A CRC64;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative ESAT-6 like protein 13.
RV3905C OR MT4024 OR MTCYISF10.06.
or send an email to license@isb-sib.ch).
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Leishmania chagasi.
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Best Local Simi
Matches 31;
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                                                                                                                                                                                                                                                                                          10 EPAVMQGFAASLDGAAEHLAVQLAELDAQVGQWLGGWRGASGSAYGSAWELWHRGAGEVQ 69
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                                                                                                                                                                                                                                                          2 DAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQK
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"Molecular coloning of a gene expressed during early embryonic development in Onchocerca volutlus ";
Mol. Biochem. Parasitol. 69:161-171(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Onchocerca volvulus.
Wararyota, Metazoa, Nematoda, Chromadorea; Spirurida, Filarioidea,
Onchocercidae, Onchocerca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=89127417; PubMed=2464764;
Donelson J.E., Duke B.O.L., Moser D., Zeng W., Erondu N.E.,
Lucius R., Renz A., Karam M., Flores G.Z.;
"Construction of Onchocerca volvulus cDNA libraries and partial
characterization of the cDNA for a major antigen.";
mol. Biochem. Parasitol. 31:241-250(1988).
-:- FUNCTION: MAY BE A MYOFIBRILLAR PROTEIN.
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                                                                                                                                                                      18.5%; Score 86; DB 1; Length 103; 23.9%; Pred. No. 0.2; ive 20; Mismatches 47; Indels
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237341 MW; B7132AACF1520317 CRC64;
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D COIL (POTENTIAL)
D COIL (POTENTIAL)
                                                           TIGR; MT4024; -.
Tuberculist; Rv3905c; -.
Hypothetical protein; Complete proteome.
SEQUENCE 103 AA; 10460 MW; 3994E272A7BDFF02 CRC64;
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25.5%; Pred. No. 4..,
... 22; Mismatches
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Last annotation update)
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MEDLINE=95287898, PubMed=7770081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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MBL; Z94121; CAB08096.1; -. MBL; AE007193; AAK48388.1; IR; B70600; B70600.
                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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01-NOV-1995 (Rel. 32,
30-MAY-2000 (Rel. 39,
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Matches 21, Conserv
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Best Local Similarity
Matches 25; Conserv
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Gaps

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41; Indels

Conservative

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                                            25
6 LAQEAGNFERISGDLKTQIDQVESTAGSLQGQ----WRGAAGTAAQAAVV-----RFQE 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Leishmania.
NCBL_TaxID=44271;
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MOTOR DOMAIN2; RINESIN MOTOR DOMAIN2; 1.

MOTOCUPOCION; MICTOCLUDALGES; TATE-DAIGHING; COLLEG COLL; Repeat.

DOMAIN 1399 KINESIN-MOTOR (BY SIMILARITY).

MODAIN 426 >955 COLLED COLL (POTENTIAL).

NP BIND 122 129 ATP (POTENTIAL).

DOMAIN 704 >955 7 X 39 AA APPROXIMATE TANDEM REPEATS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leishmania chagasi that detects specific antibody in African and American visceral leishmaniasis.";
Proc. Natl. Acad. Sci. U.S.A. 90.775-779(1993).
-!- DEVELOPMENTAL STAGE: PROCMINANT IN AMASTIGOTES.
-!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44; Indels
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                                                                                                                           56 AANKOKOELDEISTNIRQAGVOYSRADEEQQQALSSOM
                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Kinesin-like protein K39 (Fragment).
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ilarity 31.0%; Pred. No. 5.4;
Conservative 12; Mismatches
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Incerpro; 1PR001752; kinesin_motor.
Pfam; PP00225; kinesin; 1.
PRINTS; PR00380; KINESINHEAVY.
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STRAIN=MHOM/BR/82 / Isolate BA-2;
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                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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type A) (Nonmuscle myosin heavy chain-A) (NMMHC-A) MYH9.
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79 TESESLLSHARAEADRILSDAKSQVDRMASEARQHSERMLGDAREESIRIATVAKREYEA 138
             858 ATLEQQLRESEERAAELASQLESTTAAKMSAEQDRESTRATLEQQLRDSEERAAELASQL 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TDAATLAQEA-GNFERISGDLKTQIDQVESTAGS----LQGQWRGAAGTAAQAAVVRFQE 55
                                                                                                                                                                                                                                                                                                                                MEDLINE-1128732; PubMed=11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
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Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
Barrell B.G.,
"Massive gene decay in the leprosy bacillus.";
"Massive gene decay in the leprosy bacillus.";
"Mature 409:1007-1011(201).
"In TUBERCULOSIS RV2927C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MYH9 HUMAN STANDARD; PRT; 1960 AA.
P35573; O60805;
01-JUN-1994 (Rel. 29, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Myosin heavy chain, nonmuscle type A (Cellular myosin heavy chain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
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                                                                                                                                                                                                                                                   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein; Complete proteome.
SEQUENCE 245 AA; 27087 MW; C984D9ASFA49697A CRC64;
                                                                  918 EATAAAKSSAEQDR--ENTRAALEQQLRDSEERAAELASQ 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 SLNRAQSECDRL---IENGNISYBKAIQEGIKEQQRLVSQ 175
                                        53 FQEAANKOKQELDEISTNIRQAGVQYSRADEEQQQALSSQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 AANKOKQELDEISTNIRQAGVQYSRADEE---QQQALSSQ 92
                                                                                                                                                09CBS6; 066467;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FES-2003 (Rel. 41, Last annotation update)
Hypothetical protein Mil661.
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EMBL; AL583923; CAC30614.1; ALT_INIT.
                                                                                                                                       PRT;
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Best Local Similarity 27.09
Matches 27, Conservative
                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                      Mycobacterium leprae.
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Leproma; ML1661; -.
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                       YT27 MYCLE
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YT27_MYCLE
ID _YT27_M
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MYH9_HUMAN
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RRN SEQUENCE FROM N.A.

REQUIRED COSTAGE PubMed=10591208;

REDINES 20051165; PubMed=10591208;

REDINES 20051165; PubMed=10591208;

REDINES 20051165; PubMed=10591208;

RADINES 20051165; PubMed=10591208;

RADINES 20051165; PubMed=10591208;

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RADINES
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MEDLINE=91316803; PubMed=1860190;
Simons M., Wang M., McBride O.W., Kawamoto S., Yamakawa K.,
Gdula D., Adelstein R.S., Weir L.;
"Human nommuscle myosin heavy chains are encoded by two genes located
on different chromosomes.";
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Secussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P.,
Wilkinson P., Bodenteich A., Hartman K., Hu K., Khan A.S., Lane L.,
Tilahun Y., Wright H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Toochaker L.E., Gonzalez D.A., Tung N., Lemons R.S., le Beau M.M., Arnaout M.A., Clayton L.K., Tenen D.G., Cellular myosin heavy chain in human leukocytes: isolation of 5' cDNA clones, characterization of the protein, chromosomal localization, and upregulation during myeloid differentiation."; Blood 78:1826-1833(1991).
                                 Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 714-1960 FROM N.A.
MEDLINE=90138958; PubMed=1967836;
Sacz C.G., Myers J.C., Shows T.B., Leinwand L.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The DNA sequence of human chromosome 22.";
Nature 402:489-495(1999).
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MEDLINE=92003925; Pubmed=1912569;
                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rc. Res. 69:530-539(1991)
Homo sapiens (Human)
                                                                                                                          NCBI_TaxID=9606;
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Best Local Similarity 21.7
Matches 34; Conservative
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869
931
1241
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P55937;
01-NOV-1997 (
01-NOV-1997 (
15-DEC-1998 (
                                                                                                                                                                                                                                                                                Deafness.
DOMAIN
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DOMAIN
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G160 MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                     VALIANT DENALT HIS-70S.
MEDLINE=20489856; PubMed=11023810;
MEDLINE=20489856; PubMed=11023810;
Lalwani A.K., Goldstein J.A., Kelley M.J., Luxförd W., Castelein C.M.,
Mhatre A.N.;
"Human nonsyndromic hereditary deafness DFNA17 is due to a mutation in
                                                                                                                                                                                MEDLINE=20428192; PubMed=10973259;
Seri M., Cusano M., Gangarossa S., Caridi G., Bordo D., Lo Nigro C.,
Ghiggeri G.M., Ravazzolo R., Savino M., Del Vecchio M., d'Apolito M.,
Iolascon A., Zelante L.L., Savoia A., Baldmini C.L., Noris P.,
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"Mutations in MYH9 result in the May-Hegglin anomaly, and Fechtner and
Sebastian syndromes.";
Nat. Genet. 26:103-105(2000).
                                                                                                                                                                                                                                                                                                                   VARIANTS MHA ILE-1155 AND LYS-1841.
MEDLINE=20428193; PubMed=10973260;
Kelley M.J., Jawien W., Ortel T.L., Korczak J.F.;
Mutation of MH9, encoding non-muscle myosin heavy chain A, in
May-Hegglin anomaly.";
Nat. Genet. Z6:106-108(2000).
-1- FUNCTION: CELLULAR MYOSIN APPEARS TO PLAY A ROLE IN CYTOKINESIS,
CELL SHAPE, AND SPECIALIZED FUNCTIONS SUCH AS SECRETION AND
"Human nonmuscle myosin heavy chain mRNA: generation of diversity
                                                                                                                                                         VARIANTS MHA/FINS/SBS LYS-93; CYS-702; CYS-1165; HIS-1424 AND
           through alternative polyadenylylation.";
Proc. Natl. Acad. Sci. U.S.A. 87:1164-1168(1990).
                                                                                                                                J. Hum. Genet. 67:1121-1128(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z82215; CAB05105.1; -. EMBL; M81105; AAA59888.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M69180; AAA61765.1; -. M31013; AAA36349.1; -.
                                                                                                                  nonmuscle myosin MYH9."
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HSSP, P10587, 1BR2.
Genew, HGNC:7579, MYH9.
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EMBL; EMBL;

MIM;

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1738 LEEEQGNTELINDRLKKANLQIDQINTDLNLERSHAQKNENARQQLERQNKELKVKLQEM 1797
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                                                                                                               Pfam; PF00612; TC; 1.
Pfam; PF00613; Myosin head; 1.
Pfam; PF00153; Myosin head; 1.
Pram; PF01576; Myosin tail; 1.
PRINTS; PR00135; Myosin tail; 1.
PRINTS; PR00193; Myosin head; 1.
SMART; SM000155; Myosin head; 1.
SMART; SM00157; Myosin head; 1.
PR05177; PS50196; TQ; 1.
PR05177; PS50196; TQ; 1.
PR05177; PS50196; TQ; 1.
PR05177; PS50196; TQ; 1.
PR05177; PS70196; TQ; 1.
PR05177; PS70196; TQ; 1.
PR05177; PS70196; TQ; 1.
PR05177; PS70196; TQ; 1.
PR05177; PS70196; TQ; 1.
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EAI -> RGH (IN REF. 3).
T -> S (IN REF. 3).
T -> M (IN REF. 4).
C -> Y (IN REF. 4).
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COILED COIL (POTENTIAL)
ATP (POTENTIAL).
ACTIN-BINDING.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N -> K (IN MHA).
/FTId=VAR 010791.
R -> C (IN FTNS).
/FTId=VAR 010792.
R -> H (IN DENA17).
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/FTIG=VAR 010794.
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/FIId=VAR 010795.
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/FIIG=VAR 010796.
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ALKYLATION (SH-2)
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35, Last sequence update)
37, Last annotation update)
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InterPro; IPR00048; IQ_region.
InterPro; IPR001609; myosin_head.
InterPro; IPR004009; Myosin_h.
InterPro; IPR00228; Myosin_tail.
InterPro; IPR002017; Spectrin.
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The amino acid sequence of component 7c, a type II intermediate
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C -> G OR S.
C -> S.
F -> Y.
S -> V.
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Q -> H.
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LINKER 12.
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InterPro; IPR003054; Keratin_II.
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REVISIONS, AND CHARACTERIZATION.
                     filament protein from wool.";
Biochem. J. 261:1015-1022(1989).
                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR01276; TYPE2KERATIN.
PROSITE; PS00226; IF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53681 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19; Conservative
                                                                                                                                                                                                                                                                                                                                Pfam; PF00038; filament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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01-OCT-1996 (Rel. 34,
28-FEB-2003 (Rel. 41,
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Best Local Similarity
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                                                                                                                                                                                                                        "Cloning and molecular characterization of cDNA encoding a mouse male-enhanced antigen-2 (Mea-2): a putative family of the Golgi autoantigen.",

-1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN SPERMATOGENESIS AND/OR TESTIS DEVELOPMENT. PROBABLY IDENTICAL WITH THE SEROLOGICALLY DETECTABLE MALE ANTIGEN (SDM)

-1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS. TRANSCRIPTS CAN FOUND IN SPERMATIDS DURING SPERMATOGENESIS. NO EXPRESSION IN LEYDIG CELLS, SPERMATOGONIA, OR SPERMATOCYTES.
-1- SIMILARITY: HIGH, TO HUMAN GOLGIN-160.
-1- CAUTION: IT IS UNCERTAIN WHETHER MET-1, MET-19 OR MET-30 IS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Keratin, type II microfibrillar, component 7C.
Sovis axies (Sheep).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26;
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MGD; MGI:9658; Golga3.

GO; GO:0005793; C:ER-GOlgi intermediate compartment; IDA.

GO; GO:0001593; C:GOlgi membrane; IDA.

GO; GO:0005515; F:protein binding activity; IPI.

Spermatogenesis; Developmental protein.
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Sparrow L.G., Robinson C.P., McMahon D.T.W., Rubira M.R.;
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149880 MW; 3230636962C687B0 CRC64;
  Golgin-160 (Male-enhanced antigen-2) (MEA-2)
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                                                                                                                                             SEQUENCE FROM N.A.
STRAINS-CD-1, TISSUBE-Testis;
MEDIJNE=97217683; PubMed=9063644;
Kondo M., Sutou S.;
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                                             Mus musculus (Mouse)
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1325 AA;
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                        GOLGAS OR MEAS
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-:- FUNCTION: WOOLD MICRORIBARILIAR KERATIN.
-:- MISCELLANBOUS: THERE ARE TWO TYPES OF CYTOSKELETAL AND
MICROFIBRILIAR KERATIN, I AND II (40-55 AND 56-70 KILODALTONS,
RESPECTIVELY: AT LEAST ONE TYPE OF CYTOSKELETAL KERATIN IS
PRESENT IN ALL VERYEBRATE BPTHELIAL CELLS.
-:- MISCELLANGOUS: THE LOW-GULFUR, PROTEINS, DERIVED FROM THE
MISCELLANGOUS: THE LOW-GULFUR, PROTEINS, DERIVED FROM THE
FAMILIES, BACH CONSISTING OF 4 HOMOLOGOUS SUBUNITS: THE TYPE I
COMPONENTS (8C-1, 8C-2, 8A & 8B) AND THE TYPE II COMPONENTS (5,
7A, 7B, AND 7C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93064711; PubMed=1437155; Mitchbell P.J., Cooper C.S.; "The human tyr gene encodes a protein of 2094 amino acids that has extensive colled-coil regions and an acidic C-terminal domain.";
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
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Last sequence update)
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440 AA.

STANDARD;

PubMed=7798308;

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. WWW="http://www.infobiogen.fr/services/chromcancer/Genes/TPRID282.html".
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                                                                                                                                                                                                                     Byrd D.A., Sweet D.J., Pante N., Konstantinov K.N., Guan T., Saphire A.Cs., Mitchell P.J., Cooper C.S., Aebi U., Gerace L.; "Tpr, a large coiled coil protein whose amino terminus is involved in activation of oncogenic kinases, is localized to the cytoplasmic surface of the nuclear pore complex."; J. Cell Biol. 127:1515-1526(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPONENTS, INCLUDING P62.
-!- IISSUE SPECIFICITY: HIGHEST IN TESTIS, LUNG, THYMUS, SPLEEN AND BRAIN, LOWER LEVELS IN HEART, LIVER, AND KIDNEY.
-!- DISEASE: INVOLVED IN TUMORIGENIC REARRANGEMENTS WITH THE MET, TRK OR RAF GENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 76; DB 1; Length 2349;
Pred. No. 45;
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GO; GO:0005737; C:cytoplasm; TAS.
GO; GO:0005643; C:nuclear pore; TAS.
GO; GO:0006006; P:protein-nucleus import; TAS.
Coiled coil; Proto-oncogene; Chromosomal translocation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X66397; CAA47021.1; -. EMBL; Y00672; CAA68681.1; -.
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26.2%;
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2295 229
2349 AA;
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006

960 SNVEQYQAMVISLEESLNKEKQVIEEVRKNIE---VRLKESAEFQIQ 1003

43 GTAA--QAAVVRFQEAANKQKQELDEISTNIRQAGVQYSRADEEQQQ 87

Gaps

24;

16; Mismatches 39; Indels

28; Conservative

Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 SLOGOWRGAAGTAAQAAVVRFQEAANKOKOELDEISTNIRQAG-----VQYSRADEEQQO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNGGAFEGAANVESGSRVFVYEVVGMRQNEETDQTNYPIRKSGSVFIRVPYNDEMQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
Last sequence update)
16-OCT-2001 (Rel. 40, Last amnotation update)
Myosin heavy chain, nonmuscle type A (Cellular myosin heavy chain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- COFACTOR: FAD.
-!- SUBCELDULAR LOCATION: May be bound to the thylakoid membrane anchored to the thylakoid-bound phycobilisomes.
-!- SIMILARITY: WITH OTHER SPECIES FNR.
-!- SIMILARITY: Contains 1 cpcD-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R InterPro; IPRO01834; CpcD-like.
R InterPro; IPR001834; Cyt_B5_reductase.
R InterPro; IPR001834; Cyt_B5_reductase.
R InterPro; IPR001709; FAD_binding.
R InterPro; IPR001433; Oxrēd_FAD/NAD(P).
R PÉan; PF001383; CycD; 1.
R PÉan; PF001383; CycD; 1.
R PÉan; PF001383; CycD; 1.
R PÉAN; PF00167; FAD_binding_l; 1.
R PRINTS; PR00406; CYTBSRDTAŠE.
R PRINTS; PR00317; FPNCR.
R PRINTS; PR00317; FPNCR.
R PRODON; PD002838; CycD-like_C; 1.
R PCDDON; PD002838; CycD-like_C; 1.
R PCDON; PD002838; CycD-like_C; 1.
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=PCC 7937 / ATCC 29413;
Mannan R.M., Matthijs H.C.P., Pakrasi H.B.;
Mannan R.M., andlecular characterization of the petH gene in the cyanobacterium Anabaena variabilis ATCC 29413 ";
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Reduced ferredoxin + NADP(+) = oxidized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY) CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.2%; Score 75.5; DB 1; Length 440; llarity 30.0%; Pred. No. 8.4; Conservative 15; Mismatches 22; Indels
                                                                                                                                                 Anabaena variabilis.
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
NCBI_TaxID=1172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CPCD-LIKE.
NADP (RIBOSE PART)
660BAA2DCF59BB6
                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
FESEP-2013 (Rel. 42, Last annotation update)
FESTEGOXIn--NADP reductase (EC 1.18.1.2) (FNR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48826 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L26346; AAA91046.1; -. HSSP; P21890; 1QUE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ferredoxin + NADPH.
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Best Local Similarity
----- 18; Conserva
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Q44549;
01-NOV-1997
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NP BIND
SEQUENCE
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Q62812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N
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MYH9_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               엄
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01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
28-FBS-2003 (Rel. 41, Last annotation update)
Phycobiliscene 8.9 kDa linker polypeptide, phycocyanin-associated, rod
(L-8.9/R) (Rod capping linker protein).
                                                                                                                                                                                                                                                                                      MEDLINE-87246520; PubMed=3109890;
Belknap W.R., Haselkorn R.;
"Cloning and light regulation of expression of the phycocyanin operon
of the cyanobacterium Anabaena.";
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLIN237320; MEDLINE=21134097; PubMed=11237320; MEDLINE=21134097; PubMed=nayer G.J., Glazer A.N.; MITPLY O.T., Wedemayer G.J., Glazer A.N.; "Recombinant phycobiliproteins. Recombinant C-phycocyanins equipped with affinity tags, oligomerization, and biospecific recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=21595585; FubMed=11758840;
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T.,
Kaneko T., Ramura T.,
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
Yasuda M., Tabata S.,
"Complete genomic sequence of the filamentous nitrogen-fixing
Cyanobacterium Anabaena sp. strain PCC 7120.";
                                                                                                                                                            Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Res. 8:205-213(2001).
-!- SIMILARITY: TO OTHER PHYCOBILISOME LINKER PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anal. Biochem. 290:186-204(2001).
                                                                                                                                                                                                                                                                                                                                                                                         EMBO J. 6:871-884 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                           NCBI_TaxID=103690;
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Local Sim
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Matches
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                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 ERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQE------AANKQ--- 60
                                                                                                                                                                                                                                                                                                                                     SUBUNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (WHC), 2 ALKALI LIGHT CHAIN SUBUNITS (WLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2) DOMAIN: THE RODLIKE THAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEFTIDES, SHMILARITY: Contains I myosin-like globular head domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39; Gaps
                                                                 Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi; Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

Choi O.H., Park C., Itch K., Adelstein R.S., Beaven M.A.;

Choi O.H., Park C., Itch K., Adelstein R.S., Beaven M.A.;

Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: CELLULAR MYOSIN APPERRS TO PLAY A ROLE IN CYTOXINESIS,

CELL SHAPE, AND SPECIALIZED FUNCTIONS SUCH AS SECRETION AND

CAPPING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----KOELDEISTNIRQAGVQYSRADEEQQQALSSQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 1961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 ALKYLATION (SH-1) (POTENTIAL).
34 ALKYLATION (SH-2) (POTENTIAL).
226336 MW; 9B9876D9681FB19E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50096; IQ; I. Myosin, Artin-binding; Mosin, ATP-binding; Calmodulin-binding; Colled coil; Alkylation; Multigene family.

DOMAIN 1 MYOSIN HEAD-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COLLED COLL (POTENTIAL).
ATP (POTENTIAL).
ACTIN-BINDING.
type A) (Nonmuscle myosin heavy chain-A) (NMMHC-A) MYH9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.2%; Score 75.5; D:
22.8%; Pred. No. 41;
tive 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pram; Pr00062; myosin head; 1. Pram; Pr02786; myosin N. 1. Pram; Pr01276; Myosin Lail; 1. PRINTS; Pr00193; MYOSINHEAVY. Pr00m; Pr0003; Pr00193; myosin_head; 1. SMART; SM0015; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000048; IQ_region.
InterPro; IPR001609; myosin_head.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002228; Myosin_tail.
Pfam; PF00612; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U31463; AAA74950.1; -.
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174 188
654 67
694 69
704 AA;
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Best Local Simi:
Matches 26; (
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PYS1_ANASP
ID _PYS1_ANASP
AC P07124;
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MOD_RES
SEQUENCE
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NP_BIND
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 GOWRGAAGTAAQAA--VVRFQEAANKQKQELDEISTNIRQAG-----VQYSRADEEQQQ 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GOTTLGAGSVSSSASRVFRYEVVGLRQSSETDKNKYNIRNSGSVFITVPYSRMNEEYQR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 0%; Score 74.5; DB 1; Length 80; Conservative 10; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                             PIR; AB1873; AB1873.
InterPro; IPR001685; CpcD-like.
Pfam; PF01383; CpcD; 1.
Propom; P000353; CpcD-like C; 1.
Phycobilisome; Photosynthesis; Complete proteome.
SEQUENCE 80 AA; 8895 MW; 52DF2D7DEF5444D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1991 (Rel. 18, Created)
01-077-1994 (Rel. 30, Last sequence update)
01-SCF-2003 (Rel. 42, Last annotation update)
Ferredoxin--NADP reductase (EC 1.18.1.2) (FNR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    440 AA
                                                                                                                                                                                                                                                                                                    EMBL; AF178757; AAG09319.1; -. EMBL; AP003582; BAB72489.1; -.
                                                                                                                                                                                                                                                                        EMBL; X05239; CAA28865.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FENR ANASO
ID FENR AN
AC P21890
DT 01-MAY
DT 15-CCT
DT 15-CEG
GN PETH.
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PDB;
PDB;
PDB;
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PDB;
PDB;
PDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              **RAY CRYSTALLOGRAPHY (2.38 ANGSTROMS).

**MEDLINB=20508220; PubMed=11053838;

**MEDLINB=20508220; PubMed=11053838;

**Morales R., Kachalova G., Vellieux F., Charon M.-H., Frey M.;

**Morales R., Kachalova G., Vellieux F., Charon Detween the crystallographic studies of the interaction between the crystallographic studies and ferredoxin from the cyanobacterium of anabaena: looking for the elusive ferredoxin molecule.";

**Anabaena: looking for the elusive ferredoxin molecule.";

**Acta Crystallogr. D 56:1408-1412(2000).

**C. I CATALYTIC ACTIVITY: Reduced ferredoxin + NADP(+) = oxidized ferredoxin + NADPH.

**C. I CATALYTIC ACTIVITY: Reduced ferredoxin + NADP(+) = oxidized constitution or substance or substance or substance or substance to the thylakoid-bound phycobilisomes.

**C. I SIMILARITY: WITH OTHER SPECIES FRR.**

**INILARITY: Contains 1 cpcD-11ke domain.**
                                                         SEQUENCE FROM N.A.
MEDLINE-93344523; PubMed-8343609;
Fillat M.F., Flores E., Gomez-Moreno C.;
"Homology of the N-terminal domain of the petH gene product from Anabaena sp. PCC 7119 to the CpcD phycobilisome linker polypeptide.";
Plant Mol. Biol. 22:725-729(1993).
                                                                                                                                                            SEQUENCE OF 137-440 FROM N.A.
MEDLINE=91088322; PubMed=2124680;
Fillat M.F., Bakker H.A.C., Weisbeek P.J.;
"Sequence of the ferredoxin-NADP(+)-reductase gene from Anabaena PCC
                                                                                                                                                                                                                                                                                STRAIN=1403.46;
MEDLINE=88132819; PubMed=3124746;
Sancho J., Peleato M.L., Gomez-Moreno C., Edmondson D.E.;
"Purification and properties of ferredoxin-NADP+ oxidoreductase from the nitrogen-fixing cyanobacteria Anabaena variabilis.";
Arch. Biochem. Biophys. 260:200-207(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 137-440.
MEDILINE=20114461; PubMed=10651039;
MAGOTRAI T., Medina M., Sanz-Aparicio J., Gomez-Moreno C.,
Hermoso J.A.;
"Structural basis of the catalytic role of Glu301 in Anabaena PCC
7119 ferredoxin-NADP+ reductase revealed by x-ray crystallography.";
Proteins 38:60-69.(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 146-440.
MEDLINE=99119165; PubMed=9923134;
MEDLINE=99119166; PubMed=9923134;
Martinez-Julvez M., Hermoso J., Hurley J.K., Mayoral T.,
Sanz-Aparidio J., Tollin G., Gomez-Moreno C., Medina M.;
Role of Arglot and Arg264 from Anabaena PCC 7119 ferredoxin-NADP+
reductase for optimal NADP+ binding and electron transfer.";
Biochemistry 37:17680-17691(1998).
                                                                                                                                                                                                                                                                                                                                                            X-TAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 137-440.
MEDLINE=97045988; PubMed=8890910;
Serre L., Vellieux F.M.D., Medina M., Gomez-Moreno C.,
Fontecilla-Camps J.C., Frey M.;
"X-ray structure of the ferredoxin:NADP+ reductase from the
cyanobacterium Anabaena PCC 7119 at 1.8-A resolution, and
crystallographic studies of NADP+ binding at 2.25-A resolution.";
[5]
[6]
 Anabaena sp. (strain PCC 7119).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                                                                                                                       Nucleic Acids Res. 18:7161-7161(1990).
                                                                                                                                                                                                                                                                      SEQUENCE OF 152-183.
               Bacteria; Cyanoba
NCBI_TaxID=1168;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                             33 SLOGGWRGAAGTAAQAAVVRFQEAANKOKOELDEISTNIRQAG-----VQYSRADEEQQQ 87
                                                                                                                                                                                                                                                                                                                                                                                        -i- SUBCELLULAR LOCATION: May be bound to the thylakoid membrane or anchored to the thylakoid-bound phycobilisomes.
-i- SIMILARITY: WITH OTHER SPECIES FNR.
-i- SIMILARITY: Contains 1 cpcD-like domain.
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InterPro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PP01183; Oxred_FAD/NAD(P).
Pfam; PP01183; Oxred_FAD/NAD(P).
PR00175; NAD_binding_1; 1.
PR1NTS; PR00466; CYTENENTASE.
ProDom; PR00371; PPNCR.
ProDom; PR00371; PPNCR.
Prodom; PR008186; CpcD-like_C; 1.
Oxidoreductase; Plavoprotein; NADP; FAD; Thylakoid; Membrane; DoMAIN.

80 CPCD-LIKE.
                                                                                                                                                                                                                                                            Length 440;
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Bacteria: Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
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                                                                                                                                                                                                                                                            DB 1;
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28-FEB-2003 (Rel. 41, Last sequence update)
FIS-SEP-2003 (Rel. 42, Last annotation update)
FIS-Repadoxin--NADP reductase (EC 1.18.1.2) (FNR)
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30.0%; Pred. No. 13;
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InterPro; IPR001834; Cyt_BS_reductase.
InterPro; IPR001709; FPN_cyt_redctse.
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NADP (RIBOSE PART) (BY SIMILARITY) BB07AA1B99295C98 CRC64;
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15.8%; Score 73.5; D
Best Local Similarity 30.0%; Pred. No. 13;
Matches 18; Conservative 15; Mismatches
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48838 MW;
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440 AA;
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SEQUENCE
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Search completed: November 21, 2003, 16:04:18 Job time : 2.12018 secs

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01-MAR-2003 (TrEMBLrel.
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1 TDAATLAQEAGNFERISGDL.....VQYSRADEEQQQALSSQMGF 95
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

1 TDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 60 Gaps STRAIN-YS-314 / AJ 12310 / DSM 44549 / JCM 11189;

KRAMATABASASI X., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
Kawatabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
Usucki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
Usuda Y., Sugimoto S.;
"The entire genomic sequence of Corynebacterium efficiens YS-314.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, APO05215; BAC17392.1; -Hypothetical protein; Complete proteome.
SEQUENCE 106 AA; 11382 MW; 73AF6CDBEA7838A6 CRC64; . 0 24.5%; Score 114; DB 16; Length 106; 24.5%; Pred. No. 0.0051; tive 25; Mismatches 46; Indels C Corynebacterium efficiens. Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corynebacterinaea, Corynebacteriaceae, Corynebacterium. NCBI_TaxID=152794; Last sequence update)
Last annotation update) 61 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMG 94 106 AA. PRT; Created) 23, 23, Query Match Best Local Similarity 24.5% Matches 23; Conservative g g à à

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PRELIMINARY;

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691 ECAALVEELGERRRAADREKSSVAQ---QLGRLAGQARGAAGBAERSAAABERAQEALDK 747
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STRAIN-A3(2) / M45.
STRAIN-A3(2) / M45.
STRAIN-A3(2) / M45.
STRAIN-A3(2) / M45.
Bentley S.D., Chater K.E., Cerdeno-Tarraga A.-M., Challis G.L.,
Bentley S.D., Chater K.E., Cerdeno-Tarraga A.-M., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Tarper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neal S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hopwood D.A.; "Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
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                                                                                                                 SCOSS77 OR SC7A1.21.
Streptomyces coelicolor.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Streptomycineae, Streptomycetaceae, Streptomyces.
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                               Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A., Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 1186 AA; 128723 MW; CB11027815373E99 CRC64;
                                                                                                                                                                                                                                                                      Murphy L., Harris D.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
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                   1186 AA
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coelicolor A3(2).",
Nature 417.141-147(2002).

Nature 417.141-147(2002).

InterPro; IPR003439; ABC_transporter.

R InterPro; IPR003405; SMC_C.

R InterPro; IPR003829; SMC_N.

INTERPRO; IPR00829; SMC_N.

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Pfam; PF02463; SMC_N; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B., Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M., Pridoner R.D., Arigoni F., "The genome sequence of Bildobacterium longum reflects its adaptation to the human gastrointestinal tract.", Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427 (2002). EMBL, ALAJSON J. Complete protecome. Spyothetical protein; Complete protecome. SEQUENCE 96 AA; 10431 MW; 7D02BE38C6BIFGIC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AP065275; BAB97972.1; -- Hypothetical protein; Complete proteome. SEQUENCE 108 AA, 11644 MW; BOB3AFA03AE9D452 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 ERIQSSSAAVATSISÕIRQAVGGMYTNLNALÕDAWRGSAATOFTAVAEQWRAAQQQMEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERI---SGDLKTQIDQVESTAG-----SLQGQWRGAAGTAAQAAVVRFQEAANKQKQE
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                                                                                                                                                                                                             Bifidobacterium longum.
Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
Bifidobacteriaceae; Bifidobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.5%; Score 91; DB 16; Length 96; 27.3%; Pred. No. 0.53; tive 17; Mismatches 37; Indels
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19.8%; Pred. No. 0.6;
iive 26; Mismatches 47; Indels
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01-07T-2002 (TrEMBLrel. 22, Last sequence update)
01-07T-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein Cgl0579.
                                                                                  Last sequence update)
Last annotation update)
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STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
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MEDLINE=22294977; PubMed=12381787;
                                                        23,
23,
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                                 01-MAR-2003 (TrEMBLrel. 01-MAR-2003 (TrEMBLrel. 01-MAR-2003 (TrEMBLrel. by....
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                                                                                                                                                 Hypothetical protein
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es 24; Conserv
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RESULT 3 Q8G878

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550 KQAGENHYSNLSSDYETQIKSLESSL------TNSOAECVSFOEKINELNSOID 597
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STRAIN=CDC 1551 / Oshkosh;
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nalson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Middlinespozosock, Functionagesocker, Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devilin K., Feltwell T., Gentles S., Hamin N., Holroyd V. Hornsby T., Jagels K., Krogh A., Molean J., Moule S., Murphy L., Oldrer S., Osborne J., Quall M.A., Rajandram M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.", Nature 393:537-544(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                  DB 3; Length 750;
                                 STRAIN-972h.;
Wood V., Barrell B.G., Rajandream M.A.;
Submitted (BCE-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AL009227; CAA18821.1; -.
GenebB SPombe; SPAC27D7.02c; -.
InterPro; IPR000237; GRIP_domain.
PFUAFS; RIPS; GRIP, 1.
SEQUENCE. 750 AA; 87265 MW; A469AD95C5787042 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL021930; CAA17362.1; -.
EMBL; AE006937; AAK44524.1; -.
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927527DA610A1637 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1998 (TrEMBLEEL. 06, Last sequence update) 01-OCT-2002 (TrEMBLEEL. 22, Last annotation update Hypothetical 9.8 kDa protein (PE family protein). RV0287 OR MTV035.15 OR MT0300. Mycobacterium tuberculosis.
                                                                                                                                                                                                                                             19.3%; Score 90; DB 3
28.2%; Pred. No. 6.3;
tive 18; Mismatches
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Hypothetical protein; Complete
SEQUENCE 97 AA; 9778 MW; 92
                                                                                                                                                                                                                     Query Match
Best Local Similarity 28.2%,
".hes 24; Conservative 1
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01-JUN-1998 (TrEMBLrel, 06,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-A2012; PLASMID=pX01; MEDLINE=22061436; PubMed=12004073; Read T.D., Salzberg S.L., Pop M., Shumway M., Umayam L., Jiang L., Holtzapple E., Busch J.D., Smith K.L., Schupp J.M., Solomon D., Keim P., Fraser C.M.; "Comparative Genome Sequencing for Discovery of Novel Polymorphisms in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                 STRAIN-Sterne, PLASMID-virulence plasmid PX01, MEDLINE-99445483; PubMed-10515943; Okinaka R.T., Cloud K., Hampton O., Hoffmaster A.R., Hill K.K., Keim P., Koehler T.M., Lanke G., Kumano S., Mahillon J., Manter D., Martinez Y., Ricke D., Svensson R., Jackson P.J.; Sequence and organization of pX01, the large Bacillus anthracis plasmid harboring the anthrax toxin genes."; Jackson 181:6509-6515(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match , 19.4%; Score 90.5; DB 2; Length 410; Best Local Similarity 29.5%; Pred. No. 2.9; . Matches 26; Conservative 14; Mismatches 27; Indels 2:
                                                                                                                                                                                                                                      Plasmid virulence plasmid PX01, and Plasmid pX01.
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=972h , McDougall R.; McDougall R.; Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Decillus authracis...

Bacillus authracis...

Bacillus authracis...

Science 296:2028-2033(2002).

EMBL; AF065404; AAD32402.1; -..

EMBL; AE01190; AAM36135.1; -..

FROSITE; PSG0678; WD-REPEATS...

PROSITE; PSG0678; WD-REPEATS...

Hypothetical protein; Plasmid.

SEQUENCE 410 AA; 45798 MW; FIOBCO4607575C7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                              Last sequence update)
Last annotation update)
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01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-JAR-2003 (TrEMBLrel. 23, Last annotation update)
Coiled coil protein with GRIP domain.
SPAC27D7.02C.
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                                                                                                       Created)
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                                                                                               01-NOV-1999 (TrEMBLrel. 12, Cr
01-NOV-1999 (TrEMBLrel. 12, La
01-MAR-2003 (TrEMBLrel. 23, La
PXOI-99 (Hypothetical protein)
                                                         PRELIMINARY;
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Q9X367;
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Mus musculus (Mouse)
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                                                                                                                                                                                                                                                   TIGR; MT3105;
                                                                                                                                                                                                                                                                                                                                                    Local St. 29;
                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 FAAKAGLMRHTIGQAEQQAMSAQAFHQGESAAAFQGAHARFVAAAAKVNTLLDIAQANLG 77
                                                                         FERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQKQELDEISTNIR 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=9295987; PubMed=9634230; MEDLINE=9295987; PubMed=9634230; Garnier T., Churcher C., Harris D., Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eighmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., K., Skelton S., Squares R., Sulston J.E., Taylor K., Whitchead S., Barrell B.G., Barrell B.G., "Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.1%; Score 84.5; DB 16; Length 97; llarity 34.9%; Pred. No. 2.1; Conservative 7; Mismatches 44; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis.
Bacteria, Actinobacteridae, Actinomycetales, Corynebacterineae, Mycobacterineae,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97 AA; 9842 MW; BA9BCB3180EC17F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EAAGTYVAAD---AAAASSYTGF 97
                                                                                                                                                         73 QAGVQYSRADEEQQQALSSQMGF 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complete genome sequence.";
Nature 393:537-544(1998).
EMBL; AL021287; CA416105.1;
Tuberculist; Rv3020c;
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1998 (TrEMBLrel. 06,
01-JUN-1998 (TrEMBLrel. 06,
01-OCT-2002 (TrEMBLrel. 22,
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Matches 29, Conserv
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PE-family protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 FAAKAGLMRHTIGQAEQQAMSAQAFHQGESAAAFQGAHARFVAAAAKVNTLLDIAQANLG 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L. Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W.;
                                                                                                                                "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24;
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                                                                                                                                                                                                                                                                                                                                              DB 16; Length 102;
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Best Local Similarity 27.1%; Pred. No. 37;
Matches 29; Conservative 16; Mismatches 38; Indels 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87
                                                                                                                                                                                                                                                                                                                                                                                                44; Indels
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EMBL; AJ298076; CAC40701.1; -.
InterPro; IPR005613; AIP3.
Pfan; PF03915; AIP3.
NON-TER 1200 1200
                                                                                                                                                                  laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AE007129; AAK47434.1; -.
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01-DEC-2001 (TrEMBirel. 19, Last sequence update)
01-OCT-2002 (TrEMBirel. 22, Last annotation update)
Nuclear pore complex-associated protein Tpr (Fragment)
                                                                                                                                                                                                                                                                                   102 AA; 10372 MW; 03CB984D6633D2E4 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                        18.1%; Score 84.5; DE 34.9%; Pred. No. 2.2; tive 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1200 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 QAGVQYSRADEEQQQALSSQMGF 95
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                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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us-09-688-672a-10.rspt

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Strand M.;
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026589
          RESULT 13
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XX MEDLINE-22297686; PubMed=12368813;

XA Heidelborg J.F., Paulsen I.T., Nachon K.E., Gaidos E.J., Nelson W.C.,

RA Rad T.D., Eisen J.A., Seshdri R., Ward N., Methe B., Clayton R.A.,

RA Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,

RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,

RA Madupu R., Peterson J.D., Unayam L.A., White O., Wolf A.M.,

RA Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,

RA Vamathevan J., Kolonay J.F.,

RA Namler J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,

RA Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.,

RT "Genome sequence of the dissimilatory metal ion-reducing bacterium

RT Shewanella oneidensis.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 TDANAKAKTALEQARQNLEKTAEDLRKSHPDVERQAGELRTKLQAAVONTAGEVOKLAKE 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 IDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQKQELDEISTNIRQAGVQYSRADE 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Ineecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
Noctuidae; Amphipyrinae; Spodoptera.
NCBL TaxID=69820;
                                                                                                                       BEQUENCE FROM N.A.
MEDLINE=99097579; PubMed=9880904;
Kim E., Kim S.H., Choi C.S., Park Y.I., Kim H.R.;
Kloning and expression of apolipophorin-III from the common cutworm,
Spodoptera litura.";
Arch. Insect Biochem. Physiol. 39:166-173(1998).
EMBL; AF094582; AAC63377.1; -.
SEQUENCE 188 AA; 20649 MW; 7A8AE366DF8E432C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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თ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gammaproteobacteria; Alteromonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                 17.9%; Score 83.5; DB 5; Length 188; 26.7%; Pred. No. 5.3; ive 20; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 VASNVEETNEKLAPKLKEAYENFSKHVEEVQKKVHEAASKQ 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             914 AA; 98450 MW; 30189C1C218EDCD9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 AANKOKQELDEISTNIROAGVQYSRADEEQQ----QALSSQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
Prophage LambdaSo, tail length tape meausure protein.
H OR S02953.
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.4%; Score 81; DB 16;
31.2%; Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gam
Alteromonadaceae; Shewanella.
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 26.7%
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 31.2
nes 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shewanella oneidensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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SEQUENCE 914 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=70863;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Matches
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                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Muschler P.P.J., Scharf B., Schmitt R.,

Muschler P.P.J., Scharf B., Schmitt R.,

Muschler P.P.J., Scharf B., Schmitt R.,

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

BIMBL, PAB112876, AAG34154.1;

InterPro, IPR004010, Cache.

InterPro, IPR004089, Chmtaxis_transd.

InterPro, IPR003660, HAMP.

InterPro, IPR003122, TarH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              570 AVVÁQEVRELAQRSANAAKEIKALITTSGEQVHSGVTLVGD----TGRÁLQÁIVVEVQEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATLAGEAGNFERISGDLKTQIDQVESTAG-----SLQGQWRGAAGTAAQAAVVRFQE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Platyhelminthes, Trematoda, Digenea, Strigeidida,
Schistosomatoidea, Schistosomatidae, Schistosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Induction of protective immunity in mice using a 62-kDa recombinant fragment of a Schistosoma mansoni surface antigen.";
J. Immunol. 149:3612-3620(1992).
BMBJ, X65591; CA446548.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Puerto Rican;
MEDLINE=93056536; PubMed=1431131;
Soisson L.M., Masterson C.P., Tom T.D., McNally M.T., Lowell G.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 707;
                                                                                                                               Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Rhizobiaceae, Sinorhizobium.
NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            626 NKHVSAIVTATREOSTGLOFINTAVNTMDOGTOONAAMVEOOTAAS 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------AANKQKQELDEIST--NIRQAGVQYSRADEEQQQALS 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHEMOTAXIS TRANSDUC 2; 1.; 74391 MW; A82D7762FD81FFCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAX-2003 (TrEMBLrel. 23, Last annotation update)
                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39;
  707 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
17.3%; Score 80.5; D
Best Local Similarity 31.1%; Pred. No. 42;
Matches 33; Conservative 11; Mismatches
                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myosin II heavy chain (Fragment).
Schistosoma mansoni (Blood fluke)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00015; MCPsignal; 1.
Pfam; PF02203; TarH; 1.
SMART; SM00204; HAMP; 1.
SMART; SM00283; MA; 1.
PROSITE; PS0111; CHEMOTAXIS.
SEQUENCE 707 AA; 74391 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF02743; Cache; 1.
Pfam; PF00672; HAMP; 1.
PRELIMINARY;
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STRAIN=Puerto Rican;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schistosoma mansoni (Blood fluke).
Eukaryota, Metazoa, Platyhelminthes, Trematoda, Digenea, Strigeidida,
Schistosomatoidea, Schistosomatidae, Schistosoma.
NCBI_TaxID=6183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Brazilian LE;
STRAIN=Brazilian LE;
STRAIN=Brazilian LE;
MEDLINE_3211444, PubMed=8459827;
Weston D.S., Schmitz J., Kemp M., Kunz W.;
"Cloning and sequence characterization of a complete myosin heavy chain cDNA from Schistcsoma mansoni.";
Mol. Biochem. Parasitol. 58:161-164(1993).
EMBL; L01654; AAAZ9905.1;
EMSL; L01654; LMND.
                                                                                                                                                                                                                                                                                                                                                       17.2%; Score 80; DB 5; Length 528; 22.8%; Pred. No. 34; tive 21; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00015; IQ, 1.
SMART; SM02242; MYSC; 1.
PROSITE; PS00182; GLNA ADENYLATION; 1.
PROSITE; PS0096; IQ; I.
SEQUENCE 1940 AA; 222379 MW; 10FC4EAE208CA365 CRC64;
                                                                                                                                                                                                                                                                                                            528 AA; 61622 MW; AF075D13EB249B4C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     396 TRIQELEEDLEAERAARSKAEKSRQQ-LESEL 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 OELDEISTNIROAGVOYSRADEEQOOALSSOM 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1940 AA
                  UR InterPro; IPR0016098; IQ. Tegion.
DR InterPro; IPR001609; myosin_head.
DR InterPro; IPR002288; myosin_tail.
InterPro; IPR002288; myosin_tail.
InterPro; IPR00633; Tropomyosin.
IR Pfam; PF00612; IQ; 2.
R Pfam; PF000613; myosin_head; 1.
R Pfam; PF00189; myosin_tail; 1.
R PRINTS; PR00194; TROPOMYOSIN.
SMART; SM0015; IQ; 1.
PROSITE; PS00182; GLM, ADENYLATION; 1.
PROSITE; PS00182; GLM, ADENYLATION; 1.
PROSITE; PS0096; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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InterPro; IPR000048; IQ_region.
InterPro; IPR001609; myosin head.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR000333; Tropomyosin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00612; IQ; 2.
Pfam; PF00063; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
PRINTS; PR00194; TROPOMYOSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q02456;
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2003 (TrEMBLrel. 23,
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Best Local Similarity 22.8%
Matches 21; Conservative
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17.2%; Score 80; DB 5; Length 1940; 22.8%; Pred. No. 1.4e+02;

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                                      2 DAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQK 61
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1949
1 MVDFGALPPEINSARMYAGP......SGVLRVPPRPYVMPHSPAAG 391
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| SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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Mycobacterium tube
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Mycobacterium spec Description SUMMARIES AAW32449
AAW32381
AAW81702
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Mycobacterium spec			Mycobacterium spec	.~	rium	c fusi		SD	ŝ	ູດ		Mycobacterium sp.	M. tuberculosis an	Mycobacterium spec	er	rium	rium	Antigenic fusion p	ulosis	rium tu	culosis	tuberculosis r	tuberculosi	Mycobacterium tube	tuberculos	M. tuberculosis re	rium	irium t	Antigenic fusion p	rium	rium	ulosi	erium t	Mycobacterium tube	ulosis
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ALIGNMENTS

AAW32449 standard; Protein; 391 AA

RESULT 1 AAW32449

Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant; Skeiky YAW; Houghton R, Reed SG, Mycobacterium tuberculosis antigen TbH-9FL. skin testing; M.tuberculosis 96US-0680574. 95US-0523436. 95US-0533634. 96US-0620874. 96WO-US14674 Campos-neto A, Dillon DC, Twardzik DR, Vedvick TH; Mycobacterium tuberculosis. (first entry) (CORI-) CORIXA CORP. 22-SEP-1995; 22-MAR-1996; 05-JUN-1996; WO9709428-A2 30-AUG-1996; 09-JAN-1998 01-SEP-1995; 13-MAR-1997 AAW32449;

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AAW81702 standard; Protein; 391 AA
96WO-US14675
                                                                                            (CORI-) CORIXA
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Twardzik DR, V
                                01-SEP-1995;
22-SEP-1995;
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 30-AUG-1996;
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                                   New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are useful in vaccines for prevention or treatment of tuberculosis, also
                                                                                                                    (or
                                                                                                     A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (of its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M. tuberculosis antigen, TbH-9FL The immunogenic protein, and fusion proteins containing one or more of the proteins or one of the proteins BSAT-6, are useful in vaccines, preferably when formulated with a non-specific adjuvant, to induce an immune response against M.tuberculosis (for treatment or prevention).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gen; immunogen; vaccine; tuberculosis; non specific adjuvant;
testing; M.tuberculosis.
                                                                                                                                                                                                                                                 100.0%; Score 1949; DB 18; Length 391; 100.0%; Pred. No. 4.8e-143; ive 0; Mismatches 0; Indels 0;
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                                                                                   Example 3; Page 138-139; 168pp; English.
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Matches 391; Conservative
  WPI; 1997-192903/17
                                                                                                                                                                                                                             391 AA;
             N-PSDB; AAT9152]
                                                          diagnosis
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121 LIAINLLGONTPALAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, TDH-9PT The immunogenic polypeptide can be used to diagnose M.tuberculosis infection by forming complexes with specific antibodies in the sample. Fragments of DNA encoding the immunogenic polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen, especially monoclonal antibodies or equivalent polyclonal antibodies, are also used for diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                       New immunogenic polypeptide(s) from soluble M. tuberculosis antigens - useful for diagnosis of M. tuberculosis infection \,
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100.0%; Pred. No. 4.8e-143;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                      Houghton R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Page 150-152; 190pp; English
96US-0680573.
95US-0523435.
95US-0532136.
96US-0620280.
96US-0658800.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61. SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunishing against M. tuberculosis infection or may be used for the diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 LIATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLDPFEEAPEMTSAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 MYSMANNHMSMINSGVSMINISSMIKGFAPAAAQAVQIAAQNGVRAMSSIGSSIGSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
                                                         Tuberculosis, immunogenic; soluble, antigen, protective immunity, TB, vaccine, pharmaceutical, infection, diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                         Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - use to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 391;
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                                                                                                                                                                                                                                                                                                     Houghton R, Lodes MJ;
ik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1949; DB 19;
100.0%; Pred. No. 4.8e-143;
ive 0; Mismatches 0;
                            M. tuberculosis immunogenic polypeptide TbH-9FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3B; Page 128-129; 230pp; English
                                                                                                                                                                                                                                                                                                     o A, Dillon DC, Hou
Skeiky YAW, Twardzik
                                                                                                                                                                                             97WO-US18293
                                                                                                                                                                                                                        97US-0818112
96US-0730510
                                                                                                       Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                 Dillon DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 391, Conservative
                                                                                                                                                                                                                                                                                                                                                WPI; 1998-261042/23.
                                                                                                                                                                                                                                                                      (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          391 AA;
                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAV64503
                                                                                                                                  WO9816646-A2
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                                                                                                                                                                                                                          13-MAR-1997;
11-OCT-1996;
                                                                                                                                                                                                                                                                                                     Campos-Neto
27-JAN-1999
                                                                                                                                                                23-APR-1998
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                                                                                                                                                                                                                                                                                                                   Reed SG,
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181 ILEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIATNILIGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATILLPFEEAPEMTSAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This polypeptide comprises Mycobacterium tuberculosis antigen This polypeptide comprises Mycobacterium tuberculosis antigen This encoded by genomic Dim. (see AAV44375) isolated from clone TbH-9 (see AAV44371). The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAV44377) comprising an antigenic portion of a Soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, as well as DAA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic hiss for detecting M. tuberculosis inffection in a patient using these polypeptides, antibodies or oligomostocine probes and primers, for the diagnosis of tuberculosis:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated Mycobacterium tuberculosis polypeptides and DNA - used to develop products for the detection of M. tuberculosis infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                TbH-9FL.
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; Pred. No. 4.8e-143;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DC, Houghton R, Lodes M
Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                            Tuberculosis; infection; diagnosis; antigen;
                                                                                                                                                                                                             Mycobacterium tuberculosis antigen TbH-9FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Page 133-135; 250pp; English.
                                                                                                                                                                                                                                                                                                                                                   tuberculosis strain H37Rv.
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AAW64335 standard; Protein; 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0818111.
96US-0729622.
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Best Local Similarity 100.
Matches 391; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORI-) CORIXA CORP.
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                LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 360
                                                                        LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes polypeptides comprising an immunogenic are vaccines and fusion tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's, DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion tuberculosis—immune subjects. AA219249 to AA219460 and AAY39033 to AAV39225 are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antigens from Mycobacterium tuberculosis useful in diagnostic
skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis, M. tuberculosis, antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Houghton R;
                                                                                                                                                                                                                                                                             M. tuberculosis antigen TbH-9FL amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Campos-Neto A, Dillon DC, Hendrickson RC, Hc
Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                       GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1949;
100.0%; Pred. No. 4.8
:ive 0; Mismatches
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                                                                                                                                                                                                 AAY39132 standard; Protein; 391
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                                                                                                                                                                                                                                                                                                                                immune response; skin test.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0025197
                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis.
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Best Local Similarity 100.
Matches 391, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CORI-) CORIXA
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                                                                                                                                                                                                                                                                                                                                                                                    WO9942076-A2
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                                                                                                                                                                                          241 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG 300
                                                                                                                                                                                                                                      LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGOMLGGLPV 360
                                                                                                                                                                                                                                                          This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                                                                                                                                 181 LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                           LIATNLLGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG
                                                              MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                                                                                       LLEGAAAVEEASDTAAANQLMINVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antigen; diagnosis; detection; infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptide comprising antigenic portions of M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Houghton R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M. tuberculosis recombinant antigen protein TbH-9FL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dillon DC, Hendrickson RC, Ho
SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                            GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                                                                                                                                                                                                                                                                         GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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98US-0024753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Campos-Neto A, Dilla
Lodes MJ, Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccine; immunity
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18-FEB-1998;
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Length 391;

DB 20;

100.0%; Score 1949;

Query Match

1 MVDFGALPPEINSARMYAGPGSASLVAAAQMMDSVASDLFSAASAFQSVVWGLTVGSWIG 60 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG

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                                                                                                                                                                                                                                                                                                                                                                             protein; Mycobacterium; primer; PCR; amplification; probe; ation; detection; vaccine; immunisation; infection.
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Similarity 100.0%; Pred. No. 4.8e-143; )1; Conservative 0; Mismatches 0;
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methods for detecting and identifying mycobacteria, especially belonging to the M. tuberculosis complex. The encoded proteins can be used in vaccines for immunisation against a bacterial or viral infection.
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100.0%; Score 1949; DB 20;
Best Local Similarity 100.0%; Pred. No. 4.8e-143;
Matches 391; Conservative 0; Mismatches 0;
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N-PSDB; AAS03779.
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WPI; 2002-759844/82.
N-PSDB; AAD47082.
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                               as Mtb39A), an M. tuberculosis antigen. Compositions comprising at least 2 heterologous antigens, as a fushon protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially humans) against infection by Mycobacteria. The compositions contain at least 2 heterologous antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease frequently affecting patients with acquired immunodeficiency
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                     sequence represents Mycobacterium tuberculosis TbH9 (also known
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4.8e-143;
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100.0%; Pred. No. 4.8
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 Page 151-152; 168pp; English
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Matches 391; Conservative
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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous bolynucleotide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a polypeptide or its fragment. The Leishmania polynucleotide is selected from TSA, LeIF, MIS, and 6H polynucleotides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polynucleotides, as in vivo diagnostic agants and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is
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New recombinant nucleic acid molecule comprising a Leishmania TSA,
LeIF, M15 or 6H polynucleotide, useful as vaccine to elicit protective
immunity against pathogenic microogganisms e.g. Leishmania and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 391;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1949; DB 23; 100.0%; Pred. No. 4.8e-143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium species MTB39 (TbH9) protein #2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium sp. TbH9FL antigenic protein
                                                                                                                                                                                    Disclosure; Page 86-87; 155pp; English
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                                                                                                           Mycobacterium tuberculosis
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Best Local Similarity 100.
Matches 391, Conservative
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301 LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New fusion proteins useful for diagnosis, prevention and treatment of tuberculosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Di-antigen fusion protein, termed Mtb59f, composed of the antigens TbH9 and Ra35. The fusion protein is expressed in host cells using a vector carrying a polynucleotide (see AA22026) comprising the coding sequences for the 2 antigens. The invention provides fusion proteins (see AA32059-71) containing at least 2 Mtberculosis antigens. The new fusion proteins and polynucleotides encoding them are useful as vaccines for preventing tuberculosis (claimed) for diagnosis (via in vitro assays or intradermal skin tests for detection of anti-Mt tuberculosis antibodies), monitoring more effective immunogens than mixtures of the individual protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                        Tuberculosis; antigen; fusion protein; Mtb59f; TbH9; Ra35;
                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis antigen fusion protein Mtb59f.
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100.0%; Pred. No. 8.1e-143;
ive 0; Mismatches 0; 1
                                             GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                                                      361 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence represents a recombinant
                                                                                                                                                                                                                                                                                                                                                                                               diagnosis; therapy; vaccine; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Met/His tag"
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/note= "Ra12"
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/note= "TbH9"
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Best Local Similarity
Matches 391; Conserv
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                                                                                                                                                                                                                                                                                    17-JAN-2000
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                                                                                                                                                      RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with tuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention and creatment of tuberculosis infection. Sequences of the invention are useful for eliciting an immune response in a mammal, e.g., human, immunised with Mycobacterium infection. The fusion proteins and the polynucleotides are useful as diagnostic tools in patients infected with Mycobacterium, in vitro and in vivo assays for detecting hunoral antibodies or cell-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as immunogens to generate or elicit a protective immune response in a non-human patient and for raising anti-M. tuberculosis antibodies in a non-human animal. Sequences of the invention are also used as vaccines. WTB32A fusion proteins of the invention are useful as in vivo diagnostic agents for intradermal skin test. The present sequence is Mycobacterium species
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                                                                                                                                                                                                                                                                                                                                                               Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1949; DB 23; Length 391; 100.0%; Pred. No. 4.8e-143; ative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 83; Page 102-103; 136pp; English.
                                                                                                                                                                                                                                                        Skeiky Y, Reed S, Alderson M;
                                                                                                                                             20-JUN-2000; 2000US-0597796.
                                                                                                      20-JUN-2001; 2001WO-US19959
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Best Local Similarity 100.
Matches 391; Conservative
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N-PSDB; AAD28341.
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                  WO200198460-A2
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Matches 391; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polynucleoride sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a polypeptide or its fragment. The Leishmania polynucleotide is selected from TSA, LeIF, MIS, and 6H polynucleotides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic
                                                                                       188
                                                                                                             LLEGAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 240
                                                                                                                                  LLEGAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 248
                                                                                                                                                        MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG 300
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                                                                                                                                                                                                  LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 360
                                                                                                                                                                                                                New recombinant nucleic acid molecule comprising a Leishmania TSA,
LeIF, MIS or 6H polynucleotide, useful as vaccine to elicit protective
immunity against pathogenic microorganisms e.g. Leishmania and
 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                               LIATNLLGQNTPALAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPENTSAGG
                                           SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                       SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                                                                                                                                                                                                                                                                                                                agent; gene therapy; TbH9; antigen;
                                                                                                                                                                                                                                                GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                                                                                                                                                                                                                              369 GQMGARAGGGLSGVLRVPPRPYVMPHSPAAG
                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium sp. MTB59F fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 98-99; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric - Mycobacterium sp.
Chimeric - Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                             AAE29710 standard; Protein; 596
                                                                                                                                                                                                                                                                                                                                                                                                                  ne; immunity; diagnostic MTB59F; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001US-275837P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Skeiky Y, Brannon M,
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N-PSDB; AAD47086.
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microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusic polypeptides are used for enhancing the expression of polynucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is MTB59F fuelon protein. This fuelon protein comprises Ra35 protein from Mycobacterium tuberculosis and TbH9 protein from Mycobacterium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249 WVSMANNHMSMTNSGVSMINTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
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losis; infection; vaccine, MTB59F; TbH9-Ra35 protein.
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                                                                                                                                                                                                                                                         Length 596;
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                                                                                                                                                                                                                                                         Score 1949; DB 23;
Pred. No. 8.1e-143;
Mismatches 0;
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                                                                                                                                                                                                                                                            100.0%; Solarity 100.0%; Poconservative 0;
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                                                                                                                                                                                                                                                                                                                       polynucleotides are useful as diagnostic tools in patients infected with Mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or call-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as immunogens to generate or elicit a protective immune response in a patient and for raising anti-M. tuberculosis antibodies in a non-human animal. Sequences of the invention are also used as vaccines. WIB32A fusion proteins of the invention are useful as in vivo diagnostic agents for intradermal skin test. The present sequence is Mycobacterium species
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                                                                                                       The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nuclectides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with tuberculosis and methods for their use in diagnosis, prevention and useful for eliciting an immune response in a mammal, e.g., human, immunised with BCC. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the
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  Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in
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100.0%; Pred. No. 8.1e-143;
ive 0; Mismatches 0;
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                                                                             5; Page 114-115; 136pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MTB59F (TbH9-Ra35) fusion protein.
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response of Mycobacterium tuberculosis. Polypetides of the invention are useful for diagnosing, treating or preventing M. tuberculosis infection, particularly tuberculosis infection. In particular, the polypetides are useful as a vaccine formulation with an adjuvant to afford long-term protection in animals against the development of tuberculosis. The protein coding sequence may be used to encode a protein product for use as an immunogen to induce and/or enhance an immune response to M. tuberculosis. This sequence represents an M. tuberculosis fusion protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New fusion proteins of Mycobacterium tuberculosis antigens, useful for diagnosing, treating or preventing M. tuberculosis infection, particularly as vaccine for treating or preventing tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a purified polypeptide which induces an
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                                                                                                                             /note= "OTHER= Xaa. Xaa= In frame stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                               Campos-Neto A;
Fusion protein; tuberculosis; Mycobacterium tuberculosis; tuberculostatic; immunogen; vaccine; Tb59-Ra35; Mtb59f.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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100.0%; Pred. No. 8.1e-143;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Alderson M,
                                                - Mycobacterium tuberculosis
                                                                         Location/Qualifiers
597
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                                                                                                          'label= OTHER
                                                                                                                                                                                                                                                                  97US-0942578.
98US-0025197.
98US-0056556.
98US-0223040.
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Best Local Similarity 100.
Matches 391; Conservative
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SKEIKY Y A.
DILLON D C.
ALDERSON M.
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                                                                            Key
Misc-difference
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                                                                                                                                                                                                                       07-APR-1999;
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07-APR-1998;
                                                                                                                                                                                                                                                                                                                   30-DEC-1998;
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                                              Chimeric
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(ALDE/)
(CAMP/)
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MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPPAAAQAVQTAAQNGVFAMSSLGSSLGSSG 308
                                             LGGGVAANLGRAASVGSLSVPQAWAANQAVTPAARALPLTSLTSAABRGPGQMLGGLPV 360
                                                                      LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPITSLTSAAERGPGQMLGGLPV 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New fusion proteins useful for diagnosis, prevention and treatment of tuberculosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a recombinant Mycobacterium tuberculosis tri-antigen fusion protein, termed Mtb61f, composed of the antigens TDH9, DPV and MTI. The fusion protein is expressed in host cells using a vector carrying a polynucleotide (see AAZ20203) comprising the coding sequences for the 3 antigens. The invention provides fusion proteins (see AAY32059-71) containing at least 2 M. tuberculosis antigens. The new fusion proteins and polynucleotides encoding them are useful as vaccines for preventing tuberculosis (claimed), for diagnosis (via in vitro assays or intradermal skin tests for detection of anti-M. tuberculosis antibodies), monitoring more effective immunogens than mixtures of the individual protein
                                                                                                                                                                                                                                                                                                                          Tuberculosis, antigen, fusion protein, Mtb61f, TbH9, DPV, MTI, diagnosis; therapy; vaccine; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 1949; DB 20; Length 600; Best Local Similarity 100.0%; Pred. No. 8.2e-143; Matches 391; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis antigen fusion protein Mtb61f.
                                                                                                                        369 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 399
                                                                                                       GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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                                                                                                                                                                                                           AAY32068 standard; Protein; 600 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1, Fig 10A-B; 83pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0056556.
98US-0223040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US07717
                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-601610/51
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69 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 128
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                                                                                                                                                                                                 181 LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                                                                               189 LLEQAAAVEBASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                                                                                                                                                               MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                                                                                                                                                                                                                                                                                                                                         249 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSG
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                                                                                                                                        129 LIATNILGONTPALAVNEAEYGEMWAQDAAAMFGYAAATATATATLIPFEEAPEMTSAGG
                                                                                      LIATNILIGONTPALAVNEAEYGEMWAQDAAAMFGYAAATATATATLIPFEEAPEMTSAGG
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104, Appl
109, App
128, App
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APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Autonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: 153
CORRESPONDENCES: 153
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ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.411C6
TELECOMMUNICATION INPORMATION:
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 107:
US-08-095-734-2
US-08-444-623-2
US-08-441-869-2
US-09-342-563-2
US-09-342-08267-2
US-09-073-009-14
US-09-072-596-199
US-09-072-596-199
US-09-072-596-199
US-09-252-991A-26437
US-09-252-991A-26437
US-09-864-0338-3
US-08-864-0338-47
US-08-864-998A-47
US-08-861-464-8
US-08-891-998A-47
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US-08-391-333-8
US-09-323-433-8
US-09-333-8
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100.0%; Pred. No. 2.7e-154;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 107, Application US/08818112
Patent No. 6290969
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LENGTH: 391 amino acids
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 391; Conservative
      CITY: Seattle
STATE: Washington
      \begin{array}{c} \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{G} \ \mathbf{
      Sequence 107, App
Sequence 102, App
Sequence 107, App
Sequence 111, App
Sequence 111, App
Sequence 111, App
Sequence 116, App
Sequence 106, App
Sequence 109, App
Sequence 109, App
Sequence 109, App
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1126, Appl
1126, Appl
1121, Appl
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116, Appl
116, Appl
1109, Appl
1109, Appl
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1 MVDFGALPPEINSARMYAGP.....SGVLRVPPRPYVMPHSPAAG 391
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1: /cgT2_6/ptodata/1/iaa/5B_COMB.pep:*
2: /cgD2_6/ptodata/1/iaa/6B_COMB.pep:*
3: /cgD2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgD2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgD2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgD2_6/ptodata/1/iaa/pcTUS_COMB.pep:*
                                  GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
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US-08-818-111-102
US-09-072-596-102
US-09-223-040-2
US-08-818-111-106
US-08-918-111-106
US-09-056-556-111
US-09-056-556-110
US-08-818-111-104
US-08-818-111-104
US-08-818-111-104
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US-08-818-111-92
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US-09-056-556-104
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Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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                                                                       SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 120
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1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG 60
                                                 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
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APPLICANT: Reixy, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Thomas S.
APPLICANT: Twardzik, Daniel R.
NUMBER OF SEUUBNCES: 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZURINIA 2002
ZURINIA 20104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                           GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REPERENCE/DOCKET NUMBER: 210121.417C6
TELECOMOUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
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Patent No. 6338852
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
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amino acid
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TTY: Seattle
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US-08-818-111-102
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Patent No. 6350456
GENERAL INFORMATION
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
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0
     Length 391;
                                                     Indels
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APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J. 31,392
REGISTRATION NUMBER: 21,1392
REGISTRATION NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAME: (206) 682-4900
100.0%; Score 1949; DB 4;
100.0%; Pred. No. 2.7e-154;
ive 0; Mismatches 0;
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6300 Columbia Center, 701 Fifth Avenue
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MDDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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amino acid
  Query Match
Best Local Similarity 100.0
Matches 391; Conservative
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CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
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TOPOLOGY: li
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US-09-056-556-107
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TREATME

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301 LGGGVAANIGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 360
                                                                                                                                                                                                                                                                                                                                      61 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                                                                                                                                                                                                                                                                                                                      121 LIAINILGGNIPAIAVNEAEYGEMWAQDAAAMFCYAAAIAIAIAILIPFEEAPEMISAGG
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                                                                                                                                                                    Length 391,
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                                                                                                                                                                100.0%; Score 1949; DB 4;
100.0%; Pred. No. 2.7e-154;
ive 0; Mismatches 0;
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99.7%; Pred. No. 1.7e-153;
live 0; Mismatches 1;
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TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS:
                                                      LENGTH: 391 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 99.77
Matches 390; Conservative
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Matches 391; Conserv
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TOPOLOGY:
US-09-072-596-102
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US-09-223-040-2
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                                   Length 391;
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Daniel R.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Hondrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                        0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: PERADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
                                 Score 1949; DB 4;
Pred. No. 2.7e-154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       701 Fifth Avenue
               100.0%; Scolloo.0%; Pred. No. c. 0; Mismatches
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMONICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 102, Application US/09072596
Patent No. 6458366
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STREET: 6300 Columbia Center,
CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Steven G.
                               Query Match
Best Local Similarity 100.0
Matches 391, Conservative
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US-09-072-596-102
US-09-056-556-101
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ADDRESSEE:
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CITY: Se
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                                                                   LIATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG 180
                                                                                                   LIATNILIGONTPALAVNEAEYGEMWAQDAAAMFGYAAATATATILLPFEEAPEMTSAGG 321
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                            SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
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APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentII Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13 MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 532
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Patent No. 6290969
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Dillon, Davin C.
Campos-Neto, Antonio
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ATTORNEY AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-6931
INFORMATION FOR SEQ ID NO. 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
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ADDRESSEE: SEED and
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APPLICANT:
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Length 396;

DB 3;

84.8%; Score 1652.5;

Query Match

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TUBERCULOSIS
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                                                                                                                                                                                                             61 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
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APPLICANT: Campos-Neco, Anconia
APPLICANT: Houghton, Raymond
APPLICANT: Wedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
CORRESPONDENCE ADDRESS:
                            Indels
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COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David 3.
REGISTRATION NUMBER: 210121.41766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360 GLPLGOLTNSGGGFGGVSNALRMPPRAYVMPRVPAAG 396
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     Pred. No. 1.3e-129;
                         19; Mismatches
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Patent No. 6338852
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
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Dillon, Davin C.
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84.98;
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acid
TYPE: amino acid
Best Local Similarity 84.9
Matches 337; Conservative
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MEDIUM TYPE: Floppy
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                                                                                                                          Length 396;
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APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardaik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF CORRESPONDENCE ADDRESS:
                                                                                                                                                                   34; Indels
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/072,596
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                                                                                                                   84.8%; Score 1652.5; DB 4
84.9%; Pred. No. 1.3e-129;
ive 19; Mismatches 34;
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05-MAY-1998
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MG-DOS
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Patent No. 6458366
GENERAL INFORMATION:
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAK: David J.
REGISTRATION NUMBER: 31,392
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
                                                                                                              Query Match
Best Local Similarity 84.9%
Matches 337; Conservative
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STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
       TYPE: amino acid
STRANDEDNESS:
                                                       linear
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US-09-056-556-111
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Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Reekky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
                                                                                                                                         7.
                                                                                                DB 4; Length 396;
                                                                                         84.8%; Score 1652.5; DB 4; Length
84.9%; Pred. No. 1.3e-129;
ive 19; Mismatches 34; Indels
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CITY: Seattle
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
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ATTORNEY/AGENT INFORMATION:
NAME: MAXI, DAVIG J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 antino acids
                                                                                    Query Match
Best Local Similarity 84.99
Matches 337; Conservative
                        linear
; STRANDEDNESS:
; TOPOLOGY: 1;
US-08-818-111-106
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FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
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SOFTWARE: PatentI
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US-08-818-111-104
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                                                                                                                                                                                                                DB 4; Length 396;
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Patent No. 6290569
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Wedvick, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                               34; Indels
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ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                            Query Match
Best Local Similarity 84.9%; Pred. No. 1.3e-129;
Matches 337; Conservative 19; Mismatches 34;
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTPERISTICS:
LENGTH: 396 amino acids
TYPE: amino acid
STRANDEDNESS:
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US-09-072-596-106
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US-08-818-112-109
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APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ASTRFFF SEED and Define
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 76.3%; Score 1486.5; DB 3; Length Best Local Similarity 84.2%; Pred. No. 7.2e-116; Matches 303; Conservative 16; Mismatches 36; Indels
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                                                                                       210121.411C6
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IBM PC compatible
:YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 104, Application US/08818111
Patent No. 6338852
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: SEED and BERRY LLP
6300 Columbia Center,
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFRENCE/DOCKET NUMBER: 2101:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                          TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Reed, Steven G. APPLICANT: Skelky, Yasir A. WAPPLICANT: Dillon, Davin C. APPLICANT: Campos-Neto, Anto APPLICANT: Houghton, Raymonn APPLICANT: Vedvick, Thomas S. APPLICANT: Twardzik, Daniel
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TUBERCULOSIS
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APPLICANT: Reed, Steven G.

APPLICANT: Skeiky, Yasır A.W.

APPLICANT: Dillon, Davin C.

APPLICANT: Gampos-Neto, Antonia

APPLICANT: Houghton, Raymond

APPLICANT: Twardaik, Thomas S.

APPLICANT: Twardaik, Daniel R.

APPLICANT: Hendrickson, Ronald C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 350

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and NPDPL.
                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 359;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                         76.3%; Score 1486.5;
84.2%; Pred. No. 7.2e
                                                                                                                                                                                                                                                                                                                                                                                                                     16; Mismatches
                                       ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELETAX: (206) 682-693
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 104, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
                                                                                                                                                                                                                                          LENGTH: 359 amino acids
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                               amino acid
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Matches 303; Conserv
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STATE: Washingt
COUNTRY: USA
                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                  STRANDEDNESS
                                                                                                                                                                                                                                                                                                                             US-09-056-556-109
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Patent No. 6350456

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 359;
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STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: FIDEPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patcettin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                   76.3%; Score 1486.5; DB 4; 84.2%; Pred. No. 7.2e-116; iive 16; Mismatches 36;
                                  PPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAKE, David J.
NEGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C6
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR EAQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                      LENGTH: 359 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 84.2'
Matches 303; Conservative
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US-09-056-556-109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                  1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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APPLICANT: Campos-Netco, Antonio
APPLICANT: Campos-Netco, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedv. Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
NUMBER OF SEQUENCES: 153
                                                                                                                                                                                                                                                                                                                                            // Score 1486.5; DB 4; Length
// Pred. No. 7.2e-116;
16; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                             210121.41709
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 91, Application US/08818112
Patent No. 6290869
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
                                                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAK1, David J.
REGISTRATION NUMBER: 31,392
REFRENCE/POCKET NUMBER: 21012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98104-/J.COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                            76.3%;
84.2%;
                                                                                                                                                                                                                                 LENGTH: 359 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 84.28
Matches 303; Conservative
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US-09-072-596-104
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US-08-818-112-91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 TAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos Neto, Davin C.
APPLICANT: Gampos Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Tardick, Daniel R.
APPLICANT: TWANTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNSYAGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                            210121.411C6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEED and BERRY LLP
                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 210
TELECOMOUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: CO NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seattle
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/POCKET NUMBER: 210121.417C6
FILECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 92: SEQUENCE CHARACTERISTICS:
LENGTH: 263 aniho acids
TYPE: aniho acid
TYPE: aniho acid
TYPE: aniho acids
TOPOLOGY: linear
US-08-818-111-92
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0; Gaps Query Match
60.9%; Score 1187; DB 4; Length 263;
Best Local Similarity 99.6%; Pred. No. 3.9e-91;
Matches 241; Conservative 1; Mismatches 0; Indels

194 JAAANQLMINVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN 253

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254 SGVSMINTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGGVAANLGRAA 313 181 SGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANIGRAA 240 Dβ ò a

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Search completed: November 21, 2003, 16:11:39 Job time : 9.24558 secs

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November 21, 2003, 16:08:22 ; Search time 15.2499 Seconds (without alignments) 4680.740 Million cell updates/sec
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19: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        666188 seqs, 182559486 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1949
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 107, App	sequence 102, App Sequence 14, Appl		Sequence 26, Appl	Sequence 20, Appl			Seguence 18, Appl	Sequence 65, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 16, Appl	Sequence 111, App	Sequence 106, App
SUMMARIES ID	US-10-084-843-107	US-10-193-002-102 US-10-098-732A-14	US-09-287-849-26	US-10-359-460-26	US-10-098-732A-20	US-09-287-849-22	US-10-359-460-22	US-10-098-732A-18	US-10-098-732A-65	US-09-287-849-2	US-10-359-460-2	US-10-098-732A-16	US-10-084-843-111	US-10-193-002-106
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Score	1949	1949	1949	1949	1949	1949	1949	1949	1949	1944	1944	1944	1652.5	1652.5
Result No.	 	n v	4	'n	w	7	60	σv	10	11	12	13	14	15

Sequence 109, App Sequence 8, Appli Sequence 9, Appli Sequence 91, Appli Sequence 126, Appl Sequence 126, Appl Sequence 126, Appl Sequence 16, Appl Sequence 11, Appl Sequence 12, Appl Sequence 12, Appl Sequence 142, Appl Sequence 142, Appl Sequence 142, Appl Sequence 131, Appl Sequence 131, Appl Sequence 131, Appl Sequence 131, Appl Sequence 131, Appl Sequence 131, Appl Sequence 131, Appl Sequence 131, Appl Sequence 131, Appl Sequence 131, Appl Sequence 131, Appl Sequence 131, Appl Sequence 15	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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ALIGNMENTS

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US-10-084-843-107
Sequence 107, Application US/10084843
Sequence 107, Application US/10084843
Publication No. US2003041324341
GENERAL INFORMATION:
Skeiky, Yasir A.W.
Dillon, Davin C.
Gampos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADERSES:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITK: Seattle
STATE: Mashington
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Peb-2002
CLASSIFICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INPORMATION:
NAME: Maki, David J.
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us-09-688-672a-26.rapb

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APPLICANT: Brannon, Mark
APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jeffrey
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
TITLE OF INVENTION: Leishmania Antigen
FILE REFERENCE: 014058-01201008
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT FILING DATE: 2003-04-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIATNLLGONTPALAVNEAEYGEMWAQDAAANFGYAAATATATLLPFEEAPEMTSAGG
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                       OPERATING SYSTEM: PC_DOS/MS-DOS
SOFWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: MAK1, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDENESS: SINGle
;
TOPOLOGY: linear
;
SEQUENCE DESCRIPTION: SEQ ID NO: 102:
US-10-193-002-102
  IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/10098732A Publication No. US20030175294A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 391 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-098-732A-14
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Houghton, Raymond
Vedvick, Thomas S.
Twardik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
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STREET: 6300 Columbia Center, 701 Fifth Avenue
STATE: Mashington
                         REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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SEQUENCE DESCRIPTION: SEQ ID NO: 107:
US-10-084-843-107
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 102, Application US/10193002
Publication No. US20030135026A1
GENERAL INFORMATION:
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Skeiky, Yasir A.W.
Dillon, Davin C.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                        LENGTH: 391 amino acids
                                                                                                                    INFORMATION FOR SEQ ID NO: 107: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                TOPOLOGY: linear
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US-10-193-002-102
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Length 596; Indels 120 128 240

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249 WVSMANNHMSMTNSGVEMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSG 308
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; SEQ ID NO 26

LENGTH: 596

TENGTH: 596

ORGANISM: Artificial Sequence

FETURE: FETURE:

OTHER INFORMATION: Description of Artificial Sequence:bi-fusion
US-09-287-849-26
                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e-145;
Matches 391; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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SEQ ID NO 26
LENGTH: 596
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APPLICANT: Skelky, Yasir A.W.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos Netc, Antonio
APPLICANT: Campos Netc, Antonio
APPLICANT: Campos Netc, Antonio
APPLICANT: Carixa Corporation
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-00902005
CURRENT APPLICATION NUMBER: 0209204-07
FRICK PILLING DATE: 1997-03-13
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-10-01
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.1
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100.0%; Pred. No. 7.1e-146;
iive 0; Mismatches 0;
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                                                                                                                                                                         ; OTHER INFORMATION: MTB39 full length (TbH9FL) US-10-098-732A-14
      60/275,837
                                                                                                                 TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
FEATURE:
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Patent No. US20020009459A1
PRIOR APPLICATION NUMBER: US 60, PRIOR FILING DATE: 2001-03-13, NUMBER OF SEQ ID NOS: 80, SOFTWARE: PATENTIN Ver. 2.1 ERQ ID NO 14
                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.'
Matches 391; Conservative
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US-09-287-849-26
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; Patent No. US20020009459A1
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APPLICANT: Skeiky, Yasix A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Campos Neto, Antonio
APPLICANT: Corixa Corporation
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US-09-287-849-22
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US-10-098-732A-20

Sequence 20, Application US/10098732A

Publication No. US20330175294A1

GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jeffrey
APPLICANT: Grant Corporation
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
TITLE OF INVENTION: Heterologous Fusion Protein
TITLE OF INVENTION: Leishmania Antigen
FILE REFERENCE: 014058-012010US
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT APPLICATION NUMBER: US 60/275,837

PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 20

INNOTHER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER SECONDER 
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                                                 / OTHER INFORMATION: Description of Artificial Sequence:bi-fusion US-10-359-460-26
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COTHER INFORMATION: Description of Artificial Sequence:bi-fusion
FORTER INFORMATION: protein TbH9-Ra35 (designated MTB59F)
CS-10-098-732A-20
                                                                                                                                    Length 596;
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                                                                                                                                                                                        Indels
                                                                                                                                 100.0%; Score 1949; DB 12;
100.0%; Pred. No. 1.2e-145;
ive 0; Mismatches 0;
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ORGANISM: Artificial Sequence FEATURE:
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Matches 391; Conservative
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TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
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CURRENT APPLICATION NUMBER: US/09/287,849
CURRENT FILING DATE: 1999-04-07
PRIOR PRIOR PLING DATE: 1997-03-13
PRIOR FILING DATE: 1997-10-01
PRIOR PLING DATE: 1997-10-01
PRIOR PLING DATE: 1998-02-18
PRIOR PLING DATE: 1998-02-18
PRIOR PLING DATE: 1998-04-07
PRIOR PLING DATE: 1998-04-07
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PRIOR APPLICATION NUMBER: US/09/223,040
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                                           SSAGIMVAAASPYVAWMSVIAGQAELIAAQVRVAAAAYETAYGITVPPPVIAENRAELMI
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APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
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APPLICANT: Campos-Neto, Antonio
ATTLE OF INVENTION: and Their Uses
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TITLE OF INVENTION: and Their Uses
CURRENT APPLICANTON NUMBER: US/09/287,849
FRIOR FILING DATE: 1999-04-07
FRIOR FILING DATE: 1999-04-07
FRIOR FILING DATE: 1997-10-01
FRIOR FILING DATE: 1997-10-01
FRIOR FILING DATE: 1997-10-01
FRIOR FILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-04-07
FRIOR FILING DATE: 1998-04-07
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ORGANISM: Artificial Sequence
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US-10-098-732A-18
Sequence 18, Application US/10098732A
PUblication No. US20030175294A1
GENERAL INFORMATION
GENERAL INFORMATION
FAPLICANT: Skeiky, Yasir
APPLICANT: Gueiky, Yasir
APPLICANT: Grannon, Mark
APPLICANT: Grannon, Mark
FAPLICANT: Grannon, Mark
APPLICANT: Grannon, Mark
FAPLICANT: Grannon, Mark
FILLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
TITLE OF INVENTION: Leishmania Antigen
FILLE REFERENCE: 014056-01210100
CURRENT FILLIG DATE: 2003-04-29
FRICH APPLICATION NUMBER: US/10/098,732A
FRICH APPLICATION NUMBER: US/10/098,732A
FRICH FILLIG DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
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129 LIATNILGQNTPALAVNEAEYGEWWAQDAAAMFGYAAATATATTLEFEEAPEMTSAGG
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OTHER INFORMATION: Description of Artificial Sequence:WTB72FMutSA
OTHER INFORMATION: (Ral2-TbH9-Ra35MutSA)
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100.0%; Score 1949; DB 12;
Best Local Similarity 100.0%; Pred. No. 1.6e-145;
Matches 391; Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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SEQ ID NO 18
LENGTH: 729
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US-10-098-732A-18
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ORGANISM: Artificial Sequence
                                     Skeiky, Yasir A.W.
Dillon, Davin C.
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Matches 390; Conservative
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US-10-359-460-2
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442 LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 501
                                                                                                                                               Sequence 65, Application US/10098732A

| Sequence 65, Application US/10098732A
| Publication No. US20030175294A1
| GENERAL INFORMATION:
| APPLICANT: Skeiky, Yasir
| APPLICANT: Brannon, Mark
| APPLICANT: Guderian, Jeffrey
| TITLE OF INVENTION: Leishmania Antigen
| TITLE OF INVENTION: Leishmania Antigen
| TITLE OF INVENTION Leishmania Antigen
| FILE REFERENCE: 014058-012010US
| CURRENT APPLICATION NUMBER: US 60/275,837
| FRIOR FILING DATE: 2001-03-13
| NUMBER OF SEQ ID NOS: 80
| SEQ ID NO 65
| LENGTH: 930
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ORGANISM: Artificial Sequence
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Sequence 2, Application US/09287849 Patent No. US20020009459A1

RESULT 11 US-09-287-849-2

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Pred. No. 3.9e-145;
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APPLICANT: DILLON, MAYK,
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
ITILE OF INVENTION: And Their Uses
ITILE REFERENCE: 014058-009020US
FILE REFERENCE: 014058-009020US
CURRENT PILING DATE: 1999-04-07
PRIOR PILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/818,112
PRIOR PILING DATE: 1997-03-13
PRIOR PILING DATE: 1997-03-13
PRIOR PILING DATE: 1997-0-01
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-04-07
PRIOR PILING DATE: 1998-04-07
PRIOR PILING DATE: 1998-04-07
PRIOR PILING DATE: 1998-12-30
NUMBER: OF SEQ ID NOS: 46
SEQ ID NO 2
LENGTH: 729
LENGTH: 729
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; Publication No. US20030147911A1
; GENERAL INFORMATION:
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
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Gaps

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201 9

180

261

240

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61 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 120
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                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence:tri-fusion OTHER INFORMATION: protein MTB72F (Ra12-TbH9-Ra35 or MTB32-MTB39 OTHER INFORMATION: fusion)
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STREEF: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
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                         FILE REFERENCE: 014058-012010US
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT FILING DATE: 2003-04-29
FRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 729
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Skeiky, Yasir A.W.
Dayloo, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vodylck, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND ME
TITLE OF INVENTION: Leishmania Antigen
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; Sequence 111, Application US/10084843
; Publication No. US20030143243A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 99.77
Matches 390; Conservative
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                   APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their uses
FILE REFERENCE: 014058-009020US
CURRENT PAPLICATION NUMBER: US/10/359,460
CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US/09/287,849
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR PLILNG DATE: 1997-03-13
PRIOR PLILNG DATE: 1997-10-01
PRIOR PLILNG DATE: 1997-10-01
PRIOR PLILNG DATE: 1998-04-07
PRIOR PLILNG DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,56
PRIOR PLILNG DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/025,30,040
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/025,23,040
PRIOR FILING DATE: 1998-04-07
PRIOR PLILNG DATE: 1998-04-07
PRIOR PLILNG DATE: 1998-04-07
PRIOR FILING DATE: 1908-04-07
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Sequence 16, Application US/2030175294A1

Publication No. US20030175294A1

APPLICANT: Skeiky, Yasir
APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jeffrey
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence:tri-fusion US-10-359-460-2
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99.7%; Pred. No. 3.9e-145;
live 0; Mismatches 1;
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Best Local Similarity 99.7
Matches 390; Conservative
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US-10-098-732A-16
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LENGTH: 729
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METHODS FOR DIAGNOSIS
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ZIP: 98104-7032
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                          ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
STTY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/10/193,002
FILING DATE: 10-U1-2002
CLASSIFICATION: <Unknown>
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND ME
TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 106:
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                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (206) 68 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 84.99
Matches 337; Conservative
                                                                                                                                                                                                                  SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-193-002-106
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84.8%; Score 1652.5; DB 12; Lengt
Best Local Similarity 84.9%; Pred. No. 1.9e-122;
Matches 337; Conservative 19; Mismatches 34; Indels
                                                 COMPUTER READABLE FORM:
COMPUTER: PROABLE FLORDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 2-Peb-2002
FLING DATE: 2-Peb-2002
CLASSIFICATION: <a href="https://doi.org/10/084/843">UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER: UNMENDER:
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|GLPLGQLTNSGGGFGGVSNALRMPPRAYVMPRVPAAG 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: MAKI, David J.

REGISTATION NUMBER: 31,392
REPERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 622-4900
TELEFAX: (206) 622-6031
INFORMATION FOR SEQ ID NO: 111:
                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
PILING DATE: 05-WAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 111:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 106, Application US/10193002
Publication No. US20030135026A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Netc, Attonia
Houghton, Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: <Unknown>
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US-10-193-002-106
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180 121 LIATNILIGONTPAIAVNEAEYGEMWAQDAAAWFGYAATAATATEALLPFEDAPLITNPGG 180 LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 240 GSSGLGGGCVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLG 356 GSSGLGAGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAQTAPGHMLG 359 09 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG 1 VVDFGALPPEINSARMYAGPGSASLVAAAKWMDSVASDLFSAASAFOSVVWGLTTGSWIG LIATNLLGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATTLLPFEEAPEMTSAGG 61 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI LLEQAVAVEBAIDTAAANOLMNNVPQALQQLAQPTKSIWPFDQLSELWKAISPHLSPLSN 241 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSS----LGSSL Gaps 34; Indels |||:||: |GLPLGQLTNSGGGFGGVSNALRMPPRAYVMPRVPAAG 396 GLPVGQMGARAG - - GGLSGVLRVPPRPYVMPHSPAAG 391 84.8%; Score 1652.5; DB 1 84.9%; Pred. No. 1.9e-122; live 19; Mismatches 34; 360

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                                                                                                                                                                                                                                        US-09-688-672A-26
1949
1 WVDFGALPPEINSARMYAGP......SGVLRVPPRPYVMPHSPAAG 391
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score: 3
Sequence: 3
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probable PPE prote	A70647	(7)	409	21.0	409.5	45
probable PPE pro	F70825	7	645	21.1	412	44
	E70946	~	290	21.1	412	43
PPE	E70808	N	987	21.3	414.5	42
PPE	F70675	(7)	582	21.3	415	41
PPE	H70552	À	618	21.3	415.5	40
교	B70969	~	3157	21.4	418	33
크러리	A70762	N	678	21.4	418	38
五百百	E70663	N	615	21.7	422.5	37
probable PPE prote	F70846	N	2523	21.7	423.5	36
	C70780	N	443	21.9	426.5	35
	B70987	N	1053	22.0	428.5	34
probable PE prot	D70676	~	479	22.0	429.5	33
probable PPE prote	A70931	(7)	655	22.6	439.5	32
probable PPE pro	C70830	N	487	22.6	441	31
	B/0524	4	200	22.7	443	30

٠	ALIGNMENTS
RESULT 1 B70608 probable C;Species C;Date: 1	RESULT 1 B70608 probable PPE protein - Mycobacterium tuberculosis (strain H37RV) C.Species: Mycobacterium tuberculosis C.Species: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C; Access R; Cole, ; Connor Rajandre	C;Accession: B70608 C;Accession: B70608 ;Conlor, R.; Bavies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
A; Autho: A; Title: A; Refere	Nature 339, 337-348, 1330 AfAtthors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome : A;Reference number: A70500; MUID:98295987; PMID:9634230
A; Access A; Status A; Molecu A; Residu	
A;Cross-ref A;Experimen C;Genetics: A;Gene: PPE	A.Gross-references: GB:293777; GB.AL123456; NID:g3261726; PIDN:CAB07839.1; PID:e311073; F A.Experimental source: strain H37Rv C.Genetics: A.Gene: PPE
Query Best I Matche	Query Match Best Local Similarity 100.0%; Pred. No. 3.3e-108; Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
δχ	1 MVDFGALPPEINSARMYAGPGSASLVAAAQMMDSVASDLFSAASAFQSVVWGLTVGSWIG 60
QQ	1 MVDFGALPPEINSARMYAGFGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG 60
6	61 SSAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAÄAAYETAYGLTVPPPVIAENRAELMI 120
Op	61 SSAGLMVAAASPYVAWMSVTAGGAELTAAQVZVAAAAYETAYGLTVPPPVIAENRAELMI 120
δλ	121 LIATNLLGONTPALAVNBAEYGEMWAQDAAMFGYAAATATATATLLFFBEAPEMTSAGG 180
q	121 LIATNILIGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLILFFEEAPEMTSAGG 180
ολ	181 LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 240
qq	181 LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 240
λΌ	241 MVSNANNHMSMTNSGVSMINILSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSG 300
qq	241 MVSMANNHMSMINSGVSMINTLSSMLKGFAPAAAQAVQIAAQNGVRAMSSLGSSLGSSG 300
Οy	301 LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPITSITSAARROPGQMLGGLPV 360
qq	301 LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 360
δ ·	361 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391

9

Gaps . 9

47; Indels

Length 393;

120 180 240 240 296 299 121

9

Indels

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A;Residues: 1-393 <COL>
A;Cross-references: GB:AL022021; GB:AL123456; NID:g3250699; PIDN:CAA17711.1; PID:e1254600
A;Residues: 1-393 <COL>
A;Cross-references: GB:295390; GB:AL123456; NID:g3261766; PIDN:CAB08702.1; PID:e316074;
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: PPE
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A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Tille: Deciphering the biology of Mycobacterium tuberculosis from the complete genom A; Reference number: A70500; MUID:98295987; PMID:9634230
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSSGLGGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLG 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 GSSGLGAGVAANLGRAASVGSLSVPPAWAAANQAVTPAARALPLTSLTSAAQTAPGHMLG 359
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul.1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: G70929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MVDFGALPPEINSARMYAGFGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSS----LGSSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MDFGALPPEVNSVRMYAGPGSAPMVAAASAWNGLAAELSSAATGYETVITQLSSEGWLGP
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40.0%; Score 779.5; DB 2;
Best Local Similarity 43.7%; Pred. No. 4.3e-39;
Matches 179; Conservative 65; Mismatches 129;
                                                                                                                                                                                                                                                                                                 Score 1583; DB 2;
Pred. No. 1.4e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360 GLPLGH-SVNAGSGINNALRVPARAYAIPRTPAAG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            357 GLPVGQMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                                                                                                                                                                                                                                                                                                                                    20; Mismatches
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A, Gene: PPE
                                                                                                                                                                                                                                                                                             81.2%;
81.5%;
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 81.5
Matches 322; Conservative
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: H70741
R;Ocle, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Natucres 393, 537-544, 1998
A;Authors: Sqares, R.; Jouleton, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Accession: H70741
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C. Species. Mycobacterium tuberculosis

C. Species. Mycobacterium tuberculosis

C. Species. Mycobacterium tuberculosis

C. Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C. Accession: C70568

R. Cole, S.T.: Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A. Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A. Artitle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70500; MUID:98295987; PMID:9634230

A.; Status: preliminary; nucleic acid sequence not shown; translation not shown
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; Pred. No. 6.4e-91;
18; Mismatches 34;
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                                                               GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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Best Local Similarity 85.1%;
Matches 338; Conservative 1:
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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C)Species: Mycobacterium tuberculosis
C)Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C)Accession: H70931
R)Cole, S.T., Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor. R.; Davies, R.; Devlin, K.; Feltwell, T.; Gantles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome & A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: H70931
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DMS
A;Cross-references: GB:AL022021; GB:AL123456; NID:g3250699; PIDN:CAA17728.1; PID:e1254618
A;Genetics:
A;Genetics:
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Uul-1998 #sequence_revision 17-Uul-1998 #text_change 22-Oct-1999
C;Accession: B70911
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwall, T.; Garnies, S.; Hamin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, S37-544, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        223 KLGGLWKTVSPHRSPISNMVSMANNHMSMTNSGVSM-TNTLS---SMLKGFAPAAAQAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               279 OTARONGVRAMSSIGSSL----GSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFOSVVWGLTVGSWIGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 403;
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| | | | : | : | | | AAEAPGALFGEMALSSLAGRALAGTAVRSGAGARV
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A70932
probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C.Specias: Mycobacterium tuberculosis
C.Specias: Mycobacterium tuberculosis
C.Specias: Mycobacterium tuberculosis
C.Specias: Mycobacterium tuberculosis
C.Specias: Mycobacterium tuberculosis
C.Jaces 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C.Accession: A70932
R.Devihin, R.; Feltwell, T.; Gentles, S.; Hamris, D.; Gordon, S.; Connor, R.; Davies, R.; Devihin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Retenere number: A70500; MUID:9825987; PMID:9634230
A;Recession: A70932
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-409 cCOL>
A;Cross-references: GB:AL022021; GB:AL123456; NID:g3250699; PIDN:CAA17729.1; PID:e125461
A;Genetics:
C;Genetics: PPE
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                                                                                                                                                                                                                                                                                                         ONGVRAMSSLGSSLGSSGLGGGVAANLGRAASVGSLSVPQAWAA-ANQAVTPAARALPLT 341
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                                                                                                                                                233 LQSITTILANLTGPYSIIGLGAIPGGWWLTFGQILGLAQNAPGVAALLGPKAAAGALSPL
                                                                                                                                                                                                              -----TVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAA
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                      IATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                      SLTSAAERGPGOMLGGLPVGOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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                                                                                                               182 LEQAAAVEEASDTAAA--NQLMNNVPQALQQLAQPTQGTTPSSKLGGLWK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 409;
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ilarity 44.7%; Pred. No. 2.2e-37;
Conservative 53; Mismatches 138; Indels
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Best Local Similarity
Matches 177; Conserv
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180 179 214 239 272 298 332 358 388 418

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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: S:T; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.;
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Reference number: A70500; MyID:98295987; PMID:964230
A;Reference number: A70500; MyID:98295987; PMID:964230
A;Retures preclaminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-408 <COL>
A;Cross-references: GB:Z74024; GB:ALI23456; NID:g3250700; PIDN:CAA98377.1; PID:e1301025;
A;Genetics:
A;Genetics:
A;Genetics:
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                                                               MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                             61 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                                                                                                                                                                     180 LAQEVVEEVVEEVVEEVVEEVVEEVVEARQAISQAALDQAVNEGMEATVVPQVDQQVNVDVATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           215 TQGTTPSSKLGG--LWKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 QTAVPDSSSAAAPQLWGGFAQHLSPINDTLSMINNHAGMANAGLSLVNGMGSAMKSLAP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   273 AAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 TITKAAESAFKAMGSAVQSTGRGLLGSSSGGHVTAQLGRAASIGSLRVPQTWTTASQPVT
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HP4056
PPE-family protein [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: H87056
R;Ober-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: H87056
R;Davies, R.M.; Eiglineier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; HG
R;Davies, R.M.; Buthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Squares, A;Aitler massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUD:21128732; PMID:11234002
A;Accession: H87056
A;Status: preliminary
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A; Reference number: A70500; MUID:98295987; PMID:9634230
A; Reference number: D70931
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Residues: 1-423 <CD.>
A; Residues: 1-423 <CD.>
A; Residues: 1-423 <CD.>
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A;Residues: 1-421 <STO>
A;Cross-references: GB:AL450380; NID:g13093150; PIDN:CAC31563.1; GSPDB:GN00147
C;Genetics:
A;Gene: ML1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 SSTSMASAAAPYVAWMSATAVHAELAGAQARLAIAAYEAAFAATVPPPVIAANRAQLMVL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                331
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41.1%; Pred. No. 3.4e-36;
Live 55; Mismatches 160; Indels 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.8%; Score 736; DB 2; Length 42
41.8%; Pred. No. 1.7e-36;
tive 50; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----GVLPPSGVPYLLGIQSVL-
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Best Local Similarity 41.18
Matcheg 174; Conservative
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Matches 182; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         282 AQNGVRAMSSLGS--
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Probable PPB protein - Mycobacterium tuberculosis (strain H37RV)

Cipace: Mycobacterium tuberculosis

Cipace: 17-Jul.1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

Cipace: 17-Jul.1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

Cipace: 17-Jul.1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

Cipace: 17-Jul.1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

Cipace: 17-Jul.1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

Cipace: 17-Jul.1998 #sequence_revision 17-Jul.1998 #text_change 22-Oct-1999

Richers: Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Hamin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Authors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Attle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Accession: B70625

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNB

A;Cross-references: GB:292539; GB:All23456; NID:g3261714; PIDN:CAB06873.1; PID:e304546;
A;Gene: PPE

A;Gene: PPE
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                                                                                                                                              240 RLLGISYFDEGL------LQFEASLAQQAIPGTPGGAG--DSGSSVLDSWGPTIFA 287
                                                                                                                                                                                        VPQAWAAANQAVTPAARALP---LISLISAAERGPGQMLGGLPVGQMGARAGGGLSGVLR 376
                                                                                                                                                                                                                     VPPDWAARARWANPAAWRLPGDDVTALRGTAENA---LLRGFPMASAGOSTGGGF--VHK 393
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                                                      ------GGLWKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAA
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                                                                                                                       QAVQTAAQNGVRAMSSL--GSSLGS---
                                                                                                                                                                                                                                                           VPPRPYVMPHSPAAG 391
                                                                                                                                                                                                                                                                                         394 YGFRLAVMQRPPFAG 408
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166; Conservative
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Best Local Si
Matches 166;
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Gordon, S.
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                                                                                                             C)Accession: F70560
R; Cole, S. T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentlee, S.; Hamin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Ahathors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: F70560
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: C70931
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. adjandresm, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           403
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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C,Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     287 YFGLAHDLPKWASEGAKAAGEAAKALPAAVPAIPSAGL-SGVAGAVGQAASVGGLKVPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SSAASMVAAATPQVAWLRSTAGQAEQAGSQAVAAASAYEAAFFATVPPPETAANRALLMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 LIATNILGONTPALAVNEAEYGEMWAQDAAAMFGYAAATATATILLPFEEAPEMTSAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 LLEGAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : : : | | | : : | | | : : | 227 ALGLTGHTWSSDGSGLIVGGVLGDFVQGVTGSAELDASVAMDTFGKMVSPARLMVTQFKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPVGQMGARAGGGLSGVL--RVPPRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.0%; Score 702; DB 2; Le
39.1%; Pred. No. 1.7e-34;
ive 61; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 39.1%
Matches 168; Conservative
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179

227 237 291 331

181

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Cipeciaes Mycobacterium tuberculosis (Strain H3/KV)
Cipeciaes Mycobacterium tuberculosis
Cipeciaes Mycobacterium tuberculosis
Cipeciaes Mycobacterium tuberculosis
Cipeciaes Mycobacterium tuberculosis
Cipeciaes Mycobacterium tuberculosis
Cipeciaes Mycobacterium tuberculosis
Ricole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Contor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeglen, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A,Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A,Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A,Authors: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-380 <COL>
A;Residues: 1-380 <COL>
A;Cross-references: GB:Z83867; GB:AL123456; NID:g3261695; PIDN:CAB06278.1; PID:e291015; A;Experimental source: strain H37Rv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297 GSSGLGGGVAANLGRAASVGSLSVPQAWAANQAVTPAARALPLTSL--TSAAERG-PGQ 353
                                                                                                                                                                                                                                                                                                                        ------WKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQ 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 IPK------SLIGAGIĞLRSGLSAĞLAHAASAĞLĞQANLVĞDLSVPPSWASATPAV 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNMVSM -- ANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSL 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MDFALLIPPEVNSÁRMÝTGPGAGSLLAAAGGWDSLAAELATTAEAYGSVLSGLAALHWRGP
                               ---DIAAANQLMNNVPOALQOLAQPTOGTTPSSKLGGL-
                                                                                                                                                                                                                                                                       180 AGQAAATGQATALASGTNAVTTALSSAAAQFPFDIIPTLLQGLA--TLSTQYTQLMGQLI
                                                                                                                                                                                                                                                                                                                                                           238 NAIFGPTGATTYQNVFVTAANVTKESTWANDAMSARNLGMTEFKVF-----WQPPPAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                  AVQTAAQNGVRAMSSLGSSLG----SSGLGGGVAANLGRAASVGSLSVPQAWAAANQAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AAESMAVTAAPYIGWLYTTAEKTQQTALQARAALAFEQAYAMTLPPPVVAANRIQLLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 IATNLLGONTPALAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 LEQAAAVEEASDTAAANQLMNNVPQALQQLAQPT---QGTTPSSKLGGLWKTVSPHRSPI
62 SAGLMVAAASPYVAMMSVIAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL
                                                                                                          IATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGL
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34.6%; Score 675; DB 2; Length 380;
Best Local Similarity 43.1%; Pred. No. 6.1e-33;
Matches 172; Conservative 56; Mismatches 143; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             342 RLVANTLPATSLAAAPATQIPANLLGQMALGSM---TGGAL 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            332 TPAARALPLTSLTSA-AERGPGOMLGGLPVGOMGARAGGGL
                                                                                                                                                                                                                       182 LECAAAVEEAS----
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PP
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: B7093;
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gencles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUD: 98295997; PMID: 9634230
A;Accession: B70932
A;Accession: B70932
A;Gerius: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1.468 <COL>
A;Cross-references: GB:AL022021; GB:AL123456; NID: 93250699; PIDN: CAA17730.1; PID: e125462
A;Genetics:
A;Genetics:
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: C70931
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-463 <COL>
A;Cross-references: GB:AL022021; GB:AL123456; NID:G3250699; PIDN:CAA17723.1; PID:e125461
A;Experimental source: strain H37Rv
A;Genetics:
A;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 LEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVS--PHRSPI- 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 MSSLGSSLG----SSGLGG---GVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPL 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  284 -SALGAGLGLRSAISSGLGSTAPAISAGASQAGSVGGMSVPPSWAAATPAIRTVAAVPSS 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----SNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 ATOGVÁVAQÁVGASÁGN-ARSLVSEVLEFLÁ--TAGTNYNKTVASLMNAVTGVPYASSVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                        MDFGVLPPEINSGRMYAGPGSGPMLAAAAWDGLATELQSTAADYGSVISVLT-GVWSGQ
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                                                                                                                                                                                                                                                                                                                                 49;
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                                                                                                                                                                                                                                                                             DB 2; Length 463;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236 NSMLGLGFAESKAVLPANDTVISTIFGAVQFQKFFNPVTPFNPDLIPK--
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                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                             ; Score 688.5; DB 2;
; Pred. No. 1.2e-33;
48; Mismatches 136;
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 42.8%;
Matches 174; Conservative 41
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Best Local Similarity
Matches 164; Conservat
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12;

Gaps

121 120

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RESULT 15
G7081
probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: G70881
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Taitle: Decipharing the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: G70881
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Residues: 1-394 <COL>
A;Cross-references: GB:AL008967; GB:AL123456; NID:G3261491; PIDN:CAA15564.1; PID:e117389
A;Genetics:
A;Genetics: PPE
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290 GAASVGNTVLASVGRANSIGQLSVPPSWAAPSTRPVSALSPAGLTTLPGTDVAEHGMPG- 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.3%; Score 668.5; DB 2; Length 3 40.8%; Pred. No. 1.5e-32; ive 61; Mismatches 156; Indels
                                                                             354 MLGGLPVGQMGARAGGGLSGVL-RVPPRPYVMPHSPAAG 391
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Best Local Similarity 40.8
Matches 161; Conservative
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completed: November 21, 2003, 16:09:54 le : 9.15692 secs

Search comp Job time :

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

November 21, 2003, 15:51:11; Search time 4.61043 Seconds (without alignments) 3988.226 Million cell updates/sec Run on:

US-09-688-672A-26 1949 1 WVDFGALPPEINSARMYAGP......SGVLRVPPRPYVMPHSPAAG 391 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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122 121.5 121.5 121.5 121.1 121.1 121.1 118.5 118.5 118.5 117 117	

ALIGNMENTS

NESULT 1 YOG1 MYCTU AC 011031; DT 01-0CT-1990 DT 0
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EMBL; AE007119; AAK47285.1; -
PIR; G70925; G70925.
TIGR; MT2959; -.
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ID Y102 MYCTU
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SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Pleischmann R.D., Hickey E.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                              241 MYSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSS----LGSSL
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D. Gordon S.V., Eiglineier K., Gas S., Barry C.E. III, Tekaia F., Bacham D., Brown D., Chillingworth T., Comnor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., Mchean J., Moule S., Murphy L., Rutter S., Seeger K., Kardin M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitchead S., Barrell B.G., "Deciphering the blology of Mycobacterium tuberculosis from the Complete genome sequence.";
                                                                                                                                    Gaps
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                                                                                        DB 1; Length 396;
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                34; Indels
                    A -> AT (IN REF. 2).
6AFAE0D7B5F668D0 CRC64;
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                                                                                   Score 1656.5; DB
Pred. No. 4.8e-89;
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15-DEC-1998 (Rel. 37, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical PPE-family protein Rv2892c.
Mycobacterium tuberculosis.
                                                                     85.0%; Sco. No. 3.0. 85.1%; Pred. No. 3.0. 18; Mismatches
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Hypothetical protein; Complete proteome.
CONFLICT 158 159 TA -> AT (3
SEQUENCE 396 AA; 40015 MW; 6AFAE0D76
                                                                                                           Best Local Similarity 85.1
Matches 338; Conservative
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genome comparison of Mycobacterium tuberculosis clinical and
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30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
14-OCD-2001 (Rel. 40, Last annotation update)
RV1802 OR MI1851 OR MY049.24.
Mycobacterium tuberculosis.
Bacteria, Actinobacteria, Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.2%; Score 705; DB 1; Length 408; 41.8%; Pred. No. 4.4e-34; Live 47; Mismatches 134; Indels
                            laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLGK; M.1200.,
Tuberculist; Rv2892c; -.
InterPro; IPR000030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
Hypothetical protein; Transmembrane; Complete proteome.
TRANSMEM 56 76 POTENTIAL.
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284 -SALGAGLGIRSAISSGLGSTAPAISAGASQAGSVGGMSVPPSWAAATPAIRTVAAVFSS 342
                                                                              341 TSLTS--AAERGPGQML-----GGLPVGQMGARAGGGLSGVLRV
                                                                                                             laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.
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Tuberculist; Rv0442c; -.
Tuberrolist; Rv0442c; -.
InterPro; IPR000030; Microbac PPE.
InterPro; IPR00289; Mycobac pentapep.
Pfam; PF01469; Pentapeptide 2; 5.
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EMBL, ALO21392; CAA17399.1; --
EMBL, AEO06948; AAK44681.1; --
PIR, C70830; C70830.
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                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                           RESULT 4
Y442_MYCTU
ID _Y442_MYCTU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 IATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGL 181
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Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fletschmann R.D., Hickey E.,
Feterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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                                                                                      MEDLINE-8925987; PubMed=9634230; Garnier T., Churcher C., Harris I Gordon S.V., Eiglmeder K., Gas S., Barry C.E. III. Tekaia F., Badcon S.V., Eiglmeder K., Gas S., Barry C.E. III. Tekaia F., Badcock K., Bashma D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Rutter S., Seeger K., Skelton S., Squares S., Squares S., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the Nature 393:537-544 (1998)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Whole genome comparison of Mycobacterium tuberculosis clinical and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.
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EMBL, AE007044; AAK46123.1; -.
EMBL, AE007044; AAK46123.1; -.
FIR, CY0931; C70931.

TIGR, MT1851; -.
Tuberculist; Rv1802; -.
InterPro; IPR000030; Microbac_PPE.
Ffam, PF00823; PPE; 1.
Hypothetical protein; Complete proteome.
CONFLICT 401 401 8 -> L (IN REF. 2).
SEQUENCE 463 AA, 46021 MM; EB64828BF09FA551 CRC64;
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Best Local Similarity
Matches 174; Conservat
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                                              FROM N.A.
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                                                 SEQUENCE
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STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=9829597; PubMed=9634230;

Gole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III. Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Comnor R.,
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Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulsron J.E., Taylor K., Whitchead S., Barrell B.G.,
"Deciphering the biology of Mycobacterium tuberculosis from the
Complete genome sequence.",
Nature 393:537-544(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                280 TAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAASVGSLSVPQAWAANQAVTPAARALP 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  341 EAALVSSAGYATGGMSTAALSSGILASALGSTGGLQHGLANVLNSGLTNTPVAAPASAPV 400
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                                                                                                                                                                                                                                                                                                                      FGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGSSA
                                                                                                                                                                                                                                                               58;
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                         Length 487;
                                                                                                                                                                                                                                                               180; Indels
Pfam; PF00823; PPE; 1.

Hypothetical protein; Complete proteome.

CONFLICT 40 40 E -> K (IN REF. 2).

CONFLICT 96 96 I -> T (IN REF. 1).

CONFLICT 211 211 G -> GNNIG (IN REF. 1).

SEQUENCE 487 AA; 47247 MW; 97234D5B316C8C7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 NTGSGNIGFGITGDHOMGFGGFNSGSGN-IGFGNSGTGNVGLFNS-
                                                                                                                                                                                                      22.8%; Score 444; DB 1; 32.1%; Pred. No. 6.3e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical PPE-family protein Rv0878c.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                               48; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVG---SW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 IGSSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 OGPAAAAAAAAAPYLSWLNAATARAEGAAAGAKAAAAVYEAARAATAHPALVAANRNQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 MILIATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLIPFEEAPEMTSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                     rieiscnmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L. Beicher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W.;
                                                                                                                                                                                                      "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -MGNSGD-
                                                                                                                                                                                                                                     laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential)
-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 X 10 AA APPROXIMATE REPEATS.
C58BEC607F0675E2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   336 RALPLISLISAAERGPGQMLGGL - - PVGQMGARAGGGLSG 373
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ALA-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000030; Microbac PPE.
InterPro; IPR002989; Mycobac Pentapep.
Pfam; PF01469; Pentapeptide_2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, 273101, CAA97385.1, -
EMBL, AB066977, AAK45143.1, ALT_INIT.
PIR, C70780, C70780,
TIGR, MT0901, -
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58 PO
79 PO
73 PO
115 AL
270 AW;
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                         STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; TRANSMEM 38 58 TRANSMEM 38 59 79 TRANSMEM 59 79 TRANSMEM 181 201 DOMAIN 64 73 DOMAIN 81 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00823; PPE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231
443 AA;
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us-09-688-672a-26.rsp

122 IATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG-121 VASNILGONAPAIAAVEAVYEOMWAADVAAMLGYHGEASAVALSLTPFTPSPSAAATPGG -----ILEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVS PHRSPISNM--VSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., Hickey E.,
Kolonay J.F., DeBoy R., Dodson R., Gwinn M.L., Ermolaeva M.D., Salzberg S.L.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weldman J., Khouri H., Gill J., Mikula A.,
Bishai W.,
"Whole genome comparison of Mycobacterium tuberculosis clinical and
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                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis.
Bacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.
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180 200 POTENTIAL.
258 258 D -> G (IN REF. 2).
678 AA; 66736 MW; 209F1593D52533A2 CRC64;
                                                                                                                                            01-0cT-1996 (Rel. 34, Created)
15-UTL-1999 (Rel. 38, Last sequence update)
16-0cT-2001 (Rel. 40, Last unctation update)
17-0chetical PPE-family protein Rv1548c.
RV1548C OR MT1599 OR MTCY48.17.
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EMBL; AE007026; AAK45866.1; ALT_INIT.
PIR; A70762; A70762.
TIGR; MT1599; -.
Tuberculist; Rv1548c; -.
Tuberculist; Rv1548c; -.
Tuberculist; Rv1548c; -.
Tubercy: IPR000030; Microbac_PPE.
InterPro; IPR002999; Mycobac_pentapep.
Pfam; PF01469; Pentapeptide_2; 11.
Pfam; PF01823; PPE; 1.
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TRANSMEM 14 34
TRANSMEM 180 200
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Q10778;
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124 8 MYGTU

125 0107789

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DE HYPOTOR

DN RV15490

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SECUENCE FROM N.A.
MEDILTE=932383, Pubbmed=8478104;
MEDILTE=932383, Brooks I.A., Dockrell H.M., de Smet K.A.L.,
Thompson J.K., Hussain R., Stoker N.G.;
Thompson J.K., Hussain R., Stoker N.G.;
"Sequence and immunological characterization of a serine-rich antigen
Erom Woodbacterium leprae.
Infect. Immun. 61:2145-2153(1993).

01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Serine-rich antigen (25L) (45 kDa protein)
SRA OR MIOA11 OR MICL383.14.
Mycobacterium leprae.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corynebacterinese, Mycobacterium.

NCBI TaxID=1769;

Z 408

STANDARD;

SRA MYCLE Q07297;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLIRE=21128732; PubMed=11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Squares S., Stevens K., Jaylor K., Whitehead S., Woodward J.R., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                       [2]
SOUGHNEE FROM N.,
MEDLINE=58020554; PubMed=7934845;
Rinke de Wit T.F., Clark-Curtiss J.E., Abebe F., Kolkon A.H.J.,
Jonson A.A.M., Thole J.E.R.;
A Mycobacterium leprae-specific gene encoding an immunologically
recognized 45 kD protein.";
Mol. Microbiol. 10:829-838(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROM N.A.
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SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL 121

62

2 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS

9

Gaps

38;

21.4%; Score 418; DB 1; Length 678; 31.9%; Pred. No. 2.9e-17; ive 48; Mismatches 140; Indels

Best Local Similarity 31.9 Matches 106; Conservative

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Query Match

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POTENTIAL.
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InterPro; IPR00030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
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                                                                                                                                                                                                                                                         complete genome sequence.";
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276
323
419
463 AA;
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les 112;
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2 X 6 AA REPEATS OF S-V-A-Q-S-E.
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Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1773;
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S -> L (IN REF. 2).
H -> D (IN REF. 2).
P -> L (IN REF. 2).
V; 5COC2BEODGEGA9D8 CRC64;
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Live 72; Mismatches 163;
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01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical PPE-family protein Rv0096.
Mycobacterium tuberculosis.
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                                                                                                                                                                                         InterPro; IPR000030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
DOMAIN: Repeat; Complete proteome.
DOMAIN 209 235 2 X 6
DOMAIN 209 235
                                                                                      EMBL, ALS8318, CAC29919.1, -.
PIR, C86960, C86960, C86960, PIR, S33522, PIR, S39872, S39872.
Leproma, ML0411, -.
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                  EMBL, U00015, AAC43220.1; -. EMBL, X68431, CAA48480.1; -. EMBL, Z21552, CAA79950.1; -. EMBL, Z97179; CAB09938.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                             408 AA;
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CONFLICT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the FWILD custstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., Deboy R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bishai W.; "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLURAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.
MEDLINE=982999; PubMed=9634230;

Gole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harri
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekais F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Rollwell T., Gonnor R.,
Bothes R., Devilin K., Feltwell T., Gonnor R., Hanlin N., Holroy
Hornsby T., Jagels K., Kroph A., McLean J., Moule S., Murphy L.,
Oliver S., Seager K., Skelton S., Squares S.,
Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.,
"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.6%; Score 324.5; DB 1; Length 463; 27.8%; Pred. No. 4.8e-12;
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us-09-688-672a-26.rsp

an email to license@isb-sib.ch)

or send

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                                      ---GGLW-----KTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLK----GF 269
                                                                                                                APAAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAASVGSLSVPQAWAAANQ 329
----DAADTRLDVLSSIGQLIRDI---LDFIANPYKYFLEFFEQFGFSPAVTVVLALVAL 229
                                                                                                                                                     ----LGPGDQWGANLAVAVTPATAAVP----GGSP 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reductase.
-!- CAUTION: Ref.3 sequence differs from that shown due to frameshifts
in positions 294; 337 and 355.
                                                                       ------TLSALTALSALIHLLNLPPAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann T.D., DeBoy R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bishal W.; "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAINHATARY,

MEDLINE-98295987; PubMed-9634230;

Cole S.T., Parkhill J., Garnier T., Churcher C., Harris

Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

Davies R., Devlin K., Feltvall T., Gentles S., Hamlin N., Holroyd

Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

Coliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,

Rutter S., Seeger K., Skelton S., Squares S.,

Sulston J.E., Taylor K., Whitehead S., Barrell B.G.,

Complete genome sequence.

"Neciphering the biology of Mycobacterium tuberculosis from the

complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Isolate 50410;
Batki A.H., Dale J.W.;
Submitted (APR-1991) to the EMBL/GenBank/DDBJ databases.
-:- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.
-:- CAUTION: In strain Oshkosh the gene for this protein is incerrupted in position 307 by an IS6110 element.
-:- CAUTION was originally (Ref.3) thought to be a dihydrofolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bácteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI TaxID=1773;
                                                                                                                                                                                              368
                                                                                                                                                                                                                   309 PISNPAPPAPSSNSVGSASAAPGISYAVPGLAPPGVSSGPKAG 351
                                                                                                                                                                                            330 AVTPAARALPLISLISAAERGPG---QMLGGLPVG-QMGARAG
                                                                                                                                                                                                                                                                                                                                            P31500; 053265; Created)
1-JUL-1993 (Rel. 26, Created)
28-FEB-2003 (Rel. 40, Last sequence update)
Hypothetical PPEF family protein Rv3018c.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                               434 AA
                                                                         230 QLYDFLWYPYYASYGLLLLPFFTP-
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                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                   276 LPIAAA-
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125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 GGPLLGALAAVVPGVAGLAGVAGLAAL-PAVGAA--AGAPAALVGSVAPVSGGVVSPQA 354
                                                                                                                                                                                                                                                                                                                                                                                                    67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 AAVEEASDTAAAN-----QLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPH
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Gas S., Barry C.E. III. Tekaia F.,
Badcock K., Basham D., Erown D., Chillingworth T., Comnor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd & Hernsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      324 WAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPVGQMGARAGGGLSGV 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                         Length 434;
                                                                                                                                                                                                                                   41D673C4BD389DD6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          053268; 053269;

16-0CT-2001 (Rel. 40, Last sequence update)

16-0CT-2001 (Rel. 40, Last sequence update)

16-0CT-2001 (Rel. 40, Last annotation update)

Hypothetical PPE-family protein Rv3021c/Rv3022c.

RV3021C/RV3022C OR MT3106 OR MTV012.35C/MTV012.36C.
                                                                                                                                                                                                                                                                         16.6%; Score 324; DB 1; Lv
ilarity 28.0%; Pred. No. 4.7e-12;
Conservative 56; Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---RSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             435
                                                                                                                                                                  InterPro, IPR00039; Microbac PPE.
Pfam; PF00823; PPE; 1.
Hypothetical protein; Complete proteome.
EMBL, AL021287, CAA16103.1; -. EMBL, AE007129; AAK47427.1; ALT_SEQ. EMBL, AE007129; AAK47430.1; ALT_SEQ. EMBL, X59271; CAA41961.1; ALT_FRAME. PIR; E70857; E70857. TIGR, MI3009. -
TIGR; MI3009. -
TIGR; MI3101; --
Tuberculist; Rv3018c; --
                                                                                                                                                                                                                                 434 AA; 43029 MW;
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                                                                                                                                                                                                                                                                                            Local Similarity
les 115; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1773;
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                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                             Query Match
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YU21 MYCTU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 GSSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELM 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 IPAEYISNIIYEGPGADSLSAAAEQLRLMYNSANMTAKSLTDRLGELQE-----NWK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Deloher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=9892987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hensby T., Jagels K., Krogh A., McHean J., Moule S., Murphy L., Oliver S., Osborne J., Guail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the Complète genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.0%; Score 233.5; DB 1; Length 178; llarity 35.9%; Pred. No. 3e-07; Conservative 25; Mismatches 76; Indels 15.
                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              il protein; Complete proteome.
178 AA; 19811 MW; 8BEIFC025ABFBEA6 CRC64;
                                                                                                                                                                                     178 AA
                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical PPP-family protein RV3429.
RV3429 OR MT3S33 OR MTCY77.01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tuberculist; Rv3429; -.
InterPro; IPR000030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE007158; AAK47873.1; -. PIR; C70975; C70975.
TIGR; MT3533; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z95389; CAB08678.1; -.
            | : | : | : | 386 GTAGKESVGQPAGL 399
                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis.
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STRAIN=CDC 1551 / Oshkosh;
                                                                                                                                                                                     STANDARD;
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les 65; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical
SEQUENCE 17
                                                                                                                                                                               YY29 MYCTU
006246;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               249 MSMTNSGVSMTNTLSS-----MLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSGL 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----AALVGSVAPVSGGVVSPQARLVS--AVEPAPASTSVSVL--ASDRGAGAL--GF-V 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65
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                                                                                                                      SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Dogson R., Gwinn M.L., Haft D., Hickey E.,
Fotorson J.P., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 ALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGSSAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 MVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 FVAAYVPYVAWLVQASADSAAAGEHEAAAAGYVCALAEMPTLPELAANHLTHAVLVATN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 AVAAATITPFPFGELAKFLEMAAQAFTEVGELIMKSAEAWAVGFVELITGLVNFEP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                  "Whole genome comparison of Mycobacterium tuberculosis clinical and
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.5%; Score 321.5; DB 1; Length 435; 26.5%; Pred. No. 6.6e-12;
                                                                                                                                                                                                                                                                                                                                                        laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.
-!- CAUTION: Ref.1 sequence differs from that shown due to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGE; MT3106; -.
Tuberculist; Rv3021c; -.
Tuberculist; Rv3022c; -.
InterPro; IPR000030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
Hypothetical protein; Complete protecome.
CONFLICT 299 G -> A (IN REF. 2).
CONFLICT 317 320 LAGV -> VTGL (IN REF. 2).
CONFLICT 326 326 L -> V (IN REF. 2).
SEQUENCE 435 AA; 42876 MW; 3B157643EAAB484A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 LLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL021287; CAA16106.1; ALT FRAME.
EMBL; AL021287; CAA16107.1; ALT_FRAME.
EMBL; AE007129; AAK47435.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        frameshift in position 82.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 115; Conservative
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                                                                                                                                                                                                                                                                                                         Bishai W.;
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                                                                                  ADAVERYLQWLSKHSSQLKHAAWVINGLANAYNDTRRKVVPPEEIAANREERRRLIASNV 123
GSSSDLMADAAGRYLDWLTKHSRQILETAYVIDFLAYVYEETRHKVVPPATIANNREEVH 116
                                                 ILIAINLIGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 LPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGSSAGLM 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 IPAEXISNIIXEGPGADSLFFASGQLRELAXSVETTAESLEDELD-ENWKGSSSDLL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98295997; PubMed=9634210; Carnier T., Churcher C., Harris I Cole S.T., Erosch R., Parkhill J., Garnier T., Churcher C., Harris I Gordon S.V. Eiglmeier K., Parkhill J., Cannier T., Connor R., Davies R., Devin M., Rown D., Chillingworth T., Connor R., Davies R., Devin K., Feltwell T., Gentles S., Hamin N., Holroyd S Hornsby T., Jagels K., Krogh A., Rajandream M.A., Rogers J., Cliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.", Mature 393:537-544(1999).

--- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGVNTPAIADLDAQYDQYRARNVAVMNAYVSWTRSALSDLPRWREPPQIYRGG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; F70738, F70738.
Tuberculist, Rv3425; -
Interpro, IPR00030, Microbac_PPE.
Pfam, PF00823; PPE. 1.
Hypothetical protein; Complete proteome.
SEQUENCE 176 AA; 19855 MW; B8CEF2E9463B87B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.2%; Score 217.5; DB 1 33.5%; Pred. No. 2.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
18-OCT-2001 (PPE-family protein RV3425.
RV3425 OR MTCY78.04C.
                                                                                                                                                                                                                                                                                                                                      176 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z77165; CAB01031.1; -.
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Best Local Similarity 33.54
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FROM N.A.
                                                                                                                                                    180
                                                                                                                                                                                                     177
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STRAIN=H37Rv;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the burpean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENORICS 23:125-131 (1994).

-!- FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND
-!- FUNCTION: MAJOR STRUCTURAL PROTEIN CAPIDLY AND RECOVER COMPLETELY.
-!- SUBUNIT: THE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED TOGETHER
INTO AN EXTENSIBLE 3D NETWORK.
-!- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX OF ELASTIC FIBERS.
-!- FUM: THE CROSSLINKS ARE MADE OF DEAMINATED LYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGIPGVGGPGIGGPGIVGGPGAVSPAAAAAAAAAA--YGARGGVGIPTYGVGAGGFPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --IGSSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELMILIAINLLGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLP-FEEAPEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALGGLVPGAVPGALPGAVPAVPGAGGVPGAGTPAAAAAAAAAKAAKKAGLGPGVGGVPGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 GALP----PEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSW--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---LEQAAAVEEASDTAAANO---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene t
human
                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131;
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                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRATN=BALB/C; TISSUE=Lung;
STRATN=BALB/C; TISSUE=Lung;
MRDLINE=9130069; PubWed=7229060;
Wydner K.S., Sechler J.L., Boyd C.D., Passmore H.C.;
"Use of an intron polymorphism to localize the tropoelastin genues chromosome 5 in a region of linkage conservation with phromosome 7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, U08210; AAA80155.1; -.
PIR; A55721; EAMS.
MGD; MGI-95317; Eln.
InterPro; IPR0013979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
Structural protein; Repeat; Signal; Connective tissue.
SIGNAL.
1 27 POTENITAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
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                                                   01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Elastin precursor (Tropoelastin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELASTIN.
BY SIMILARITY.
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855 BY
71955 MW;
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STANDARD;
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850 8
860 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 115; Conserv
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
ELS MOUSE
P54320;
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DISULFID
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491

us-09-688-672a-26.rsp

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124 AG 125
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                                                                                                                                     01-OCT-1996
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         splicing."
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                                                                                                 ELS RAT
                                                        RESULT 15
ELS_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                               346
                                                                                                                  784
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                                       672 YGAAGGLGGPGGLGGPGGLGGPGGLGGAGVPGRVAGAAPPAAAAAAAAAAAAAAAAAAAAA 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 ADAALRYLDWLSKHSRQILRTARVIESLVMAYEETLLRVVPPATIANNREEVRRLIASNV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99
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MEDILINE=9829897; PubMed=9634230;

A Gordon S.V., Erglmeier K., Gas S., Barry C.E. III, Tekaia F.,

A Gordon S.V., Basham D., Brown D., Chillingworth T., Connor R.,

B Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

A Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

A Hornsby T., Jagels K., Kregh A., McLean J., Moule S., Murghy L.,

A Rutter S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,

Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the

I complete genome. Eequence.";

I complete genome.

I nature 393:537-544(1998).
HMSMTN--------SGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRA
                                                                                                                IPABYISNVIYEGPRADSLYAADQRLRQLADSVRTTAESLNTTLDELH-ENWKGSSSEWM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 VAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNL
                                                                               289 MSSLGS-SLGSSGLG-GGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 LPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGSSAGLM
                                                                                                                                                          347 AERGP---GOMLGG--LPVGOMGARAGGGLS------GVLRVPPRPY 382
                                                                                                                                                                                             785 AKYGAAGLGGVLGARPFPGGGVAARPGFGLSPIYPGGGAGGLGVGGKPPKPY 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; Complete proteome.
2 AA; 25872 MW; D76512D49EB272C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                              update)
                                                                                                                                                                                                                                                                                               232 AA
                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence upda
116-OCT-2001 (Rel. 40, Last annotation up
Hypothetical PPE-family protein RV3426.
RV3426 OR MTCY78.03C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z77165; CAB01030.1; -.
PIR; G70738; G70738.
Tuberculiar; R9426; -.
InterPro; IPR000030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 LG 128
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SEQUENCE 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomics 12,651-658(1992).

-!-FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND
-!-FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND
NUCHAL LIGAMENT, WHICH MUST EXPAND RAPIDLY AND RECOVER COMPLETELY.
-!-SUBUNIT: THE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED TOGETHER
-!-SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX OF ELASTIC FIBERS.
-!-ALTERNATIVE PRODUCTS:
                                                                                                                                                Bukaryota, Métazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 264-533 AND 558-864 FROM N.A., AND ALTERNATIVE SPLICING. MEDILTE=92941859; PubMed=157537; Pierce R.A., Alatawi A. Deak S. B., Boyd C.D.; "Elements of the rat tropoelastin gene associated with alternative
                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE-91104868; PubMed=1702999;
Blerce R.A., Deak S.B., Stolle C.A., Boyd C.D.;
"Heterogeneity of rat tropoelastin.mRNA revealed by cDNA cloning.";
Blochemistry 29:9677-9683(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=099372-8; Sequence=VSP 004244, VSP 004245, VSP_004246; -:- PTM: THE CROSSLINKS ARE MADE OF DEAMINATED_LYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=8; Comment=Experimental confirmation may be lacking for some
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 781-864 FROM N.A.
MEDLINE=88330868; PubMed=2971041;
Deak S.B., Pierce R.A., Belsky S.A., Riley D.J., Boyd C.D.;
"Rat tropoelastin is synthesized from a 3.5-kilobase mRWA.";
J. Biol. Chem. 263:13504-13507(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=099372-5; Sequence=VSP_004244, VSP_004245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSP_004246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSP_004246;
                                                   01-0CT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Elastin precursor (Tropoelastin) (Fragment).
864 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q99372-7; Sequence=VSP_004244,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q99372-6; Sequence=VSP_004245,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q99372-2; Sequence=VSP_004244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q99372-3; Sequence=VSP_004245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=Q99372-4; Sequence=VSP_004246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q99372-1; Sequence=Displayed;
                                 34, Created)
34, Last seq
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EMBL; J04035; AAA42268.1; -.
EMBL; M86372; AAA42271.1; -.
STANDARD;
                                                                                                                                    Rattus norvegicus (Rat).
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BY SIMILARITY.

ELASTIN.

BY SIMILARITY.

Missing (in iseform 2, iseform 5, iseform 7 and iseform 8).

/FITG=VSP 00424.

Missing (in iseform 3, iseform 5, iseform 6 and iseform 8).

/FITG=VSP 004245.

Missing (in-iseform 4, iseform 6, iseform 7 and iseform 8).

/FITG=VSP 004246.

/FITG=VSP 004246.

/FITG=VSP 004246.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 --IGSSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  457 YGVGAGAĞL------GGASQAAAA----AAAAKAAKYGAG------ 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 ELMILIATNLIGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 SAGGLL---EQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSS-KLGGLWKTVS 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 PHRSPISNMVSMANNHMSMTNSGVSM-TNTLSSMLKGF-APAAAAQAVQTAAQNGVRAMS 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               291 SLGSSLGSSGLGGGV----AANLGRAASV---GSLSVPQAWAAANQAVTPAARALPLT 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           487 -----GAGTLGGLVPG------AVPGALPGAVPGALPGAVPGALP-GAVPGVP 527
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Best Local Similarity 25.9%; Pred. No. 0.11;
Matches 102; Conservative 31; Mismatches 153; Indels 108; Gaps
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EMBL, M86364; AAA42271.1; JOINED.
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EMBL, M86376; AAA42271.1; JOINED.
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Scoring table:

Searched:

Database

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3..8
/label= Histidine tag
/note= "Nickel chelating region used for purifying
the fusion protein"
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ABB81982
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AAE04867
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AAR40846
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/label= MtB81_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
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Misc-difference
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AAU01900
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M. tuberculosis po
Mycobacterium tube
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C glucamicum prote
Corynebacterium gl
Corynebacterium gl
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                                                                                                                                             November 21, 2003, 15:50:31; Search time 70.9578 Seconds (without alignments) 2621.664 Million cell updates/sec
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6061
1 MQHHHHHHTDRVSVGNLRIA......SAATRRPRCTRGRDGRWACQ 1172
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                GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                1107863 seqs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Score

Result

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M. tuberculosis re
Novel human diagno

Corynebacterium sp C. glutamicum aspa Propionibacterium Novel human diagno Methylophilus meth

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TQLLYDDHIGKVSLIGAGMRSHPGVTATFCEALAAVGVNIELISTSEDORSRCCAATPNW 1140
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                                                                                                                                                        LHRRRRREFKARABAEKPAPSDRAGDDARVOKYGGSSVADAERIRRVAERIVATKKOGNDV
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                                                                                                                                                                                                                                                                                                                                               TAVAMAAALGADVCEIYTDVDGIFSADPRIVRNARKLDTVTFEEMLEMAACGAKVLMLRC
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                               601 IREEVDNNCQSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRHGVI
                                                                                                   TSADVRASLERMAPLVDRQNAGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTEPI
                                                                                                                                      LHRRRREFKARAAEKPAPSDRAGDDAARVQKYGGSSVADAERIRRVAERIVATKKQGNDV
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IREEVDNNCOSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATIRISSQLLANWLRHGVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis; antigen; Mtb-91; Mtb-67.2; antigen presenting cell; serodiagnosis; detection; human immunodeficiency virus; HIV;
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                                                                                                                                                                                                                                                                                    The sequence represents Mycobacterium fusion protein antigen TbF14 consisting of a His tag for purification, antigen MtB81 and antigen Mo2. Compositions comprising at least 2 heterologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially humans) against infection by Mycobacteria. The compositions contain at least 2 heterologous antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease frequently affecting patients with acquired immunodeficiency disease, AIDS.
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iive 0; Mismatches
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99US-0158425
 2000WO-US28095
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Novel Mycobacterium tuberculosis polypeptide comprising an immunogenic portion of M. tuberculosis antigens Mtb-81 and Mtb-67.2, useful for diagnosis, treatment and monitoring therapy of tuberculosis Polypeptides comprising an immunogenic portion of Mycobacterium tuberculosis antigens Mtb-81 or Mtb-67.2 or variants that differ by substitutions, additions, insertions and/or deletions but which still react with antigen specific antisera or T-cells are described. 'note= "Encoded by TAA stop codon" note= "Encoded by TAA stop codon" note= "Encoded by TAA stop codon" /note= "Encoded by TAA stop codon" 1348 note= "Encoded by TGA stop codon" note= "Encoded by TGA stop codon" note= "Encoded by TGA stop codon" 'note= "Encoded by TGA stop codon" 'note= "Encoded by TGA stop codon" note= "Encoded by TAA stop codon" 'note= "Encoded by TAA stop codon" 'note= "Encoded by TAG stop codon" 'note= "Encoded by TGA stop codon" note= "Encoded by TGA stop codon" /note= "Encoded by TAA stop codon" 'note= "Encoded by TAA stop codon" note= "Encoded by TAA stop codon" 'note= "Encoded by TGA stop codon" stop stop note= "Encoded by TGA stop note= "Encoded by TAA stop 'note = "Encoded by TAA stop 1691..2438 /label= Mtb-81 polypeptide Houghton RL; by TGA 'note= "Encoded by TGA Claim 1; Fig 1a-f; 91pp; English. "Encoded 17-MAR-2000; 2000WO-US07196. 99US-0272975. Hendrickson RC, Lodes MJ, 'note= Misc-difference 1211 Misc-difference 1582 Misc-difference 1616 Misc-difference 1643 2478 Misc-difference 1527 Misc-difference 1579 WPI; 2000-638180/61. (CORI-) CORIXA CORP N-PSDB; AAA53971. Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference WO200055194-A2 18-MAR-1999; 21-SEP-2000. Protein

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Also described are polynucleotides encoding the polypeptides. The polypeptides, expression vectors expressing the polypeptides or comprising an antisense polynucleotide, or an antigen presenting cell comprising a sequence encoding the polypeptides are useful for determining the presence or absence of M.tuberculosis in whole blood, serum, sputum, plasma, saliva, cerebrospinal fluid or urine in a patient infected with human immunodeficiency virus (HIV).
                                                                                                                                                                                                                                  DB 21; Length 2502;
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88.3%; Pred. No. 3.8e-286;
iive 8; Mismatches 27;
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The present invention relates to a method for early detection of active mycobacterial disease or infection comprises assaying a biological fluid sample for the presence of early antibodies specific for an 88-kDa Mycobacterium tuberculosis (Mt) protein or immune complexes consisting of an 88-kDa M. tuberculosis protein or immune complexes consisting of specific for the antigen. The method is useful for the early and rapid electric nof mycobacterial disease, particularly tuberculosis, in individuals at heightened risk of developing tuberculosis. This individuals include human immunodeficiency virus (HIV)-infected subjects or other immunocompromised individuals. The method is a rapid and inexpensive screening procedure for detecting mycobacterial disease. The present sequence is a Mt 88 kDa secreted protein early antigen, used in the exemplification of the invention.
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                                                                                                                                                            Mycobacterial disease, infection, 88-kDa protein, tuberculosis, TB, early antigen, human immunodeficiency virus, HIV, secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detecting a mycobacterial disease (tuberculosis) in individuals comprise assaying a biological sample for the presence of anti-Mycobacterium tuberculosis antibodies or M. tuberculosis
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                                                                                                                                Mycobacterium tuberculosis 88 kDa secreted protein.
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100.0%; Pred. No. 1.3e-282;
tive 0; Mismatches 0;
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                               AAE05665 standard; peptide; 741 AA.
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Page 7-8; 12pp; German.
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                                                                AVDKDGTAFLRVLNRDRNYTAPGGGGFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEG 361
                                                                                                                               TWKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAGASTAW 541
                                                                                                                                                                                                       VPSPTAATLHALHYHQVDVAAVQQGLAGKRATIEQLLTIPLAKELAWAPDBIREEVDNN 601
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LSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEI
                              LIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAA
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                 LIDPESQVGTTDRAGVKDVILESALTTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA contg. upstream regulatory region from malate synthase gene of coryneform bacteria - used for regulated synthesis of protein in coryneform(8), regardless of nutrient medium compsn..
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AAR77501 is encoded by an approx. 3 kb BfrI-PvuI fragment contg. the aceB gene from Cornyeform glutuanicum (see AA705501). Nucleorides 1 to 574 can be isolated and used to regulate the expression of a protein-encoding structural gene placed downstream of it, after incorporation into a vector and transfer into a Cornyeform bacterium. Induction of protein expression occurs even when the culture medium contains carbon sources other than acetate.
                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                    37.8%; Score 2289; DB 16;
61.3%; Pred. No. 3.6e-166;
iive 90; Mismatches 184;
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les 444; Conservative
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Corynebacterium glutamicum; carbon metabolism and energy production; SMP protein; sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; diagnosis; Corynebacterium diphtheriae; evolutionary study.
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                                                                                                                                                                                                                                                                                                          555 VPSPIGATHATHYHLVDVFKVQDELRAAGRRDSLRNILTIFTAPNTNWSEEEKKEEMDN
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                                              309 AVDKDGTAFLRVINRDRNYTAFGGGQFTLPGRSLMFVRNVGHLMTNDALVDTDGSEVFEG
                                                                 IMDALFTGLIAIHGLKASDVNGPLINSRTGSIYIVKPKMHGPAEVAFTCELFSRVEDVLG
                                                                                                                                                                  LPONTMKIGIMDEERRTTVMLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMVRKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of agene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium. Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium, according the region of gene derived from coryneform bacterium, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
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                                                                                              amino acid synthesis; vitamin; saccharide;
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; Pred. No. 3.6e-166;
90; Mismatches 184;
                                                                                                                                                                                                                                                                                                                                                       Ando S, Hayashi M,
la M, Ozaki A;
                                                                   protein fragment SEQ ID NO: 6988.
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Ikeda M,
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61.3%;
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2000JP-0280988.
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                                                                                                                                            Corynebacterium glutamicum.
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Senoh A,
                                                                                                              organic acid synthesis.
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                                                                                              Coryneform bacterium;
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Best Local Similarity
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                                                                   C glutamicum
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Tateishi N,
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                                           249 LIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAA
                                                                   259 QIDPVHPIGKADKTGLKDIVLESAITTIMDFEDSVAAVDAEDKTLGYSNWFGLNTGELKE
                                                                                                                                 309 AVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEG
                                                                                                                                                            319 EMSKNGRIFTRELNKDRVYIGRNGTELVLHGRSLLFVRNVGHLMQNPSIL-IDGEEIFEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated Corynebacterium glutamicum nucleic acid encoding a metabolism and oxidative phosphorylation protein for production modulation of production of fine chemicals e.g. amino acids, carbohydrates or enzymes -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; Page 992-995; 1246pp; English.
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              99DE-1031634
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99DE-1042123.
99DE-1042125.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     AG.
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                                                                                                                                                                                           27-AUG-1999;
31-AUG-1999;
03-SEP-1999;
03-SEP-1999;
03-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                          03-SEP-1999;
03-SEP-1999;
03-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BADI ) BASF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pompejus M,
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03-SEP-1999
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180 VEKYNIIDGKLAAHIGDSVYRLKONESYRGFIGNFLDPEAILLEINGLHIELQIDPVHPI 239
                                                                                                                                                                                                                                                                                                               GVMDEERRISVNLDASIMEVADRLAFINIGFLDRIGDEIHISMEAGAMVRKADMQTAPWK 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRHGVITSADVRASLERMAPL 675
                                                                                                                                                                   FTREINKDRVYIGRNGTELVLHGRSLLFVRNVGHLMQNPSIL-IDGEEIFBGIMDAVLTT
                                                                                                                                                                                                                                   596 VVRWVEHGVGCSKVPDIHDIDLMEDRATLRISSOMLANWIRHDVVSKEQVLESLERMAVV
                                                                                                                                                 FLRVLNRDRNYTAPGGGOFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEGIMDALFTG
                                                                                GTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAAAVDKDGTA
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                                                                                                                                                                                                                LIAIHGLKASDVNGPLINSRTGSIYIVKPKWHGPAEVAFTCELFSRVEDVLGLPQNTMKI
                                                                                                                                                                                                                                                                                                                                                  497 LAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAGASTAWVPSPTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                 LHALHYHQVDVAAVQQGL-AGKRRATIEQLLTIPLAKELAWAPDEIREEVDNNCQSILGY
                                                                                                                                                                                                                                                                                                                                                                                                                                    GIMDEBRRITVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMBAGPMVRKGTMKSQPWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VDRONAGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTEPILHRRRREFKAR 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tuberculosis, Mycobacterium infection, gene therapy, anti bacterial, immunostimulant, MO-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lodes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Encoded by GAC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-FEB-2000; 2000US-0185037.
08-AUG-2000; 2000US-0223828.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243 to AAB 79633 which are involved in carbon metabolism and carbon are involved in carbon metabolism and carbon are involved in carbon metabolism and carboy production. The C. glutamicum SMP gene can be used in vectors (II) for expression in host cells and production or modulation of production of fine chemicals, such as, an organic acid, a proteinogenic or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a uncleotide, a seturated or unsaturated fauty acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a coffactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins (III) encoded by them are used for diagnosing the presence or activity of corprebactorium diphtheriae in a subject. (I), (II), (III) or host cells containing them are used to map genomes of corganisms related to c. glutamicum, identify and localise C. glutamicum sequences of interest, in evolutionary studies, in determining SMP protein regions required for the function, in medulating SMP protein activity, in modulating the metabolism of sugars, and in modulating high-energy molecule production in a cell (i.e. ATP, NADPH).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 RRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPVLNARFALN 136
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or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVPLSSGSFGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 LRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQAQIDKWHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOVAKVLYDFVTEAVLPRVGVDAEKFWSGFAAIARDLTPRNRELLARRDELOMLIDDYHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated Corynebacterium glutamicum nucleic acid encoding a metabolism and oxidative phosphorylation protein for production modulation of production of fine chemicals e.g. amino acids, carbohydrates or enzymes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar
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                                                                                                                                                                                                                                                                                                                                                                                                                 Zelder O, Haberhauer G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 2253; DB 22; Length
; Pred. No. 1.9e-163;
89; Mismatches 183; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; Page 998-1000; 1246pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                 Schroeder H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.2%;
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99DE-1032180
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99DE-1042076
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Best Local Similarity
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09-70L-1999

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13-A0G-1999

27-A0G-1999

23-A0G-1999

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIVENARKLDTVTFEEMLEMAACGARVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELDMLLTAGERISNALVAMAIESLGAHARSFIGSQAGVITTGTHGNAKIIDVTPGRLQTA 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIVRNARKLDTVTFBEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS 988
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                                                                                                         The present invention relates to the isolation of Mycobacterium tuberculosis antigen polypeptides (e.g. TD224) and the mucleic acids encoding them. The invention describes compounds and methods for the diagnosis of tuberculosis or for inducing protective immunity against tuberculosis. The compounds comprise at least one immunogenic portion of one or more Mycobacterium proteins and nucleic acid molecules encoding such polypeptides. The Mycobacterium proteins and nucleic acid molecules encoding them can be used in diagnostic kits for the detection of Mycobacterium infection in patients and biological samples. The compounds of the invention and antibodies directed against the Mycobacterium proteins may be used in vaccines for immunisation against Mycobacterium infections. The mucleic acids encoding the Mycobacterium proteins may be used in service acids encoding the Mycobacterium proteins may be used in gene therapy. The present sequence represents Mycobacterium polypeptide for MO-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEBGRAVILVAGFÓGVSÓDTKDVTTLGRGGSDTTAVAMAAALGADVCELYTDVDGIFSADP 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    296 VLONVSKVEKGKTDITFTCSRDVGPAAVEKLDSLRNEIGFSOLLYDDHIGKVSLIGAGMR 355
                                                                                                                                                                                                                                                                                                                                                                                                                                      64
                         An isolated polypeptide comprising a Mycobacterium antigen, e.g., from Mycobacterium tuberculosis, useful in a vaccine for enhancing an immune response to and inhibiting development of a Mycobacterium infection -
                                                                                                                                                                                                                                                                                                                                                                                                          749 VOKYGGSSVADAERIRRVAERIVATKKOGNDVVVVVSAMGDITDDLLDLAQQVCPAPPPR
                                                                                                                                                                                                                                                                                                                                                                                                                             VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feedback inhibition release aspartokinase, Brevibacterium flavum,
Corynebacterium, L-lysine production.
                                                                                                                                                                                                                                                                                                                                                     DB 22; Length 421;
                                                                                                                                                                                                                                                                                                                                                                                 17;
                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Feedback inhibition release aspartokinase 279Ala,
                                                                                                                                                                                                                                                                                                                                                  26.7%; Score 1619.5; DB 27
85.1%; Pred. No. 2.7e-115;
iive 8; Mismatches 34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                842
                                                                                Claim 1; Fig 17; 161pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 VAGFQGVNKETRDVTTLGRGGSDTTAVALAAALNADVCEIYSDVDGVYTADPRIVPNAQK
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                                                                                                                                                                                                                                                                                                                                                                                         AAQ72693 encodes AAR63567 Brevibacterium flavum feedback inhibition release agpartokinase, it was used in the construction of a plasmid. The plasmid was used to transform Corynebacterium cells, where the expression of AAQ72693 resulted in incresed L-lysine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   579 RATIEQLLTIP-----LAKELAMAPDEIREEVDNNCQSILGYVVRWVDQ----
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                                                                                                                                                                                                                                                   encoding feedback inhibition release asparto-kinase - used the production of L-Lysine.
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1e-86;
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                                                                                                             CO LID
                                                                                                             PETROCHEMICAL
                                                                                                                                                                                                                                                                                                                                      Claim 4; pl6; 28pp; Japanese.
93JP-0055451
                                                     93JP-0055451
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les 346; Conserv
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  16-MAR-1993;
                                                     16-MAR-1993;
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Db 60	OY 623 GVGCSKVPDHHDVALMEDRATLRISSQLLANWIRHGVITSADVRASLERMAPLUDRQNAG 682 351 GAGMKSHPGV-TAEFMBALRDVNVNIEL	QY 1033 RRRQHRHGAABELQGRGRQD-RHHLHLLPQTSGPPPWGWTRSETRSASTQLLYDDH1 1089 Db 720 NFSSVEDGTTDITFICPRSDGRRAMEILKKLQVGGTNVLYDDQV 765 QY 1090 GKVSLIGAGMRSHPGVTAFFCBALAAVGVNIELISTSE 1127 CA 1090 GKVSLIGAGMRSHPGVTAFFCBALAAVGVNIELISTSE 803 RESULT 11 AAG64046 ID AAG64046; XX AC AAG64046; XX AC AAG64046; XX COTYNEbacterium thermoaminogenes lysin biosynthetic enzyme lysc. XX CAC Corynebacterium thermoaminogenes: lysc. XX XX XX XX XX XX XX XX XX
Qy 863 GRLQTALEEGRVVLVAGFQGVSQDTKDVTTLGRGSBTTAVAMAAALGADVCEIYTDVDG 922	RESULT 10 AAR63570 ID AAR63570 ID AAR63570 ID AAR63570; XX AC AAR63570; XX DT 29-JUN-1995 (first entry) XX DE Peedback inhibition release aspartokinase, Brevibacterium flavum, XX Corynebacterium; L-lysine production. XX XX DD B Sevibacterium flavum. XX XX DF Corynebacterium flavum. XX XX DF Corynebacterium flavum. XX XX DF Corynebacterium flavum. XX XX DF Corynebacterium flavum. XX XX DF Corynebacterium flavum. XX XX PR 16-MAR-1993; 93JP-0055451. XX XX PR 16-MAR-1993; 93JP-0055451. XX XX XX XX XX XX XX XX XX XX XX XX XX	3es fat

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842 AA;
                                                                                                                      N-PSDB; AAQ72694
           Brevibacterium
                          JP06261766-A
                                                            16-MAR-1993;
                                                                             16-MAR-1993;
                                            20-SEP-1994
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                                                                                                                                                                                                                                                                                               VOKYGGSSLESAERIRNVAERIVATKKAGNDVVVVCSAMGDTTDELLDLAAAVNPVPPAR
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                                                                                                                                                                                                                                                                                                                                                                                   RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                                             The invention relates to a gene from a high temperature-resistant coryneform microbe that encodes a heat-resistant lysin biosynthetic enzyme. The enzyme asspartate-semialdehydd dehydrogenase activity and can be used for growing amino acid-producing microbes. The present amino acid sequence corresponds to an enzyme of the
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                                                                                                                                                                                                                                           20.6%; Score 1248.5; DB 22; Lengt
65.2%; Pred. No. 6.9e-87;
iive 58; Mismatches 63; Indels
                                                                                                                     A heat-resistant lysin biosynthetic system enzyme gene temperature-resistant coryneform microbe
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                                                                                                                                             Claim 6; Page 21-22; 27pp; Japanese.
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251; Conservative
                                                                           (AJIN ) AJINOMOTO KK.
                                                                                           WPI; 2001-364760/38.
N-PSDB; AAH45374.
                                                                                                                                                                                                                           421 AA;
         JP2001120270-A
                                          01-NOV-1999;
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                        08-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BEAV--LTGVATDXSEAKVTV--LGISDK--PGEVAKVFRALADAEINIDMVLQNVSSVE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        375 TGLIAIHGLKASDVNGPLINSRIGSIYIVKPKMHGPAEVAFTCELFSRVEDVL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ72694 encodes AAR63568 Brevibacterium flavum feedback inhibiti release aspartockinase, it was used in the construction of a plasmid. The plasmid was used to transform Corynebacterium cells, where the expression of AAQ72694 resulted in incresed L-lysine
                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding feedback inhibition release asparto-kinase - used for the production of L-Lysine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----GLPQNTMKIGIMDE--ERRTTVNLKACIKA-
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1033 RRROHRHGAAERLOGRGROD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHI 1089
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           TAFLEVLNRDENYTAPGGGQFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEGIMDALF 374
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                                                                                                                                                                                         LDRTGDEIHTSMEA-GPMVRKGTMKSQPWILAY-----EDHNVDAG-LAAGFSGRAQV
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                                                                                     82 AMAIESLGAEAQSFIG----SQAG---VLTTERHGNARIVDVTP--GRVREALDEGKICI
                                                                                                                                                                                                                                                  GKGMWIMTELMADMVETKIAQPRAGASTAWVPSPTAATLHALHYHQVDVAAVQQGLAGKR
                                                                     TGLIAIHGLKASDVNGPLINSRIGSIYIVKPKMHGPAEVAFTCELFSRVEDVL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified Corynebacterium glutamicum aspartokinase, T311I.
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                                                                                                                                ----GLPQNTMKIGIMDE--ERRTTVNLKACIKA
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                                                                                                                                                                                                                                       1033 RRRQHRHGAAERLQGRGRQD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHI 1089
                                                                                                                                                                            TVVVGSIKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA-----R 1032
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               PVPPAREMDMLLTAGERISNALVAWAIESLGAEAQSFTGSQAGVLTTERHGNARIVDVTP
                                                                                                                   IFSADPRIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPG
                                                                                                                                      GRVREALDEGKICIVAGFQGVNKETRDVTTLGRGGSDTTAVALAAALNADVCEIYSDVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     255 OVGTIDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAAAVDKDG
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                                                         GRLQTALEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Feedback inhibition release aspartokinase, Brevibacterium flavum,
Corynebacterium, L-lysine production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feedback inhibition release aspartokinase 279Val, 301Ser, 308Thr.
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larity 36.8%; Pred. No. 2.1e-86;
Conservative 128; Mismatches 241; Indels 224
                                                                                                                                                                                                                                                                                                GKVSLIGAGMRSHPGVTATFCEALAAVGVNIELISTSE 1127
                                                                                                                                                                                                                                                                                                                   766 GKVSLVGAGMKSHPGVTAEFMEALRDVNVNIELISTSE 803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brevibacterium flavum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1994-337417/42.
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Matches 345; Conserv
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The specification describes Coryneform bacteria which produce chemical compounds, which instead of a single copy of an open reading frame (ORF), gene or allale maturally present at a desired locus have at least two copies of the ORF, gene or allale, preferably in tandem arrangement. The modified bacteria are is useful for producing chemical compounds including Leamino acids, vitamins, nucleosides and nucleotides. The present sequence is encoded by a lysc gene, and represents an aspartate kinase carrying the T3111 mutation. Tandem duplications of the lysc gene are used to construct the bacteria of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   809 ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMDMLLTAGERISNALVAMAIESLGAEAQSFTGSQAGVLTTERHGNARIVDVTPGRVREA 124
   -- TNVLYDDQVGKVSLV 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coryneform bacteria to produce chemical compounds e.g. L-lysine, has at least two copies of open reading frame, gene or allele in question at a particular desired site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         749 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bacteria; chemical compound; L-amino acid; vitamin; lysC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of a aspartate kinase carrying T3111 mutation.
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                                                           1127
   305 DGTTDIIFTCPRSDGRRAMEILKKLQVQG-----NW--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Met encoded by GTG'
                                                                                                  GAGMKSHPGVTAEFMEALRDVNVNIELISTSE
                                                           GAGMRSHPGVTATFCEALAAVGVNIELISTSE
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Corynebacterium glutamicum.
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Best Local Similarity 64.0%
Matches 251; Conservative
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N-PSDB; ABZ77392.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coryneform bacter aspartate kinase.
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                                    95 G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a modified aspartokinase from Corynebacterium glutamicum (e.g., AAB25607) and to DNA encoding the modified aspartokinase (e.g., AAC64119). The aspartokinase of the invention is modified to remove its sensitivity to feedback inhibition by L-threonine or L-lysine. This is achieved by substituting the wild-type Thr 311 with any other amino acid; for example, in AAB29607 Thr 311 is substituted by Ile. The invention also relates to expression vectors and host coryneform bacteria containing the modified DNA, and to the preparation of L-lysine using coryneform bacteria transformed with the modified aspartokinase-encoding DNA. Culturing coryneform bacteria transformed with the modified aspartokinase DNA of the invention provides efficient production of L-lysine. The present sequence represents a modified Corynebacterium glutamicum aspartokinase of the invention, T3111.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding modified aspartokinase without synergistic feedback inhibition by L-lysine and L-threonine for efficient production of L-lysine by coryneform bacterium fermentation
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                                                                                                                                                                                 Key
Misc-difference 311
/note= "Wild-type Thr replaced with Ile"
L-lysine; L-threonine; insensitive; product inhibition; coryneform bacterium; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ochiai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KYOW ) KYOWA HAKKO KOGYO KK
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                                                                                        Corynebacterium glutamicum
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N-PSDB; AAC64119.
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1 MQHHFHHHTDRVSVGNLRIA.....SAATRRPRCTRGRDGRWACQ 1172
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3: /cgnZ_6/ptodata/1/iaa/6A_COMB.pep:*
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6: /cgnZ_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd
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US-09-252-911A-2554
US-08-836-943-2
US-08-836-943-2
US-08-312-7603
US-08-311-731A-30
US-08-311-731A-30
US-08-596-6
US-08-596-6
US-08-967-104-6
US-08-965-104-6
US-08-965-104-6
US-08-955-366-6
US-08-955-366-6
US-08-955-916-5
US-08-955-916-5
US-08-525-911A-29720
US-07-556-227
US-09-056-556-227
US-09-056-556-227
US-09-056-556-227
US-09-056-556-227
US-09-056-556-227
US-09-328-332-6511
US-09-328-332-6511
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US-08-950-737-2
US-08-973-461A-8
                                                                                                                                                                                                                                                                                                                                                                           328717 segs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                              November 21, 2003, 15:58:31
                                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
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                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                              Run on:
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8,	Sequence 20, Appl	41	Seguence 5, Appli	Sequence 11, Appl	7	Sequence 16, Appl	Sequence 7, Appli	9	Sequence 8, Appli	ω̈	11	Sequence 6090, Ap	55	14	Sequence 8, Appli	'n	Sequence 6, Appli
US-08-648-010-8	US-08-380-182-20	US-09-134-001C-4160	US-08-532-828B-5	US-08-700-359-11	US-08-985-908-7	US-08-852-730-16	US-08-985-916-7	US-08-532-828B-6	US-08-596-366-8	US-08-967-104-8	US-09-198-452A-1124	US-09-107-532A-6090	US-09-328-352-5503	US-08-804-227C-14	US-08-804-227C-8	US-08-804-198-2	US-09-335-409-6
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310.5	310.5	294.5	285.5	285.5	285.5	285.5	285.5	281.5	281.5	281.5	241	226	181.5	172.5	172.5	172.5	171
28	29	30	31		33	34	35	36	37	38	39	40	41	42	43	44	4. 17.

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 AQIDKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 LNARFALNAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVP 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 LIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAA 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 LSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQPAGYTGAAESPTSVLLINHGLHIEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 LSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEI
Sequence 106, Application US/09001984C

| Sequence 106, Application US/09001984C
| Patent No. 6245331
| Patent No. 6245331
| GENERAL INFORMATION:
| APPLICANT: Lia1, Suman
| APPLICANT: Lia1, Patent Suman
| APPLICANT: Belisle, John T
| TILE OF INVENTION: BAELY DETECTION OF MYCOBACTERIAL DISEASE
| TILE REFERENCE: NYU-011
| CURRENT APPLICATION NUMBER: US/09/001,984C
| CURRENT FILING DATE: 1997-12-31
| PRIOR PILING DATE: 1996-12-31
| NUMBER OF SEQ ID NOS: 106
| SOFTWARE: PatentIN Ver: 2.1
| LENGTH: 741
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100.0%; Pred. No. 0;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-001-984C-106
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Best Local Similarity 100.0
Matches 740, Conservative
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488

481

421

548

541

608

601

668

661

721

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Sequence 2254, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
APPLICATION: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PRILING DATE: 1998-02-18
PRIOR PRILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               669 LERMAPLVDRONAGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTEPILHRRRREF 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 LIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAA 301
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                                                                                                                                          362 IMDALFTGLIAIHGLKASDVNGPLINSRTGSIYIVKPKNHGPAEVAFTCELFSRVEDVLG
                                                                                                                                                                                                                                                                                                                                                                          542 VPSPTAATLHALHYHQVDVAAVQQGLAGKRRATIEQLLTIPLAKELAWAPDEIREEVDNN
                                                                                                                                                                                                                   LPONTWKIGIMDEERRTTVNLKACIKAAADRVVFINTGFLDRIGDEIHTSMEAGEMVRKG
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                                                                          302 AVDKDGTAFLRVINRDRNYTAPGGGOFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEG
                                                                                                                IMDALFIGLIAIHGLKASDVNGPLINSRIGSIYIVKPKWHGPAEVAFICELFSRVEDVLG
                                                                                                                                                                                           LPQNTMKIGIMDEERRTTVMLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMVRKG
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69.1%; Pred. No. 9.6e-222;
live 77; Mismatches 139;
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502; Conser
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; ORGANISM: Pseudor
US-09-252-991A-22524
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US-09-252-991A-22524
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Matches 50
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IMDALFTGLIAIHGLKASDVNGPLINSRTGSIYIVKPKMHGPAEVAFTCELFSRVEDVLG
                            IMDALFIGLIAIHGLKASDVNGPLINSRIGSIYIVKPKWHGPAEVAFICELFSRVEDVLG
                                                                                                            LPQNIMKIGIMDEERRITVNLKACIKAADRVVFINTGFLDRTGDEIHTSMEAGPMVRKG
                                                                                                                                                                                                                                                                                                                                CQSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRHGVITSADVRAS
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                                                                          LPONTMKIGIMDEERRITVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMVRKG
                                                                                                                                                    TMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAGASTAW
                                                                                                                                                                                     TMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAGASTAW
                                                                                                                                                                                                                             VPSPTAATLHALHYHQVDVAAVQQGLAGKRRATIEQLLTIPLAKELAWAPDEIREEVDNN
                                                                                                                                                                                                                                                               VPSPTAATLHALHYHQVDVAAVQQGLAGKRRATIEQLLTIPLAKELAWAPDEIREEVDNN
                                                                                                                                                                                                                                                                                                       COSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRHGVITSADVRAS
                                                                                                                                                                                                                                                                                                                                                                                LERMAPLVDRQNAGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTEPILHRRRREF
                                                                                                                                                                                                                                                                                                                                                                                                                    LERMAPLVDRONAGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTEPILHRRRREF
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0
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APPLICANT: Lal, Suman
APPLICANT: Zolla-Pazner, Susan
APPLICANT: Zolla-Pazner, Susan
APPLICANT: Belisle, John T
TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
FILE REFERENCE: 32044-169276
CURRENT APPLICATION NUMBER: US/09/396,347F
CURRENT APPLICATION NUMBER: 09/001,984
PRIOR FILING DATE: 1997-12-31
PRIOR FILING DATE: 1997-12-31
NUMBER OF SEQ ID NOS: 106
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 741;
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62.9%; Score 3810; D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 740; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 106, Application US/09396347F Patent No. 6506384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Mycobacterium tuberculosis
US-09-396-347F-106
                                                                                                                                                                                                                                                                                                                                                                                                                                                            KARAAEKPAPSDRAGDDAAR 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KARAAEKPAPSDRAGDDAAR 741
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US-09-396-347F-106
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259 QIDPVHPIGKADKTGLKDIVLESALTTIMDFEDSVAAVDAEDKTLGYSNWFGLNTGELKE
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                                                                                                                                                                                                Length 739;
                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                  90; Mismatches 184;
                                                                                                                                                                                              37.8%; Score 2289; DB 2; 61.3%; Pred. No. 1.7e-196;
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Patent No. 6562958
GENERAL INFORMATION:
 (718) 884-6600
                                                      2
                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: SEQUENCE TRAFACTERISTICS: TYPE: amino acids TOPOLOGY: linear
                                                                                                                                                                                            Query Match
Best Local Similarity 61.3
Matches 444; Conservative
                718/601-1099
                                                                                                                                           , MOLECULE TYPE: protein US-08-836-943-2
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US-09-328-352-7603
TELEPHONE:
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                                                                     /KDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLA 307
                                                                                                                                       AAVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFE 367
                                                                                                                                                                BEVSKGGSTFTRTMNPDRVYTRADGSELTLHGRSLLFVRNVGHLMTNDALLDKDGNEVPE 367
                                                                                                                                                                                                             GIMDALFTGLIAIHGLKASDVNGPLI--NSRTGSIYIVKPKMHGPAEVAFTCELFSRVED 425
                                                                                                                                                                                                                                  VLGLPQNTMKIGIMDEERRITVNLKACIKAAADRVVFINTGFLDRIGDEIHTSMEAGPMV 485
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                                                                                                   248 iQidəsspyqqidaaqvxdvlmbaalttimdcedsvaavdaddxvviyrnwlglmxgdla 307
                  DNNAQGILGYVVRWIDQGVGCSKVPDINDVGLMEDRATLRISSQLLANWLRHGVISQEQV
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,943
FILING DATE: 08-MAY-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: Myers, Jonathan
REFERENCZ/DOCKET NUMBER: 201957
TELECOMMUNICATION INFORMATION:
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APPLICANT: Reinscheid, Dieter
APPLICANT: Eikmanns, Bernhard
APPLICANT: Eikmann
TITLE OF INVENTION: DNA WHICH REGULATES
TITLE OF INVENTION: CORYNEFORM BACTERIA
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: The Firm of Karl F. I
STREET: 5676 Riverdale Ave.
CITY: Bronx
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08836943
Patent No. 5965391
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US-08-836-943-2
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248

258 308

128 138 188 198

89 9 368

377 428 434 488 494 548 554 607 614 667

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Query Match
Best Local Similarity 80.4<sup>3</sup>
Matches 319; Conservative
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                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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ORGANISM: MYC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCQSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRHGVITSADVRA 667
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                                                                                                                                                                                                                                                       10 TARIQKGKLAIAKELYDFIENEALPGSGLDSETYWKNFEQVVVDLSPKNKALLAKRDELQ
                                                                                                                                                                                                                                                                                             AQIDKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          543 WVPSPTGAVIHAMHYHQVNVKARQDQLKAEEMLSLDDLLTPPFATDTNWSAEEINNELEN
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                                                                                                                                                                                                                                                                                                            LSSGSFGDATGFTVQDGQLVVALPD-KSTGLANPGQFAGYTGAAESPTSVLLINHGLHIE
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                                                                                                                                                                                                              Gaps
                AND AMINO ACID SEQUENCES RELATING TO DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                 Length 729;
                                                                                                                                                                               36.7%; Score 2225; DB 4; Length 7
59.8%; Pred. No. 9.5e-191;
ive 97; Mismatches 185; Indels
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO A; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTIC;
; TILE REFERENCE: GTC99-03PA; CURRENT APPLICATION NUMBER: US/09/328,352; CURRENT FILING DATE: 1999-06-04; NUMBER OF SEQ ID NOS: 8252; SEQ ID NO 7603
                                                                                                                                        ORGANISM: Acinetobacter baumannii
US-09-328-352-7603
                                                                                                                                                                                                           432; Conservative
                                                                                                                                                                                 Query Match
Best Local Similarity
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US-08-311-731A-30
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; Sequence 30, Application US/08311731A

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Patent No. 6583266
GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR TITLE OF INVENTION: DAGNOSTICS AND THERAPEUTICS
INTREE OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
ADDRESSES: WOLF, GREENFIELD & SACKS, P.C.
ATREET: ______
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1044 RLQGRGRQDRHHLHL---LPQTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLIGAGMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                749 VOKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER REALMANDE FORM:
MEDIUW TYER: FIPOPDY 4:
MEDIUW TYER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INPORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C0044/7125
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION 100-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHPGVTATFCEALAAVGVNIELISTSEDQRSRCCAAT 1137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.5%; Score 1545.5; DB 4
80.4%; Pred. No. 4.2e-130;
iive 18; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MYCOBACTERIUM LEPRAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERICSICS:
LENGTH: 421 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1101
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1039 HGAAERLQGRGRQD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 1095
989 IKDVPMEDPILTGVAHDRSBAKVTIVGLPDIPGYAAKVFRAVA-------RRRRQHR 1038
                                                                                                              305 DGTTDIIFTCPRADGRRAMEILKKLQVQG-----NW------TNVLYDDQVGKVSLV 350
                          869 LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59; Indels
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SUGIMOTO, MASAKAZU
APPLICANT: SUGIMOTO, WASAKAZU
APPLICANT: USUDA, YOSHHHIRO
APPLICANT: TANAKA, AKIKO
APPLICANT: TANAKA, AKIKO
APPLICANT: MATSUI, HIROSHI
TITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.2%; Score 1223.5; DB 164.0%; Pred. No. 3.6e-101; ive 55; Mismatches 59;
                                                                                                                                                                 1096 GAGMRSHPGVTATFCEALAAVGVNIELISTSE 1127
                                                                                                                                                                                                        351 GAGMKSHPGVTAEFMEALRDVNVNIELISTSE 382
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS TEXT EDITOR
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,359
FILING DATE: 08-OCT-1996
CLASSIPICATION: 435
PROOR APPLICATION ATA:
APPLICATION TO ATA:
APPLICATION NUMBER: US/08/700,359
FILING DATE: 04-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/08700359
Patent No. 5766925
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET UNBER: 10
TELECOMMUNICATION:
TELEPHONE: 703-413-3000
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Best Local Similarity 64.0<sup>§</sup>
Matches 251; Conservative
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INFORMATION FOR SEQ ID NO:
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MOLECULE TYPE: protein
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US-08-700-359-9
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                                                                  Sequence 3, Application US/08532828B
Fatent No. 568871
GENERAL INFORMATION.
APPLICANT: GGMA, Yuri
APPLICANT: GGMA, Yuri
APPLICANT: SUCIMOTO, Masakazu
APPLICANT: SIZUKI, Tomoko
APPLICANT: TANAKA, Akiko
APPLICANT: TANAKA, Akiko
APPLICANT: MATSUI, Hiroshi
TITLE OF INVENTION: MITANT ASPARTOKINASE GENE
TITLE OF INVENTION: MITANT ASPARTOKINASE GENE
TORRESPONDENCE ADDRESS: 2
ADDRESSE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.2%; Score 1223.5; DB 1; Length 421; 64.0%; Pred. No. 3.6e-101; tive 55; Mismatches 59; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Flappy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS TEXT EDITOR
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/532,828B
FILING DATE: 27-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24,618
RR: 10-764-0 PCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2, CLE
CLASSIFICATION: 435
PRIOR APPLICATION: DATA:
APPLICATION NAMER: JF 5-101450
FILING DATE: 27-APR-193
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 10-764-0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAC: 703-413-220
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
TEMMOTH: 421 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 421 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                         STREET: 1755
CITY: ARLING
STATE: VA
COUNTRY: US/
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM:
                                 RESULT 7
US-08-532-828B-3
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US-08-532-828B-3
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Best Local &
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Matches
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Gaps

27;

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989 IKDVPMEDPILIGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA-------RRRROHR 1038
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                                                                                                                                                                                                                                                                                                                                            DGTTDITFTCPRADGRRAMEILKKLÖVQG----NW------TNVLYDDQVGKVSLV 350
                                                                                                                                                         809 ELDMILTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 868
                                                                                                                                                                                 65 EMDMLLITAGERISNALVAWAIESLGAEAQSFTGSQAGVLTTERHGNARIVDVTPGRVREA 124
                                                                                                                                                                                                                                                                  RESULT 10

US-08-967-104-6

1 Sequence 6, Application US/08967104

2 Sequence 6, Application US/08967104

3 Patent No. 5919694

GENERAL INFORMATION:
APPLICANT: SUGINCY, Masakazu
APPLICANT: ATSUL, Tomoko

APPLICANT: ATSUL, Hiroshi
APPLICANT: ATSUL, Hiroshi
APPLICANT: ATSUL, Matsura

TITLE OF INVENTION: ITS GENE, AND PRODUCTION METHOD OF AMINO ACID
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSE

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER, & NEUSTADT,
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER, & NEUSTADT,
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER, & NEUSTADT,
STATE: VIRGINIA

COUNTRY: USA
ZIP- ATLINGTON
                                                                          749 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPR
                                                                                                                                                                                                                                        869 LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP
                                                                                                                                                                                                                                                                                                                       929 RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                 5 VOKYGGSSLESAERIRNVAERIVATKKAGNDVVVVCSAMGDTTDELLELAAAVNPVPPAR
Length 421;
20.2%; Score 1223.5; DB 2; Length 64.0%; Pred. No. 3.6e-101; tive 55; Mismatches 59; Indels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,104
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGMRSHPGVTATFCEALAAVGVNIELISTSE 1127
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PRICEATION: 130
PRICEATION NUMBER: US 08/596,366
FILING DATE: 29-APR-1996
APPLICATION NUMBER: UP 5-209775
FILING DATE: 24-AUG-1993
PRICEATION NUMBER: UP 5-209776
FILING DATE: 24-AUG-1993
PRICEATION NUMBER: UP 5-209776
FILING DATE: 24-AUG-1993
PRICEATION NUMBER: UP 6-153876
FILING DATE: 05-UUL-1994
                                        251; Conservative
                     Similarity
Query Match
Best Local S
Matches 251
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                                                               929 RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS 988
                                                                                                                                                 245 MEDIPVEEAVLITGVATDKSEAKVITVLGISDKPGEAAKVFRALADAEINIDMVLQNVSSVE 304
                                                                                                                                                                                                                             ----TNVLYDDQVGKVSLV 350
  125 LDEGKICIVAGFQGVNKETRDVTTLGRGGSDTTAVALAAALNADVCEIYSDVDGVYTADP 184
                                                                                                                                                                                                                                                                                                                     COMPUTER: USAS

ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/596,366
FLING DATE: 29-APR-1996
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/596,366
FLING DATE: 24-AUG-1993
PRIOR APPLICATION NUMBER: US/08/596,366
FILING DATE: 24-AUG-1993
PRIOR APPLICATION NUMBER: US/08/59776
FILING DATE: 24-AUG-1993
PRIOR APPLICATION NUMBER: US-010-1994
ATPONEY/AGENT INPORMATION:
NAME: OSLON, NORMAN TO:
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 10-784-0 PCT
TELECHOME (700) 413-3000
TELECHOME
                                                                                                                                                                                                                                    305 DGTTDITFTCPRADGRRAMBILKKLÖVQG-----NW---
                                                                                                                                                                                                                                                                                       1096 GAGMRSHPGVTATFCEALAAVGVNIELISTSE 1127
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SEQUENCE CHARACTERISTICS:

TENERY 248855 OPAT UR

INFORMATION FOR SEQ ID NO:

SEQUENCE CHARACTERISTICS:

TYPER 421 amit
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Sequence 14, Application US/08852730

Patent No. 6090597

GENERAL INFORMATION:
APPLICANT: MASAKO IZUI, ATSUSHI HAYAKAWA, YASUHIKO YOSHIHARA, AND TSUYOSHI
APPLICANT: MASAMO IZUI, ATSUSHI HAYAKAWA, YASUHIKO YOSHIHARA, AND TSUYOSHI
APPLICANT: MASAMO IZUI, ATSUSHI HAYAKAWA, YASUHIKO YOSHIHARA, AND TSUYOSHI
APPLICANT: MASAMOTSU
APPLICANT: METHOD OF PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER AND NEUSTADT, P.C.
CITY: ARLINGTON
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   989 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA-------RRRRQHR 1038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP
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                                                                                                                                                                                                                                                                                                                                                                                                               Score 1223.5; DB 3; Length 421;
Pred. No. 3.6e-101;
55; Mismatches 59; Indels 27;
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,730
FILING DATE: 05-07-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         305 DGTTDITFTCPRADGRRAMEILKKLOVOG----NW----
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          APPLICATION NUMBER: JP 8-3256E
FILING DATE: 05-DE0-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-300
TELEPHONE: 703-413-300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 mmino acids
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 64.0%;
Matches 251; Conservative 55
                                                                                                                                                                                                                                                                    : 421 amino acids
amino acid
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MOLECULE TYPE: protein
US-08-985-908-5
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Patent No. 6004773

GENERAL INFORMATION:
APPLICANT: MASAYIR ARAKI, MASAKAZU SUGIMOTO, YASUHIKO YOSHIHARA, AND TSUYOSHI NA TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --RRRRQHR 1038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       809 ELDMILTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA
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245 MEDIPVERAVLTGVATDKSBAKVTVLGISDKPGBAAKVFRALADABINIDMVLQNVSSVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           749 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             989 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA---
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/985,908
FILING DATE: 05-DEC-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 20.2%; Score 1223.5; DB 2; Best Local Similarity 64.0%; Pred. No. 3.6e-101; Matches 251; Conservative 55; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DGTTDITFTCPRADGRRAMEILKKLOVOG-----NW--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-784-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-2220
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
                                                                                                                                                                                                                                                              : 421 amino acids
amino acid
                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-967-104-6
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 05-DEC-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-08-985-908-5
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989 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA-------RRRRQHR 1038
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----TNVLYDDQVGKVSLV 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEEGRIVILVAGFOGUSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27;
                                                                                                                                                                                                                                                                                                                                                                                                                                20.2%; Score 1223.5; DB 3; Length 64.0%; Pred. No. 3.6e-101; iive 55; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08532828B
; Sequence 4, Application US/08532828B
; Patent No. 5688671
; GENERAL INPORMATION:
; APPLICANT: SUZUMOTO, Masakazu
; APPLICANT: SUZUMOTO, Wasakazu
; APPLICANT: TANAKA, Yuxi
; APPLICANT: TANAKA, Hixosh
; TILLE OF INVENTION: MUTANT ASPARTOKINASE GENE
; TULE OF INVENTION: MUTANT ASPARTOKINASE GENE
; TULE OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK
; STREE: 1755 s
CITV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      305 DGTTDITFTCPRADGRRAMEILKKLÖVOG-----NW----
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-325658
FILING DATA: 05-DEC-1996
ATTORNEY AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-220
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acid
TYPE: .... linear
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 64.0<sup>§</sup>
Matches 251; Conservative
                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                       US-08-985-916-5
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STATE:
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APPLICANT: ATSUSHI HAYAKAWA, MASAKAZU SUGIMOTO, YASUHIKO YOSHIHARA, AND TSUYOSHI
TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
COUNTRY: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .039 HGAAERLQGRGRQD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     809 ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 MEDIPVEEAVLIGVATDKSEAKVTVLGISDKPGEAAKVFRALADAEINIDMVLQNVSSVE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----TNVLYDDQVGKVSLV 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIVRNARKLDTVT FEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           749 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27;
                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3; Length 421;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    20.2%; Score 1223.5; DB 3; Length
64.0%; Pred. No. 3.6e-101;
tive 55; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 22152
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,916
FILING DATE: 05-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           305 DGTTDITFTCPRADGRRAMEILKKLÖVQG-----NW----
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                          CLASSIPICATION: 435
PRIOR APPLICATION DATA:
3 APPLICATION NUMBER: JP 8-142812
FILING DATE: 05-UUN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-985-916-5
; Sequence 5, Application US/08985916
; Patent No. 6221636
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TOTAL TOTAL
TELEFAN.
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SEQUENCE CHARACTERISTICS:
                                                                                                                                        NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,610
TELECOMMUNICATION INFORMATION
TELESPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                      421 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251; Conservative
                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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Best Local Similarity
Matches 251; Conserv
                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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963 YARRHNIPVHVRSSYSDRPGTVVVGSIKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGY 1022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 VALAAALKADECQIYTDVDGVYTTDPRVVPQARRLDKITFEEMLEMASLGSKVLQIRAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   327 AFKILGPISAANVEVDMIVQNVAHDNTTDFTFTVHRNDYLNALE-------ILKQT
                                                                                                                                                                                                                                                                              663 ADVRASLERMAPLVDRQNAGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTEPILH
                                                                                                                                                                                                                                                                                                                 6 APERCGAGRPAPLDARP----AVRPASP-----GSERMWQVQKGALH
                                                                                                                                                                                                                                                                                                                                                   723 RRRREFKARAAEKPAPSDRAGDDAARVQKYGGSSVADAERIRRVAERIVATKKQGNDVVV
                                                                                                                                                                                                                                                                                                                                                                                      44 GIRR-------FEMALIVQKFGGTSVGTVERIEQVAEKVKKFREAGDDVVV
                                                                                                                                                                                                                                                                                                                                                                                                                        783 VVSAMGDITDDLLDLAQQVCPAPPPRELDMLLIAGERISNALVAMAIESLGAHARSFIGS
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                                                                                                                                                                                                       13.6%; Score 827; DB 4; L
38.6%; Pred. No. 1.8e-65;
ive 86; Mismatches 130;
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he: 26.7156 secs
   PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 SEQ ID NOS: 33142 LENGTH: 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1023 AAKVFRAVARRRRQ------
                                                                                                                                                 ORGANISM: Pseudomonas aeruginosa
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Best Lócal Similarity 38.6'
Matches 187; Conservative
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US-09-252-991A-29720
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               989 IKDVPMEDPILIGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA------RRRRQHR 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HGAAERLQGRGRQD-RHHLHLLP--QTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 1095
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63.8%; Pred. No. 8.3e-101;
iive 55; Mismatches 60;
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                                                                                                                                                                                                                                                                                                                                                                                                                          יייסבאונט Corynebacterium glutamicum
;
US-08-532-828B-4
                                                   APPLICATION NUMBER: US/08/532,828B
FILING DATE: 27-OCT-1995
CLASSIPICATION: 435
                                                                                                 PULGATION 1935
PULGATION DATA
APPLICATION NUMBER: UP 5-101450
FILING DATE: 27-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 10-764-0
FELERANG/DOCKET NUMBER: 10-764-0
TELEPHONE: 703-413-320
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acids
TYPE: amino acids
OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MS-DOS TEXT EDITOR CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 63.8
Matches 250; Conservative
                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
US-09-252-991A-29720
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TOPOLOGY:
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us-09-688-672a-52.rapb

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:	November 21, 2003; 16:08:22 ; Search time 45.7107 Seconds (without alignments) 4680.740 Million cell updates/sec
Title: Perfect score: Seguence:	US-09-688-672A-52 6061 1 MQHHHHHHTDRVSVGNLRIASAATRRPRCTRGRDGRWACQ 1172
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched:	666188 segs, 182559486 residues
Total number of	Total number of hits satisfying chosen parameters: 666188
Minimum DB seq Maximum DB seq	Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Sequence 2, Appli	Sequence 58, Appl	Sequence 6988, Ap	Sequence 163, App	Sequence 3781, Ap	Sequence 24, Appl	Sequence 5, Appli	Sequence 2, Appli	Sequence 16, Appl	Sequence 12093, A	Sequence 227, App	Sequence 222, App	Sequence 290, App	Sequence 17, Appl	Sequence 8, Appli
SUMMARIES			DI	US-09-272-975-2	US-09-272-975-58	US-09-738-626-6988	US-09-793-306-163	US-09-738-626-3781	US-09-746-660A-24	US-10-226-136-5	US-10-067-974-2	US-10-067-974-16	US-10-156-761-12093	US-10-084-843-227	US-10-193-002-222	US-09-882-227-290	US-09-890-813-17	US-09-890-813-8
			- 1	11	11	10	σ	10	11	15	15	15	15	12	12	12	10	10
			Match Length DB	748	753	739	421	421	421	421	421	421	430	156	156	394	564	555
,	o ∤ o	Query	Match	63.8	63.8	37.8	26.7	20.2	20.2	20.2	20.1	20.0	18.9	12.7	12.7	11.1	6.2	0.9
			Score	3868	3868	2289	1615.5	1224.5	1224.5	1223.5	1217.5	1211.5	1144.5	770	770	673	377	365
		Result	No.	н	7	М	4	w	9	7	ω	σı	10	11	12	13	14	15

Sequence 6, Appli	23	equence 23	equence 16,	7,	equence 1	equence 34,	14	equence 9582, A	e 142	equence 11, App	Appl	equence 10429,	e 7964	72, App	equence 45	equence 79	Sequence 10436, A	equence 6,	equence 6,	9	equence 49	e 6,	10	ednence 79	e) C)	e 9538,	e 539, p	e O	5064,
	-997-2	-09-989-339-2	-890-	-136-	9-890-81	-022-832-	US-09-976-059-14	-10-156-761-958	US-10-156-761-14293	9-079-	-10-014-717-	-10-156-761-10	-10-156-761-796	B-7	9-4	1-796	10-156-76	-09-861-28	0-846-	6-82	∞	8-384B-	1-104	10-156-761-79		1-95	10-080-170-5	US-10-132-134-34	1
10	12	11	10	15	10	15	10	15	15	12	14	15	15	12	12	15	15	10	10	11		11		15	14	15	16	12	σ
560	262	449	439	172	281	440	4999	530	304	5245	3798	3970	3564	9689	5245	7746	6146	11877	11877	11877	11877	12199	4840	3352	7257	541	1624	8360	2472
5. 9.	٠	5.1	5.1	4.7	٠	4.0			3.0			•		٠			2.5				•				٠,	2.4	2.4	2.4	2.4
S	14.	10.	•	85.	48	4	g	œ	179	7	7	9	9	9	160	151.5	S	94	49.	49.	149.5	49.	∞	4,	4	-	4	145	
16	17	18	19	20	21	22	23	24	25	26	27	28	0,	30	31	32	33	34	32	36	37	38	8	40	41			44	45

ALIGNMENTS

	0	09	120	180	240
pplication US/09272975 o. US200300277441 MATION: MATION: Machine C. Lodes, Michael J. Houghton, Raymond L. ENTION: TUBERCULOSIS ANTIGENS AND METHO CE: 210121.474 ICATION NUMBER: US/09/272,975 O. ID NOS: 63 astSEQ for Windows Version 4.0	63.8%; Score 3868; DB 11; Length 748; Similarity 100.0%; Pred. No. 0; 8; Conservative 0; Mismatches 0; Indels 0; Gaps	1 MQHHHHHHTDRVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQAL 60 	61 LNARDELÇAÇIDKWHRRRVIEBIDMDAYRÇFLTEIGYLLPEPDDFTITTSGVDAEITTTA 120 	GPQLVVPVLNARFALNAANAEWGSLYDALYGTDVIBETDGAEKGPTYNKVRGDKVIAYAR 	KFLDDSVPLSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLI
LT 1 quence 2, A quence 2, A blication N NERAL INFOR PPLICANT: PREMARE:	atch cal Si 748;			121 0	181 F
RESULT 1 US-09-272-975-2 US-09-272-975-2 PUBLICACTON OF GENERAL INFOR APPLICANT: APPLICA	Query Match Best Local Matches 74	Sý Pp	oy du	oy D	ζ

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GPQLVVPVLNARFALNAANARWGSLYDALYGTDVIPBTDGABKGPTYNKVRGDKVIAYAR 180
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APPLICANT: NAKAGANA, SATOSHI
APPLICANT: NAKAGANA, SATOSHI
APPLICANT: HANDO, SELKO
APPLICANT: HANDO, SELKO
APPLICANT: CHAAL, KELKO
APPLICANT: OCKIAI, HARUHIKO
APPLICANT: TATELSHI, NAGKO
APPLICANT: TEDA, MASITO
APPLICANT: TECA, MASITO
APPLICANT: SENGH, AKIHIRO
APPLICANT: SENGH, AKINO
APPLICANT: SENGH, AKIO
TITLE OF INVENITON: NOVEL POLYNUCLEOTIDES
FILE REFRENCE: 249-125
CURRENT APPLICATION NUMBER: US 99/377484
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR PELING DATE: 1999-112-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SEQ ID NO 6988
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                                                         NHGLHIEILIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLG
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Publication No. US20030027774A1
GENERAL INFORMATION:
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: TUBERCULOSIS ANTIGENS AND METHODS
TITLE OF INVENTION: OF USE THEREFOR
TITLE OF INVENTION: OF USE THEREFOR
FILE REFERENCE: 210121.474
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 748; Conservative 0; Mismatches
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CURRENT FILING DATE: 1999-03-18
NUMBER OF FIGUR DATE: 3
SOFTWARE: FASCESQ for Windows Version 4.0
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; ORGANISM: Mycobacterium tuberculosis
US-09-272-975-58
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US-09-272-975-58
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296 VLQNVSKVEDGKTDITFTCSRDVGPAAVEKLDSLRNEIGFSQLLYDDHIGKVSLIGAGMR
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26.7%; Score 1615.5; DB 9
Best Local Similarity 85.1%; Pred. No. 1.3e-130;
Matches 338; Conservative 7; Mismatches 35;
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Sequence 3781, Application US/09738626
Publication No. US20020197605A1

SEQUENCAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: NAZOGUHI, HIROSHI
APPLICANT: MIZOGUHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: YOKOJ, HARUHIKO
APPLICANT: YOKOJ, HARUHIKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
                                                                                                                                                                                                                                                                GRGANISM: Mycobacterium tuberculosis
CTHER INFORMATION: MO-2 (aspartokinase)
US-09-793-306-163
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                                                                                               Length 739;
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                                                                                           37.8%; Score 2289; DB 10;
61.3%; Pred. No. 2.2e-188;
ive .90; Mismatches 184;
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Patent No. US20020098200A1
GENERAL INFORMATION:
APPLICANT: Campos-Neto, Antonio
APPLICANT: Skeiky, Yasir
APPLICANT: Ovendale, Pamela
APPLICANT: Lodes, Michael
APPLICANT: Lodes, Michael
                     TYPE: PRT
ORGANISM: Corynebacterium glutamicum
                                                                                                               Best_Local Similarity 61.33
Matches 444; Conservative
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                                             ; ORGANISM: COLY
US-09-738-626-6988
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US-09-793-306-163
   LENGTH: 739
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989 IKDVPMEDPILIGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVA------RRRRQHR 1038
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                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                  59; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/226,136
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HAYAKAWA, Atsushi
NAKANO, Eiichi
KOBAYASHI, Masaki
YOSHIHARA, Yasuhiko
NAKAMATSU, Tsuyoshi
TITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                       DB 11;
                                                                                                                                                                                                                          Score 1224.5; DB Pred. No. 7.7e-97;
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                                                                                                                                                                                                           20.2%; Scc. No. /...
64.0%; Pred. No. /...
... 55; Mismatches
PRIOR FILING DATE: 2000-03-09
PRIOR PEDLICATION NUMBER: DE 19931420.9
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 125
SOFTWARE: Patentin Vers. 2.0
SEQ ID NO 24
LENGTH: 421
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US-10-226-136-5
Sequence 5, Application US/10226136
; Publication No. US20030054506A1
; Publication To. US20030054506A1
; GENERAL INFORMATION:
; APPLICANT: OTSUNA, Seiko
; APPLICANT: OTSUNA, Seiko
                                                                                                                                      TYPE: PRT ; ORGANISM: Corynebacterium glutamicum US-09-746-660A-24
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COMPUTER READABLE FORM:
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APPLICANT: SCHOOLS, BATEWAY
APPLICANT: Schools, Casar
APPLICANT: Aberhauer, Gregor
APPLICANT: Haberhauer, Gregor
APPLICANT: Haberhauer, Gregor
APPLICANT: Head-Schick
APPLICANT: Lee, Heung-Schick
APPLICANT: Lee, Heung-Schick
APPLICANT: Lee, Heung-Schick
APPLICANT: METABOLIC PATHWAY PROTEINS
TITLE OF INVENTION: ORRNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
FILE REPREBACE: BGI-121CP2
CURRENT APPLICATION NUMBER: US/09/746,660A
CURRENT APPLICATION NUMBER: 09/603124
PRIOR APPLICATION NUMBER: 09/603124
PRIOR PILING DATE: 2000-06-23
PRIOR PELING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/14101
PRIOR PILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/148613
PRIOR PILING DATE: 1999-08-12
PRIOR PILING DATE: 1999-08-12
PRIOR PILING DATE: 1999-08-12
                                                                                                                                                                                                                              Length 421;
                                                                                                                                                                                                                                                                  59; Indels
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PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION WHMER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 3781
LENGTH: 421
                                                                                                                                                                , ORGANISM: Corynebacterium glutamicum US-09-738-626-3781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Sequence 24, Application US/09746660A, Publication No. US20030049804A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
APPLICANT: Kim, Jun-Won
APPLICANT: Lee, Heung-Schick
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Best Local Similarity 64.0°
Matches 251; Conservative
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, ORGANISM: Corynebacterium glutamicum
US-10-067-974-2
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Publication No. US2030055232A1

GENERAL INFORMATION:

APPLICANT: Li, Lhing-Yew

APPLICANT: Trei, Kelli J.

TITLE OF INVENTION: Polymucleotide Constructs for Increased Lysine Production
FILE REFERENCE: 1533.2640001

CURRENT APPLICATION NUMBER: US/10/067,974

CURRENT PILING DATE: 2002-02-08

PRIOR FILING DATE: 2001-02-08

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin version 3.1

TYPE: PRI

TYPE: PRI

TYPE: PRI

TYPE: PRI
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64.0%; Pred. No. 9.4e-97;
tive 55; Mismatches 59; In
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                    PRIOR APPLICATION: CULLIUM...

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/952,976
FILING DATE: 8-DEC-1997
APPLICATION NUMBER: UP 7-140614
FILING DATE: 07-0UL-1995
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN P. OBLON
REGISTRATION NUMBER: 24,618
TELEFONE: 703-413-300
TELEFPONE: 703-413-300
TELEFPONE: 703-413-3220
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
FELDERAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-226-136-5
                                                                                                                                                                                                                                                              LENGTH: 421 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 64.0%
Matches 251; Conservative
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US-10-067-974-2
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US-10-067-974-16
| Sequence 16, Application US/10067974
| Sequence 16, Application No. US20030055232A1
| Publication No. US20030055232A1
| GENERAL INFORMATION:
| APPLICANT: Li, Lhing-Yew
| APPLICANT: Li, Lhing-Yew
| TILL OF INVENTION: Polynucleotide Constructs for Increased Lysine Production
| TILL OF INVENTION: Polynucleotide Constructs for Increased Lysine Production
| TILL OF INVENTION: VOLUMER: US/10/067,974
| CURRENT FILING DATE: 2002-02-08
| PRIOR FILING DATE: 2001-02-08
| NUMBER OF SEQ ID NOS: 25
| SEQTIMARE: Patentin version 3.1
| ENGTH: 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 039 HGAAERLOGRGROD-RHHLHLLP--QTSGPPFWKNWTRSETRSASTQLLYDDHIGKVSLI 1095
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-----TNVLYDDQVGKVSLV 350
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                                                                                                                                                                                                                                                                                                                               869 LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 928
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                                                                                                                                                                                                                                                                                                                                                                                                                                             929 RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS 988
                                                                                                                                                                  64
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                                                                                                                                                                                                                      809 ELDMLITAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA
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                                                       27;
     DB 15; Length 421;
                                                       60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 20.1%; Score 1217.5; DB Best Local Similarity 63.8%; Pred. No. 3.1e-96; Matches 250; Conservative 55; Mismatches 60
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NAME/KSY: MISC FEATURE
LOCATION: (317)..(317)
OTHER INFORMATION: May be either Ser or Ala
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NAME/KEY: MISC_FEATURE
LOCATION: (40)...(40)
OTHER INFORMATION: May be either Cys
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LOCATION: (380)...(380)
OTHER INFORMATION: May be either Thr
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TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 227:
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ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: SEED and BERRY LLP
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TYPE: amino acid
STRANDEDNESS: single
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(206) 682-6031
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STATE: Washington
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                                                                                                                                                                                                                                                                                      749 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDITDDLLDLAQQVCPAPPPR
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                                                                                      ; Score 1211.5; DB 15; Lengtl
; Pred. No. 1e-95;
55; Mismatches 61; Indels
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: ARATORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
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, Publication No. US20030119018A1
, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-12093
                                                                                           20.0%;
                                                                                                                                                                                           Matches 249; Conservative
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                                                                                                                                             Best Local Similarity
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Matches 239; Conserv
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US-10-156-761-12093
JS-10-067-974-16
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1035 ----RQHRHGAAERLQGRGRQDRHHLHLLPQTSGPPPWKWWTRSETRSASTQLLYDDHIG 1090
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LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP
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US-10-084-843-227
Sequence 227, Application US/10084843
Sequence 227, Application US/10084843
Sequence 227, Application US/10084843
SEGUENCE 227, Application US/10084843
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SEGUENCE 227, Application US/10084843
SEGUENCE 227, Application US/10084843
SEGUENCE 227, Application US/100879410
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SEGUENCE 227, Application US/1
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMINICATION INFORMATION:
TELEPHONE: (206) 622-4900
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1111 EALAAVGVNIELISTSE 1127
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US-09-882-227-290
                Conservative
Best Local Similarity
Matches 156; Conserv
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US-09-882-227-290
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                                                              Gaps
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Dillon, Davin C.
Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Micheal J.
Hendrickson, Ronald C.
Hendrickson, Ronald C.
INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS
                              Length 156;
                                                              Indels
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ZIP: 98104-709

ZOMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: SYSTEM: PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                         EEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAM 905
                                                                                                                                                                                                                                           BEGRUVLVAGFOGVSQDTXDVTTLGRGSDTTAVAM 156
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                              Score 770; DB 12;
Pred. No. 2.7e-58;
                    CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: US/10/193,002
FILING DATE: 10-JUJ-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TUBERCULOSIS
                                                                                                                                                                                                                                                                                                              3-10-193-002-222
Sequence 222, Application US/10193002
Publication No. US20030135026A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (206) 682-6031
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SEQUENCE CHARACTERISTICS:
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STATE: Washington
                                                              Matches 156; Conservative
                              Query Match
Best Local Similarity
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US-10-084-843-227
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DB 12;

Score 770;

12.7%;

Query Match

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APPLICANT: Al-darawi, Amai Applicant: Arguments, Amai Applicant: Arguments, Amai Applicant: Al-darawi, Amai Applicant: Miler, Charles Applicant: Miler, Charles Applicant: Tomb, Jean-Francois Applicant: Tomb, Jean-Francois Applicant: Ocomen, Raymond P. TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Genome FILE REFERENCE: 06132/047002
CURRENT APPLICATION NUMBER: US/09/882,227
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 08/902,615
PRIOR APPLICATION NUMBER: US 08/902,615
NUMBER OF SEQ ID NOS: 638
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 290
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                                                                                                                                    1 OKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDITDDLLDLAQQVCPAPPRE
                                                                                                                                                                                                         810 LDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTFGRLQTAL
                         Indels
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11.1%; Score 673; DB 12;
Best Local Similarity 40.1%; Pred. No. 3e-49;
Matches 151; Conservative 83; Mismatches 119;
100.0%; Pred. No. 2.7e-58; iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 290, Application US/0988227; Publication No. US2030158396A1
GENERAL INFORMATION: APPLICANT: Kleanthous, Harold
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992 VPMEDPILIGVAHDRSEAKVTIVGLPDIP--GYAAKVFRAVARRRRQHRHGAAERLQGRG 1049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         382 RDMSKAVLTSIVLKRNVTMLDIASTRMLGQYGFLAKVFSIFEELGISVDVVATSEVSVSL 441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               749 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLL--
                              Sequence 17, Application US/09890813
Publication No. US20020183486A1
GENERAL INFORMATION:
FAPPLICANT: E.I. du Pont de Nemours and Company
TITLE OF INVENTION: Aspartate Kinase
FILE REFRENCE: BB1430 PCT
CURRENT APPLICATION NUMBER: US/09/890,813
CURRENT FILING DATE: 2001.08-02
PRIOR FILING DATE: 1999-12-21
NUMBER: OF SEQ ID NOS: 24
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Publication NG. US20020183486A1

Publication NG. US20020183486A1

GENERAL INFORMATION

TITLE OF INVENTION: Aspartate Kinase

FILE REFERENCE: BB1430 PCT

CURRENT APPLICATION NUMBER: US/09/890,813

CURRENT FILING DATE: 1999-12-21

PRIOR FILING DATE: 1999-12-21

NUMBER OF SEQ ID NOS: 24
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                                                                                                                                                                                                                                                                                                        TYPE: PRT

CORGANISM: Glycine max

US-09-890-813-17
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RESULT 14
US-09-890-813-17
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LENGTH: 564
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US-09-890-813-8
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6.0%; Score 365; DB 10; Length 5:
Best Local Similarity 29.9%; Pred. No. 2.1e-22;
Matches 103; Conservative 58; Mismatches 119; Indels
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1 MQHHHHHHTDRVGVGNLRIA......SAATRRPRCTRGRDGRWACQ 1172
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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	705	703	694.5	656	959	632	585	562	533	524	52	20	492	480.5	46

ALIGNMENTS

RESULT 1. PRESULT 1. Probable glob probable glob p. C. Species: Myco C. Dacession: F7 R. Cole, S.T.; B. R. Jandream, M. A. Mature 393, S37 A. Title: Sqar A. Title: Status: prelia, A. Reference mum A. Residues: 1-7 A. Residues: 1-7 A. Experimental C. Genetics: A. Ge	RESULT 1. PRESULT 1. PRODACT 2. PRODACT 3. PRODACT
Query Me Best Loc Matches	Query Match 62.9%; Score 3810; DB 2; Length 741; Best Local Similarity 100.0%; Pred. No. 7.1e-221; Matches 740; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
γò	9 TDRVSVGNLRIARVLYDFVNNBALPGTDIDPDSFWAGYDKVYADLTPONQALLNARDELQ 68
qq	2 TDRVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGYDKVVADLTPQNQALLNARDELQ 61
δλ	9 AQIDKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTGGVDAEITTTAGPQLVVPV
qq	62 AQIDKWHRRRVIEPIDMDAYRQFLTEIGYLLPBPDDFTITTSGVDAEITTTAGPQLVVPV 121
oy D	129 INARFALNAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVP 188
ζō	189 LSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEI 248
qq	182 LSSGSFGDATGFTVQDGQLVVALFDKSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEI 241
δλ	249 LIDPESQYGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAA 308
qq	242 LIDPESQVGTTBRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAA 301
δλ	309 AVDKDGTAFLRVLNRDRNYTAPGGGGFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEG 368
Ор	302 AVDKDGTAFLRVLNRDRNYTAPGGGGFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEG 361
ζ	369 IMDALFIGLIAIHGLKASDVNGPLINSRTGSIYIVKPKMHGPARVAFTCELFSRVEDVLG 428

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| ILIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRWWLGLNKGDLA 307
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                                                                            TWKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAGASTAW 548
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                                                                                                                                                                                              CQSILGYVVRWYDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRHGVITSADVRAS 661
                                                                                                                                                                                                                                 LERMAPLVDRQNAGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTEPILHRRRREF 728
                                                                                                                                                                                                                                                   LERMAPLVDRQNAGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTEPILHRRREF 721
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362 IMDALFTGLIAIHGLKASDVNGPLINSRTGSIYIVKPKMHGPAEVAFTCELFSRVEDVLG 421
                                          LPQNIMKIGIMDEERRITVNLKACIKAAADRVVFINIGFLDRIGDEIHTSMEAGPMVRKG 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A)Residues: 1-731 <PAR>
A)Cross-references: EMBL:AL008609; PIDN:CAA15459.1
A)Cross-inental source: cosmid B1788
C;Genetics:
A,Note: glob
C;Keywords: carbon-carbon lyase; coenzyme A; oxo-acid-lyase
                                                                                                                                                                                                                                                                                    KARAAEKPAPSDRAGDDAAR 748
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Matches 597; Conservative
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RESULT 3
H83586
malate synthase G PA0482 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000
C;Accesion: H83586
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Briadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, M. Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Reference type: DNA
A;Residues: 1-72 <STO>
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A;Genetics:
A;Genetics:
A;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AKIDGWHQARAGQAHDAVAYKAFLEEIGYLLPEAEDFQAGTQNVDDEIARMAGPQLVVPV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                    362 EVFEGIIDAVFIGLAAIHGLKIGEANGPLINSRIGSIYIVKPKMHGPAEVAFICELFSRV
                                                                                                                                                              EDVLGLPOGTLKVGIMDEERRTTLNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGP
                                                                                                                                                                                                                         WVRKGTMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAG
                                                                                                                                                                                                                                                                                                                                    544 ASTAWVPSPTAATLHALHYHQVDVAAVQQGLAGKRRATIEQLLTIPLAKELAWAPDEIRE
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Best Local Similarity 69.1%; Pred. No. 2.3e-146;
Matches 502; Conservative 77; Mismatches 139;
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                                   PLSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLINHGLHIE
                                                     PLETGSWSDVTGFNIADGLLQLAIGAATTGLKDAVQFKGFSGEAAKPATILLGKNGLHTE
                                                                                                    ILIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLA
                                                                                                                                                                     AAVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSIMFVRNVGHLMTNDAIVDTDGSEVFE
                                                                                                                                                                                                                                       GIMDALFTGLIAIHGLKASDVNGPLINSRTGSIYIVKPKMHGPAEVAFTCELFSRVEDVL
                                                                                                                                                                                                                                                           GLPQNTMKIGIMDEERRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMVRK
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Best Local S:
Matches 461
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malate synthase G [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C, Species: Agrobacterium tumefaciens
C, Species: Agrobacterium tumefaciens
C, Species: Agrobacterium tumefaciens
C, Species: Agrobacterium tumefaciens
C, Species: Agrobacterium tumefaciens
C, Accession: AH3582
R, Wood, D. W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Strile: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AH3582
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-744 <KCNR>
A;Residues: 1-744 <KCNR>
A;Coss-references: GB:AE008688; PIDN:AAL41078.1; PID:g17738367; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
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                                                                                                                      GIQDGLFTSLIAIH-----DLNGNTSRKNSRTGSVXIVKPKWHGPERAAFTNELFGRVED 416
                                                                                                                                                                                       417 VLGEPRNTLKVGIMDEERRTTVNLKACIKAAKDRVVFINTGFLDRTGDEIHTSMEAGAVV 476
                                                                                                                                                                                                                                       RKGTMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAGAS 545
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                                308 AAVDKDGTAFLRVLNRDRNYTAPGGGOFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFE 367
IQIDPSSPVGQTDAAGVKDVLMEAALTTIMDCEDSVAAVDADDKVVIYRNWLGLMKGDLA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HVSRTDKFGLSIDDRLYAFLTDEVLPGTGLDSETFFEGFSAIVHELSPKNRELLAKRDAL 81
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                                                     EEVSKGGSTFTRTMNPDRVYTRADGSELTLHGRSLLFVRNVGHLMTNDALLDKDGNEVPE
                                                                                                                                                                                                                                                         597 DNNAQGILGYVVRWIDQGVGCSKVPDINDVGLMEDRATLRISSQLLANWLRHGVISQEQV
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                                                                                                    GIMDALFIGLIAIHGLKASDVNGPLI--NSRIGSIYIVKPKMHGPAEVAFTCELFSRVED
                                                                                                                                                                   VLGLPQNTMKIGIMDEERRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMV
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.larity 63.5%; Pred. No. 5.3e-135;
Conservative 91; Mismatches 170;
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A, Map position: circular chromosome
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461; Conserv
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Best Local S:
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Malate synthase (BC 4.1.3.2) - Corynebacterium glutamicum
C; Species: Corynebacterium glutamicum
C; Species: Corynebacterium glutamicum
C; Species: Corynebacterium glutamicum
C; Species: Corynebacterium glutamicum
C; Species: L40215; L40836
C; Accession: 140715; L40836
R; Reinscheid, D.J.; Elkmanns, B.J.; Sahm, H.
Microbiology 140, 3099-3108, 1994
A; Title: Malate synthase from Corynebacterium glutamicum: sequence analysis of the gene
A; Recession: 140715
A; Recession: 140715
A; Residues: 1-739 < RES
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                                                                                                                            DKDGTAFLRVLNRDRNYTAPGGGOFTLPGRSLMFVRNVGHLMTNDALVDTDGSEVFEGIM
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EKNGKQMTRRLNGDRTYTAPDGSTLTLKGRSLMLVRNVGHLMTNPAILDAEGNEVPEGIM
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                                                                                            DKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPVLNA
                                                                                                                                                                                                                                                                                    GSFGDATGFTVQDGQLVVALPDKS-TGLANPGQFAGYTGAAESPTSVLLINHGLHIEILI
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    VSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQAQI
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AF229
malate synthase (EC 4.1.3.2) [imported] - Brucella melitensis (strain 16M)
C.Species: Brucella melitensis
C.Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002
C.Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002
C.Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002
C.Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002
R.DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
R.DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 43-448, 2002
A;fitle: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AB3299
A;Status: preliminary
A;Roteus: preliminary
A;Roteus: preliminary
A;Roteus: preliminary
A;Roteus: Breliminary
A;Resperimental source: strain 16M
A;Resperimental source: strain 16M
A;Reperimental source: strain 16M
A;Gene: BME10380
A;Map position: I
C;Reywords: carbon-carbon lyase; coenzyme A; oxo-acid-lyase
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                                            VLNARFALNAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSV 187
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                                                                             PLSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLINHGLHIE
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PIDN:BAB05852.1; GSPDB:GN001
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851788
malate synthase (EC 4.1.3.2) isoenzyme G - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Species: 23-Aug-1995 #sequence_revision 13-Mar-1997 #text_change 01-Mar-2002
C;Accession: S51788; P65083
R;Molina, I.; Pellicer, M.T.; Baddia, J.; Aguilar, J.; Baldoma, L.
Bur. J. Blochem. 224, 541-548, 1994
A;Title: Molecular characterization of Escherichia coli malate synthase G. I
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                                                                                         Length 727
                                                                                                                Indels
A,Molecule type: DNA
A,Residues: 1-727 <STO>
A,Cross-references: GB:AP001514; GB:BA000004; NID:g10174613;
A,Experimental source: strain C-125
C,Genetics:
A,Gene: BH2133
                                                                                      37.3%; Score 2258; DB 2;
59.9%; Pred. No. 1.1e-127;
iive 97; Mismatches 186;
                                                                                                    Best Local Similarity 59.9%;
Matches 441; Conservative
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C;Species: Bacillus halodurans
C;Date: 01-0ec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: B8316
R;Takani, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.;
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83550; MUD:20512582; PMID:11058132
A;Accession: B83916
A;Status: preliminary
                                                                                                                                                     128
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                                                                                                                  AQIDKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPV
                                                                                                                                                                                                       INARFALNAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVP
                                                                                                                                                                                                                                                          LSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEI
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                                                                          Gaps
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                                                   739;
                                                                          Indels
                                                   Length
                           oxo-acid-lyase
                                                Query Match 37.8%; Score 2289; DB 2; Best Local Similarity 61.3%; Pred. No. 1.5e-129; Matches 444; Conservative 90; Mismatches 184;
                           Ä
                           coenzyme
             'Gene: aceB
'Keywords: carbon-carbon lyase;
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Differentiation

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probable ask protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Sacession: F70794
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Hamris, D.; Gordon, S.; Colnor, R.; Davish, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 333, 537-544, 1998
A;Authors: Sagares, R.; Sultson, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome fareference number: A70500; MUID: 98295987; PMID: 9634230
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome fareference: P7094
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Status: Leferences: GB: AL02121; GB: AL123456; NID: 93261559; PIDN: CAA18031.1; PID: 9296013: A;Genetics:
A;Genetics: A;Genetics: Strain H37Rv
C;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;
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C;Species: Mycobacterium leprae
C;Date: 20.Apr-2001 #sequence_revision 20.Apr-2001 #text_change 14-Dec-2001
C;Accession: 687199
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hor R:, Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Squ
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Pred. No. 1.8e-89;
7; Mismatches 35;
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Best Local Similarity 85.1%;
Matches 338; Conservative
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A; Reference number: S51788, MUD: 95010032; PMID: 7925370
A; Accession: S51788
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-723 < MOL>
A; Cross.references: EMBL: X74547; NID: 9517246; PIDN: CAA52639.1; PID: 9517247
A; Cross.references: EMBL: X74547; NID: 9517246; PIDN: CAA52639.1; PID: 9517247
B; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Rose, D.J.; Mau, B.; Shao, Y.
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A; Accession: F65083
A; Accession: F65083
A; Accession: F65083
A; Residues: 1723 < BLAT>
A; Residues: 1723 < BLAT>
A; Residues: 1723 < BLAT>
A; Residues: 1723 < BLAT>
A; Cross.references: GB; Accoss GB; Uno096; NID: 91789344; PIDN: AAC76012.1; PID: 91789348; A; Gene: 9108
C; Genetics:
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Alternate kinase (EC 2.7.2.4) alpha chain - Corynebacterium glutamicum NiAlternate names: aspartokinase alpha chain Cispecies: Corynebacterium glutamicum Cispecies: Corynebacterium glutamicum Cispecies: Corynebacterium glutamicum Cispecies: Corynebacterium glutamicum Cispecies: Corynebacterium glutamicum Cispecies: Corynebacterium glutamicum Cispecies: Organica Sizof; Sapari Cispecies: Corynebacterium J. Cremetry J. Cremetry J. Sachmann, B.; Eggeling, L.; Sahm, H.; Puehler, A. Rialinowski, J.; Cremetry J. 1997-1204, 1991
A;Title: Genetic and biochemical analysis of the aspartokinase from Corynebacterium glut A;Reference number: S15276; MUD:92065816; PMID:1956296
A;Accession: S15276
A;Accession: S15276
A;Accession: S15276
A;Accession: S15276
A;Accession: S15276; MUD:940509; PIDN:CAA40502.1; PID:9580983
A;Cross-references: EMBL:X57226; NID:940509; PIDN:CAA40502.1; PID:9580983
A;Cross-references: EMBL:X57226; NID:940509; PIDN:CAA40502.1; PID:9580983
A;Cross-references: EMBL:X57226; November 1994
A;Accession: S15276
A;Accession: S49977
A;Accession: S49977
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A; Residues: 329-421 <SER>
A; Residues: 329-421 <SER>
A; Cross-references: Embi.K82928; NID:g599716; PIDN:CAAS8100.1; PID:g599717
A; Atalinowski, J.; Bachmann, B.; Thierbach, G.; Puehler, A.
Mol. Gen. Genet. 224, 317-324, 1990
A; Title: Aspartokinase genes lysC-alpha and lysC-beta overlap and are adjacent the Aspartokinase genes lysC-alpha and lysC-beta overlap and are adjacent the Contents: annotation
C; Genetics:
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         5 VQXYGGSSVADAERIRRVAERIVETXKAGNDVVVVVSAMGDTTDDLLDLARQVSPAPPPR
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                                                                                                ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA
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A)Gene: codon: GTG
C;Superfamily: aspartate kinase; aspartate kinase homology
C;Superfamily: aspartate initiators; phosphotransferase
C;Keywords: alternative initiators; phosphotransferase
F;3-406/Domain: aspartate kinase homology <DKI>
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NyAlternate names: aspartokinase alpha chain
C;Species: Mycobacterium smegmatis
C;Date: 07-May-1998 #sequence_revision 15-May-1998 #text_change 18-Jun-1999
C;Accession: $42422; $31801
R;Cirillo, J., D.; Waisbrod, T. R.; Pascopella, L.; Bloom, B.R.; Jacobs Jr., W.R.
Mol. Microbiol. 11, 629-639, 1994
A;Title: Isolation and characterization of the aspartokinase and aspartate semialdehyde
A;Reference number: $42421; MUID:94254720; PMID:7910936
A;Reference number: $42421; MUID:94254720; PMID:7910936
A;Reference: EMBL:217372; MID:944506; PIDN:CAA78984.1; PID:9581352
A;Note: the authors translated the initiation codon GTG for residue 1 as Val
C;Genetics:
A;Start codon: GTG
C;Superfamily: aspartate kinase; aspartate kinase homology
C;Keywords: alternative initiators; phosphorransferase
F;1-421/Product: aspartate kinase alpha chain #status predicted <ASA>
F;3-406/Domain: aspartate kinase beta chain #status predicted <ASA>
F;250-421/Product: aspartate kinase beta chain #status predicted <ASB>
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25.5%; Score 1545.5; DB 2; Length 421;
Best Local Similarity 80.4%; Pred. No. 2.9e-85;
Matches 319; Conservative 18; Mismatches 43; Indels 17;
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24.4%; Score 1478.5; DB.2; Length 421;
Best Local Similarity 77.6%; Pred. No. 3.1e-81;
Matches 302; Conservative 31; Mismatches 35; Indels 21;
A; Title: Massive gene decay in the leprosy bacillus.
A; Reference number: A66909; MUD:21128732; PMID:11234002
A; Accession: GR7199
A; Accession: GR7199
A; Residues: preliminary
A; Residues: 1-421 <STO>
A; Residues: 1-421 <STO>
C; Genetics:
A; Cross-references: GB:AL450380; NID:g13093941; PIDN:CAC31839.1; C; Genetics:
A; Gene: ask
C; Superfamily: aspartate kinase; aspartate kinase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHPGVTATFCEALAAVGVNIELISTSEDQRSRCCAAT 1137
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Nature 406, 959-964, 2000
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                                                                                                                                                                                  asparetate kinase alpha and beta chain PA0904 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa () Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 14-Dec-2001 C;Accession: C83531 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br. Stover, C.K.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Jature 406, 959-964, 2000
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        358 KSNPGVTADFFTALSDAGVNIELISTSE 385
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Best Local Similarity 42.6%;
Matches 170; Conservative 8
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probable aspartokinase - Streptomyces coelicolor
C;Bate: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 31-Jan-2000
C;Accession: T35383
R;Murshy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Date Library, June 1999
A;Reference number: Z21576
A;Reference number: Z21576
A;Retaus: preliminary; translated from GB/EMBL/DDBJ
A;Gtatus: preliminary;
A;Molecule type: DNA
A;Rocession: 1-452 kMUR.
A;Rocessides: 1-452 kMUR.
A;Cross-references: EMBL:AL079348; PIDN:CAB45482.1; GSPDB:GN00070; SCOEDB:SC66T3.26c
A;Experimental source: strain A3(2)
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C;Superfamily: aspartate kinase; aspartate kinase homology
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; Search time 13.8195 Seconds (without alignments) 3988.226 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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6061 1 MQHHHHHHHDRVSVGNLRIA......SAATRRFRCTRGRDGRWACQ 1172 BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-688-672A-52 Title: Perfect score: Scoring table: Sequence:

Total number of hits satisfying chosen parameters:

127863 seqs, 47026705 residues

Searched:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

050596 mycobacteri 032913 mycobacteri 032913 mycobacteri 091636 pseudomonas 081878 pseudomonas 081912 pseudomonas 081912 pseudomonas 081913 pseudomonas 081913 pseudomonas 081777 rhizobium 1 092734 rhizobium 1 09273 preacheria 081750 brucella su 081750 brucella su 081750 brucella su 081750 brucella su 081750 brucella su 081750 brucella su 081750 brucella su 081750 brucella su 081750 brucella su 081750 brucella su 081750 brucella su 081750 brucella su 081772 pseudomonas 081773 oscherichia 081701 mycobacteri 081701 corynebacte 06171 pseudomonas 081711 thermus the 05922 bacillus st 06172 qquifex aeo rhizobium lagrobacteri rhizobium l rhizobium m brucella me Description SUMMARIES MASZ_MYCTU
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O25827 helicobacte	Q04795 bacillus su			P27725 serratia ma	P00561 escherichia	P37142 daucus caro	P44505 haemophilus	P08660 escherichia	P94417 bacillus su	P57290 buchnera ap	O84367 chlamydia t
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ALIGNMENTS

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AK2_BACST AK_AQUAE AK_HELPJ AK2_BACSU

corynebacte corynebacte corynebacte pseudomonas thermus the

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CATALYTIC BASE (BY SIMILARITY)

ACT SITE 633 633 CATALYTIC ACID (BY SIMILARITY)

SEQÜENCE 741 AA; 80403 MW; A92P54E0PE8B7C64 CRC64;
                                                                                            Pfam, PP01274; Malate synthass; 1.
TIGRFAMs; TIGR01345; malate syn G; 1.
Transferase; Glyoxylate bypass; Tricarboxylic acid cycle;
                                                                                                                                                                                                                 0; Indels
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100.0%; Pred. No. 1.5e-205;
ive 0; Mismatches 0;
                                                          HAMAP; MF 00641; -; 1.
InterPro; IPR001465; Malate_synthase.
InterPro; IPR006253; Malate_synthG.
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ses 740; Conservative
                                    TIGR; MT1885; -.
Tuberculist; Rv1837c; -.
             PDB; 1N8I; 18-DEC-02.
PDB; 1N8W; 18-DEC-02.
F70722; F70722.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-i- SUBDNIT: Monomer (By similarity).
-i- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-i- SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21128732; PubMed=11234002;
Cole S.T., Edilmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnher T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Fellwell T., Fraser A., Hamlin N.,
Murphy L., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-!- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate = S-malate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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                                                                                                                                                                                                                                             Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales;
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CATALYTIC ACID (BY SIMILARITY)
3878CADA45DB416C CRC64;
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Transferase; Glyoxylate bypass; Tricarboxylic acid cycle;
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NCBI_TaxID=1769;
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82.0%; Pred. No. 7.4e-167;
M.cmatches 72;
                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Malate synthase G (EC 2.3.3.9)
GLOB OR ML2069 OR MLCB1788.27.
Mycobacterium leprae.
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731
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InterPro; IPR001465; Malate_synthase.
InterPro; IPR006253; Malate_synthG.
Pfam; PF01274; Malate_synthase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AL008609, CAA15459.1; -. EMBL, AL583924; CAC31024.1; -. PIR, T44752, T44752.
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Matches 597; Conservative
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43.5%; Score 2634; DB 1;
69.0%; Pred. No. 7.5e-140;
tive 82; Mismatches 138;
                                                                                                             EMBL; AJ301559; CAC35701.1; -. HSSP; P37330; 1D8C.
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SUBUNIT: Monomer. (By similarity).
SUBCELULAR LOCATION: Cytoplasmic (By similarity).
SINILARITY: Belongs to the malate synthase family. GlcB subfamily.
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                                                                    EDVLGLPQGTLKVGIMDEERRTTLNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGP
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LNARFALNAANARWGSLYDALYGTDTI PETEGAEKGSEYNKIRGDKVI AYARKFMDQAVP
                                         LSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQFAGYTGAAESPT-SVLLINHGLHIE
                                                                                                                                                                                                                                                                                                                   EVFEGIMDALFTGLIAIHGLKASDVNGPLINSRIGSIYIVKPWMGPAEVAFTCELFSRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Characterization of a chromosomal locus that affects pathogenicity Abodococcus fascians."; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate = S-malate.
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Vereecke D.M., Cornelis K., Van Montagu M., Bl Jaziri M., Holsters
Goethals K.;
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15-SE57,
15-SE2-2003 (Rel. 42, Last sequence update)
15-SE2-2003 (Rel. 42, Last sequence update)
15-SE2-2003 (Rel. 42, Last annotation update)
16-SE2-2003 (Rel. 42, Last annotation update)
16-SE3-2003 (Rel. 42, Last annotation update)
16-SE3-2003 (Rel. 42, Last annotation update)
16-SE3-2003 (Rel. 42, Last annotation update)
18-SE3-2003 (Rel. 42, Last annotation update)
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the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). CA CA 128 188 181 247 241 307 367 361 427 418 487 478 538 607 598 667 727 718 121 301 19 LNARFALNAANARWGSLYDALYGTDVI PETDGAEKGPTYNKVRGDKVIAYARKFLDDSVP ILIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLA EEVSKGGKTFTRAMMKDRTYTSVDGSELTLHGRSLLFVRNVGHLMTSDAILDADGNEVPE WVPSPTAATLHALHYHQVDVAAVQQGLAGKRRATIEQLLTIPLAKELAWAPDEIREEVDN NCOSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRHGVITSADVRA AAVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFE GIMDALFIGLIAIHGLKASDVNGPLINSRIGSIYIVKPKMHGPAEVAFTCELFSRVEDVL GILDALFTSLAGLHSLTPDNV---LSNSRTGSLYIVKPKMHGPDEVAFTAELFGRVEQVL GLPQNTMKIGIMDEERRTTVNLKACIKAAADRVVFINTGFLDRTGDEIHTSMEAGPMVRK GLPINILKVGIMDEERRITVNIKACIQAASERVVFINTGFLDRIGDEIHTSMEAGPVVRK GTMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAGASTA SLKRMAPVVDRONASDPTYKPLAPDFDINIAFQAASDLIFQGTSQPNGYTEPILHRRRRE 69 AQIDKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPV LSSGSFGDATGFTVQDGQLVVALPDKST-GLANPGQFAGYTGAAESPTSVLLINHGLHIE NSOSILGYVVRWIDHGVGCSKVPDINDIALMEDRATIRISSOFIANWIRHGIVTEEOVRE SLERMAPLVDRQNAGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTEPILHRRRRE 9 TDRVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQ GKVDAWHGEHAGAEYDRAAYKAFLKEIGYLLDEPADFQIHTSGVDTEITTTAGPQLVVPV Gaps 4 724; HAMAP; MF_00641; -; 1.

InterPro; IPR001465; Malate_synthase.

InterPro; IPR006253; Malate_synthG.

Pfam; PF01274; Malate_synthG.

IGRPAMs; TIGR01345; malate_syn_G; 1.

ITARNEFAMS; TIGR01345; malate_syn_G; 1.

ACT_SITE 340 340 CATALYTIC BASE (BY SIMILARITY)

ACT_SITE 631 CATALYTIC ACID (BY SIMILARITY)

SEQUENCE 724 AA; 78609 MW; F889PE883890995E CRC64;

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LSSGSFGDATGFTVQDGQLVVALPDKS-TGLANPGQFAGYTGAAESPTSVLLINHGLHIE
                                                        11.1DPESQVGTTDRAGVKDV1LESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLA
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15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Malate synthase G (EC 2.3.3.9).
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Pseudomonadaceae; Pseudomonas.
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717 REFKAK 722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LNARFALNAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVP 188
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SEQUENCE FROM N.A.

SEQUENCE 15692 / PAO1;

MEDLINE=2043737; PubMed=10984043;

MEDLINE=2043737; PubMed=10984043;

MEDLINE=2043737; PubMed=10984043;

MEDLINE=2043737; PubMed=10984043;

MEDLINE=2043737; PubMed=10984043;

MEDLINE=2043737; PubMed=10984043;

MEDLINE=2047, Explain X.-Q.T., Hufnagle W.O., Kowalik D.J., Lagrou M., Acarber R.L., Golltry L., Tolentino B., Westbrock-Radman S., Yuan Y., Brody L.L., Coulter S.N., Folger W. Mestbrock-Radman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.-S., Wu Z., Paulisen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";

Nature 406:959-964(2000).

"L. CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate = S-malate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT: Monomer (By Similarity).
-!- SUBCELLUTAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TDRVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQ
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                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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CATALYTIC ACID (BY SIMILARITY).
3669670A9E38D391 CRC64;
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TIGRFAMs; TIGR01345; malate syn G; 1.
Transferase; Glyoxylate bypass; Tricarboxylic acid cycle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.4%; Score 2569; DB 1; Length 7 69.1%; Pred. No. 3.2e-136; cive 77; Mismatches 139; Indels
                                                                                   15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
115-SEP-2003 (Rel. 42, Last annotation update)
Malate synthase G (EC 2.3.3.9).
                                                        725 AA
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InterPro; IPR001465; Malate synthase.
InterPro; IPR006253; Malate synthG.
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HSSP; P37330; 1D8C.
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Best Local Similarity
Matches 502; Conserv
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ACT_SITE 340
ACT_SITE 631
                                                                                                                                                 GLCB OR PA0482.
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                                                          MASZ PSEAE
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        308 AAVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFE
                                                   417 VLGLPRNTLKVGIMDEERRTTVNLKACIKAAKDRVVFINTGFLDRTGDEIHTSMEAGAVV
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Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
Berinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,
Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
Eauber J., Stiepandic D., Hohelsel J., Straetz M., Heim S.,
Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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Environ. Microbiol. 4:799-808(2002).
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-!- SUBUNIT: Monomer (By similarity).
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FKAR
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                                                                                                                                                                                                                                                                                  AQIDKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPV 128
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                                                                                                                                                                                                                                                      9 TDRVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQ
                                                                                                                                                                                                                                                                                                    AKIDAWHQARKGQAHDAAAYKAFLQEIGYLLPQADDFQATTQNVDEEIAHMAGPQLVVPV
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SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: Belongs to the malate synthase family. GlcB subfamily
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                                                                                                                                                                                                    Length 725;
                                                                                                                                                            340 CATALYTIC BASE (BY SIMILARITY)
631 CATALYTIC ACID (BY SIMILARITY)
78346 MW, 8363F218E6116AE1 CRC64;
                                                                                                         EMBL; AEÒ16775; AAN65987.1; -.
TIGR; PP0356; -.
HAMAP; MF_00641; -; 1.
Transferase; Glyoxylate bypass; Tricarboxylic acid cycle;
                                                                                                                                                                                                  41.9%; Score 2541; DB 1; Length 7 67.1%; Pred. No. 1.2e-134; ive 95; Mismatches 139; Indels
                                                                                                                                                                                                                      486; Conservative
                                                                                                                                                            340
631
725 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- PATHWAY: Glyoxylate bypass; second step.
-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Artiguenave F.M., Delecu M., Vilagines R., Danglot C.;
"A functional glyoxylate bypass is mandatory for utilization of
alkanes by Pseudomonas fluorescens.";
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate = S-malate
                                                                                                                                                                                                                                                                                                                                                                                                              Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.
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HAWAP; MF 00641; -; 1.

InterPro; IPR001465; Malate_synthase.

InterPro; IRR00623; Malate_synthG.

Pfam; PF01274; Malate_synthGse; 1.

TIGRFAMs; TIGR01345; malate_synthG.

Transferase; Glyoxylate bypass; Tricarboxylic acid cycle.

Transferase; Glyoxylate bypass; Tricarboxylic acid cycle.

ACT SITE 340 CATALYTIC BASE (BY SIMILARITY).

ACT SITE 710 A31 CATALYTIC ACID (BY SIMILARITY).
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Local Similarity 66.7%; Pred. No. 3.4e-132;
les 483; Conservative 85; Mismatches 152;
                                                                                                                                                                          005137;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
Malate synthase G (EC 2.3.3.9).
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Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas fluorescens.
722
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MF 00641
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  242 IQIDASTPVGQTDAAGVKDVLMEAALTTIMDCEDSVAAVDADDKVVIYRNWLGLMKGDLA 301
                                                                                                                                                         GILDGLLTSLAAIHSLNG---NSSRKNSRTGSVYIVKPRMHGPESAAFTNELFGRIEDVL
                                                                                                                                                                                                                                          479 AAMKTEKWIGAYENWNVDIGLSTGLQGRAQIGKGMWAMPDLMAAMLEQKIAHPLAGANTA
                                                                                                                                                                                                                                                                                                                                                                                                                  -!- PATHWAY: Glyoxylate bypass; second step.
-!- SUBDMT: Monomer By similaticy).
-!- SUBCELLULAR LOCATION: Cycloplesmic (By similarity).
-!- SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
                                                                  302 BEVAKGGKTFTRIMNPDRVYTGVDGQDVTLHGRSLLFVRNVGHLMTIDAILDKAGNEVPE
                                                                                                                                GIMDALFTGLIAIHGLKASDVNGPLINSRTGSIYIVKPKWHGPAEVAFTCELFSRVEDVL
                                                                                                                                                                                                                   GLPQNTMKIGIMDEERRITVNLKACIKAAADRVVFINIGFLDRTGDEIHTSMEAGPMVRK
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                                             AAVDKDGTAFLRVLNRDRNYTAPGGQQFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFE
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"Complete sequence of Pseudomonas syringae.";
"Complete Sequence of Pseudomonas syringae.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Malate synthase G 1 (EC 2.3.3.9).
GLCB1 OR GLCB-1 OR PSPT00480.
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                                                                                                                                                                                                                                                                                                                                     62 AQIDAWHQSRAGQAHDASAYKAFLQEIGYLLPEAADFQITTQNVDEBIATMAGPQLVVPV
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                                                                                                                                                                                                                                                            TEYVQVGDLQVARVLFDFVQNEATPGTGVDAGAFWAGADQLIHDLAPKNKALLAQRDELQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               308 AAVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFE
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                                                                                                                                                                                      Gaps
                                                                                                                                                                                      4.
                                                                                                                                                    Length 725;
                                                                      CATALYTIC BASE (BY SIMILARITY)
CATALYTIC ACID (BY SIMILARITY)
F1993264E8083660 CRC64;
                                     Transferase, Glyoxylate bypass; Tricarboxylic acid cycle;
                                                                                                                                                                                      Indels
                                                                                                                                              41.1%; Score 2489; DB 1;
65.3%; Pred. No. 9.5e-132;
iive 97; Mismatches 150;
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Last annotation update)
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                                                                                                             79143 MW;
                                                                                                                                                                    Best Local Similarity 65.3
Matches 473; Conservative
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                                                                                             631
                                                                                                               725 AA;
                                                      Complete proteome.
ACT_SITE 340
ACT_SITE 631
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PSPT00480;
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Science 294:2317-2323(2001).
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Q8UJB5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LNARFALNAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVP 188
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                                                                                                                         MEDLINE=21082930; PubMed=11214968; MEDLINE=21082930; PubMed=11214968; MEDLINE=21082930; PubMed=11214968; MEDLINE=21082930; PubMed=11214968; Mendia T., Kankana Y., Sato T., Sasamoto S., Watanabo A., Idesawa K., Ishikawa A., Kawashina K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Moorizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Sugimoto M., Tabata S.; "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                           PATHWAY: Glyoxylate bypass; second step.
SUBUNTT: Monomer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TDRVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQ
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                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate = S-malate
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               GLCB OR MIR4664.
Mizobium loti (Mesorhizobium loti).
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC BASE (BY SIMILARITY)
CATALYTIC ACID (BY SIMILARITY)
65376311A7E1BFDF CRC64;
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InterPro; IPR001465; Malate_synthase.
InterPro; IPR006253; Malate_synthG.
IPR01274 PF01274; Malate_synthase; 1.
TIGR01345; Malate_syn G; 1.
Transferame; Glyoxylate bypass; Tricarboxylic acid cycle;
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synthase G (EC 2.3.3.9)
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Best Local Similarity 64.4%
                                                                                                                                                                                                                                                            Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
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629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
ACT_SITE 338
ACT_SITE 629
SEQUENCE 721 AA;
                                                                                                                FROM N.A
                                                                               NCBI TaxID=381;
                                                                                                                                                                                                                                                                              Res.
                                                                                                              SEQUENCE
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IMDALFTGLIAIHGLKASDV--NGPLINSRTGSIYIVKPKMHGPAEVAFTCELFSRVEDV
                                                                                                               LGMPRNIIKMGIMDEERRITVNLKEAIRAARERVVFINIGFLDRIGDEIHISMEAGEMIR
                                                                                                                                                                                                                                                                    AWVPSPTAATLHALHYHQVDVAAVQQGLAGKRATIEQLLTIPLAKELAWAPDEIREEVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASLERMAPLVDRONAGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTEPILHRRRR
                                                                                                                                                                             KGTMKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGWWTMTELMADMVETKIAQPRAGAST
                                                                                                                                                                                                                         KGDMKQAAWISAYEAWNVDTGLECGLAGHAQIGKGMWAMPDLMAAMLEQKIAHPKAGANT
                          NNCQSILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRHGVITSADVR
                                                                                                                                                                                                                                                                                                                                                                                                       596 NNAQGILGYVVRWIDQGVGCSKVPDINDVGLMEDRATLRISSQHIANWLRHKVCSEIQVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WEDLINE-2168856; PubMed=11743193;
Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R. Li M.-J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŗ.,
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Science 294:3232-2328 (2001).
-!- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate = S-malate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE=21608551; PubMed=11743194;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin I
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Mollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Protecobacteria; Alphaphroteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Malate synthase G (EC 2.3.3.9)
GLCB OR ATU0047 OR AGR_C_78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           731 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARFALNAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVPLS 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 SGSFGDATGFTVQDGQLVVALPDKSTGLANPGQ-FAGYTGAAESPTSVLLINHGLHIEIL 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDDWYRRHG-APADMDEYOSFLREIGYLLPEGSDFOVSTONVDPEIASIAGPOLVVPVMN 121
                                                                                           NAQGILGYVVRWVDQGVGCSKVPDINNIGLMEDRATLRISAQHMANWLRHGVVTEAQIIK
                                                             SLERMAPLVDRQNAGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTEPILHRRRRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 RVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PATHWAY: Glyoxylate bypass; second step.
SUBUNIT: Monomer. (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 RVDKNGLAIETVLHDFLVEEVLPGLAVDADKFFADFSAIVHDLAPKNCALLAKRDELQVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                = S-malate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AV059637; AAL17965.1; -.

R EMBL; AV059637; AAL17965.1; -.

R EMBL; AV059637; AAL17965.1; -.

R EMBL; AV059637; AAL17965.1; -.

R InterPro; IPR001465; Malate synthase.

DR InterPro; IPR001465; Malate synthase.

DR InterPro; IPR001345; Malate synthase; I.

R ITGREAMS; TIGR1345; Malate syn G; I.

TIGREAMS; TIGR1345; Malate syn G; I.

RW Transferase; Glyoxylate bypass; Tricarboxylic acid cycle.

ACT SITE 629 CATALYTIC ACID (BY SIMILARITY).

ACT SITE 729 629 CATALYTIC ACID (BY SIMILARITY).

ACT SITE 729 77 MW; 4E879906CFD64444 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhizobium leguminosarum (biovar viciae).
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Rhizobiaceae, Rhizobium/Agrobacterium group, Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ate synthase gene from Rhizobium leguminosarum.", nitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. CATALYTIC ACTIVITY: Acetyl-COA + H(2)O + glyoxylate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8e-125;
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Malate synthase G (EC 2.3.3.9).
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                                                                                                                                                                                                                                                                                                                                                                                                       723
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LKAKQA 730
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SEQUENCE FROM N.A.
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                                                                                                                                                                                      728
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                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    428 GLPQNTMKIGIMDEERRTTVNLKACIKAAADRVVFINTGFLDRTGDBIHTSMEAGPMVRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC BASE (BY SIMILARITY)
CATALYTIC ACID (BY SIMILARITY)
69F304D5D6F8EFFB CRC64;
                                                                                                                                                                                                                                                                                                                                                            EMBL; AE008979; AAL41078.1; ALT_INIT.
PMR1; AB007447; AAK85871.1; ALT_INIT.
PMR; A4D2582.
PIR; P97364; F97364.
PIR; P97364; F97364.
IN EMPRP; MR 00641; -1, 1.
InterPro; IPR006253; Malate_synthase.
InterPro; IPR006253; Malate_synthase.
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                                                                                                                                                                                                                                                                                                                PONTMKIGIMDEERRITVNLKACIKAAADRVVFINTGFLDRIGDEIHTSMEAGPMVRKGT 489
                                                                                                                                                                                                                                                                                                                                         MKSQPWILAYEDHNVDAGLAAGFSGRAQVGKGMWTMTELMADMVETKIAQPRAGASTAWV 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSPTAATLHALHYHQVDVAAVQQGLAGKRRATIEQLLTIPLAKELAWAPDEIREEVDNNC 609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QGILGYVVRWVDQGGGGKVPDINNVGLMEDRATLRISAQHMANWLHHKVVTEAQIIETM 658
IDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAAA 309
                                                                                                                                                                      -!- PATHWAY: Glyoxylate bypass; second step.
-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Malate synthas 66 (EC. 3.3.3)
6LCB OR R006c2 OR SMC02581.
Rhizoblum meliloti (Sinorhizoblum meliloti).
Radiceria; Proteobacteria; Alphaproteobacteria; Rhizoblale.
Rhizoblaceae; Sinorhizoblum/Ensifer group; Sinorhizoblum.
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MEDLINE=21396507; PubMed=11481430;
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between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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CATALYTIC ACID (BY SIMILARITY)
A0E95E8A5164BE58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length
                                                                                                                                                                                                                                           Pfam, PF01274; Malate synthase; 1.
TIGRFAMs; TIGR01345; malate_syn_G; 1.
Transferase; Glyoxylate bypass; Tricarboxylic acid cycle;
                                                                                                                                                                                                                                                                                                                                                                                                                            38.8%; Score 2351.5; DB 1
llarity 62.9%; Pred. No. 4.6e-124;
Conservative 94; Mismatches 169;
                                                                                                                                                                             HAMAP; MF 00641; -; 1.
InterPro; IPR001465; Malate_synthase.
InterPro; IPR006253; Malate_synthG.
                                                                                                                                                        EMBL; AL591782; CAC41449.1; -.
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78853 MW;
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ACT_SITE 338
ACT_SITE 629
SEQUENCE 723 AA;
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                                                                                                                                                                                                                                                                  DALFIGLIAIHGLKASDVNGPLINSRIGSIYIVKPKWHGPAEVAFTCELFSRVEDVLGLP 430
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                                                                                                        DXDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEGIM
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                                                                       DPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAAAV
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-!- SUBUNIT: Monomer (By similarity).
-!- SUBCINIT: MORGET (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
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MEDIINE=22247741; PubMed=12271122;

Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
Read T.D., Dodon R.J., Umayam L., Brinkac L.M., Beanan M.J.,
Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.
Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
Hoover D.L., Lindlar L.E., Halling S.M., Boyle S.M., Fraser C.M.;
"The Brucella suis genome reveals fundamental similarities between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RMAPLVDRQNAGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTEFILHRRRREFK
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. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate = S-malate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Malce synthase G (EC 2.3.3.9).
GLCB OR BR1648.
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                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=16M / APICC 21456 / Biotype 1;
MEDLINB=20020109; PubMed=1175668;
DelVecchio V.G., Kaparral V., Redkar R.J., Patra G., Mujer C., Los T.,
Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
Selkov E., Elzer P.H., Hagius S., O'Cellaghan D., Letesson J.-J.,
Haselkorn R., Kyrpides N., Overbeek R.;
"The genome sequence of the facultative intracellular pathogen
Brucella melitensis.";
Droc. Natl. Acad. Sci., U.S.A. 99:443-448(2002).
--- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate = S-malate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: Monomer (By Similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By Similarity).
SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 VSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQAQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 728;
                                                                                                                                                                                                                                                                                                           Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Brucellaceae, Brucella.
NCBI_TaxID=29459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR, AP2299, AF3299.

HAWAP; MF 00641; -; 1.

HAWAP; MF 006641; -; 1.

InterPro; IPR001465, Malate_syntha.

Pfam; PF01274; Malate_synthae, 1.

TIGRFAMS; TIGR01345; malate_syn_G; 1.

Transferase; Glyoxylate bypass; Tricarboxylic acid cycle;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.2%; Score 2318; DB 1; 61.8%; Pred. No. 3.4e-122; iive 97; Mismatches 174;
                                                                                                                                                                      (Rel. 42, Created)
(Rel. 42, last sequence update)
(Rel. 42, last annotation update)
nase G (EC 2.3.3.9).

    -!- PATHWAY: Glyoxylate bypass; second step.

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                                                                                                                          STANDARD;
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636
                                                                                                                                                                                                                                                                                              Brucella melitensis.
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ACT_SITE 345
                                                                                                                                                                                                                                           Malate synthase (
GLCB OR BMEI0380
       718 KAK
                                                                                                                                                                        L5-SEP-2003
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                                                                                                                                                                                                                      15-SEP-2003
                                                                                                                          MASZ BRUME
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SEQUENCE
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Matches
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SEQUENCE FROM N.A., SEQUENCE OF 1-10, AND CHARACTERIZATION.
STRAIN=ATC (21302 / DSM 20300 / NCIB 10025;
MEDINE=55111631; PubMed=781249;
Reinscheid D.J., Eikmanns B.J., Sahm H.;
"Malate synthase from Corynebacternium glutamicum: sequence and the gene and blochemical characterization of the enzyme.", Microbiology 140:3099-3108(1994).
             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Malate synthase G (EC 2.33.9)
GLCB OR ACEB OR CGL2329.
Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria, Actinobacteria, Actinobacteriade, Actinomycetales, Corynebacterineae, Corynebacterium.
                                                                                                                                                                                                                                             | [2]
SEQUENCE FROM N.A.
STRAIN=ATCC 13059 / AS019;
A Lee H.S., Sinskey A.J.;
T "Molecular characterization of aceB, a gene enc
T in Corynebacterium glutamicum.";
T in Corynebacterium glutamicum.";
XL J. Microbiol. Biotechnol. 4:256-263(1994).
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
                                                                                                                         NCBI_TaxID=1718;
                                                                                                                                                                                                                                                                                                                                                                                      Nakagawa S.;
    'n
 removed. Usage by and for commercial sut (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                      GKWADVAGLAVNDGKLEIRLTDGSATTLKDESQFKGYNGDAASPTNVLLAKHNMHVDIVI 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPTAATLHALHYHQVDVAAVQQGLAGKRRATIEQLLTIPLAKELAWAPDEIREEVDNNCQ 610
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CATALYTIC ACID (BY SIMILARITY)
F95669D002A14EDE CRC64;
                                                                  TIGR; BR1648; -. 1.
HAMAP; MF 00641; -; 1.
InterPro; IPR001465; Malate_synthase.
InterPro; IPR0006253; Malate_synthG.
Pfam; PF01274; Malate_synthase; 1.
TIGRFAMs; TIGR01145; malate_syn G; 1.
Transferase; Glyoxylate bypass; Tricarboxylic acid cycle;
modified and this statement is not remo
entities requires a license agreement (
or send an email to license@isb-sib.ch)
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636 636 C
728 AA; 79966 MW;
                                                        EMBL; AE014458; AAN30550.1;
                                                                                                                                                                                                                                                               443; Conservative
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ACT_SITE 345
ACT_SITE 636 6
SEQUENCE 728 AA;
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encoding malate synthase

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"Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate = S-malate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TERVDAGGMQVAKVLYDFVTEAVLPRVGVDAEKFWSGFAAIARDLTPRNRELLARRDELQ
                                                                                                                                                                         -!- SUBCELLUIAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the malate synthase family, GlcB subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 TDRVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQ
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                                                                                         -!- ENZYME REGULATION: Inhibited by oxalate, glycolate and ATP-!- PATHWAY: Glyoxylate bypass; second step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 738;
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SIMILARITY)
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InterPro; IPR01465; Malate_synthase.
InterPro; IPR06253; Malate_synthG.
Pfam; PF01274; Malate_synthase; 1.
TIGRRAMS; TIGR01345; malate syn_G; 1.
Transferase; Glyoxylate bypass; Tricarboxyllc acid cycle;
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61.3%; Pred. No. 1.5e-120;
cive 90; Mismatches 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AP005281; BAB99722.1; -. PIR; 140715; I40715.
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738 AA;
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RESULT 14 MASZ_CORGL ID MASZ_C

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    SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: Belongs to the malate synthase family. GlcB subfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              265 QIDPTHPIGKEDKTGLKDIILESAITTIMDFEDSVAAVDAEDKTLGYRNWFLLNTGELTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LNARFALNAANARWGSLYDALYGTDV1PETDGAEKGPTYNKVRGDKV1AYARKFLDDSVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 748;
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CATALYTIC ACID (BY SIMILARITY)
F9550473EC4E9A09 CRC64;
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HAMAP; MF 00641, -; 1.
InterPro; IPR001465; Malate synthase.
InterPro; IPR001653; Malate_synthG.
Ffam; PF01274; Malate synthase, 1.
TIGRPAMS; TIGR01915; malate syn G; 1.
TIGRPAMS; Glyoxylate bypāss; Tricarboxylic acid cycle;
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61.5%; Pred. No. 1.2e-119;
tive 90; Mismatches 182;
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ACT_SITE 362
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                                                                                                            LNARFALNAANARWGSLYDALYGTNAIPETDGAEKGKEYNPVRGCKVIEWGREFLDSVVP
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
Itkeo K., Sugimoto S.; Jene G. Corynebacterium efficiens YS-314.";
"The entire genomic sequence of Corynebacterium efficiens YS-314.";
Submitted (WAY-2002) to the EMBL/GenBank/DDBJ databases.
---- CATALYIIC ACTIVITY: Acetyl-CoA + H(2)O + glyoxylate = S-malate +
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Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=152794;
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Malate synthase G (EC 2.3.3.9).
GLCB OR MASZ OR CE2231.
Corynebacterium efficiens.
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Vereecke D.M., Cornelis K., Van Montagu M., El Jaziri M., Holsters M.,
Goethals K.,
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43.5%; Score 2634; DB 2; Length 724;
Best Local Similarity 69.0%; Pred. No. 3.2e-144;
Matches 499; Conservative 82; Mismatches 138; Indels 4
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Corynebacterineae; Nocardiaceae; Rhodococcus.
NCBI_TaxID=1828;
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STRAIN=ATCC 15692 / PAO1;

MEDLINE=C104373.7; PubMed=10984043;

Stroy T. F. Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou N. Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou N. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadnan S., Yuan Y., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Smith K.A., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";

Nature 406:959-964(2000).
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01-6AR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Malate synthase G.
GLCB OR PA0482.
Pseudomonas aeruginosa.
Pseudomonas aeruginosa.
Pseudomonas aeruginosa.
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Pseudomonas aeruginosa.
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YKA 721
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                                                                                                                                                                                                                                                                                                                                                         AQIDKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVPV
                                                                                                                                                                                                                                                                                                                                                                                                 62 AKIDGWHQARAGQAHDAVAYKAFLEEIGYLLPEAEDFQAGTQNVDDEIARMAGPQLVVPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                LNARFALNAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILIDPESQVGTTDRAGVKDVILESAITTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLA
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                                                                                                                                                                                                                                                                  9 TDRVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLIPQNQALLNARDELQ
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                                                                                                                                   725 AA; 78659 MW; 3669670A9E38D391 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                           42.4%; Score 2569; DB 16;
69.1%; Pred. No. 1.9e-140;
ive 77; Mismatches 139;
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HSSP, P3730; 1D8C.
InterPro; IPR001465; Malate_synthase.
InterPro; IPR001625; Malate_synthG.
Pfam; PF01274; Malate_synthase; 1.
TIGRFAMs; TIGR01345; malate_syn_G; 1.
CSCMPLE proteon?
SEQUENCE 725 AA; 78659 MW; 366967
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18,
23,
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Matches 502; Conservative
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128 VLNARFALNAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYARKFLDDSV 187
                           ASLERMAPLVDRONAGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTEPILHRRRR
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GLCB OR AUTU0047 OR AGK C. 78.

GLCB CATU0047 OR AGE C. 78.

Bacberium tumefaciens (strain C58 / ATCC 33970).

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

Rhizobiaceae; Rhizobium.
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Last annotation update)
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                                                                                                                                                                                                                                                             744 AA
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TIGRFAMs; TIGR01345; malate_syn_G; 1.
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Interpro, IPR006253; Malate synthG.
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01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2003 (TrEMBLrel. 23,
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SEQUENCE 744 AA;
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Best Local Simil
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SEQUENCE FROM N.A.
STRAIN-MAFF303099;
MEDLINE-21082930. PubMed=11214968;
MEDLINE-21082930. PubMed=11214968;
MEDLINE-21082930. PubMed=11214968;
MATANAPA T., Nakamura Y., Sato S., Aamizu E., Kato T., Sasamoto S., Aatanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Xiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Makayawa C., Kohara M., Matsumoto M., Matsuno A., Aakeuchi C., Yamada M., Tabata S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., Nakazaki N., Shimpo S., Sugimoto M., Tabata S., Nakazaki N., Shimpo S., Sugimoto M., Mochizuki Y., Nakashi S., Nakazaki N., Shimpo S., Sugimoto M., Tabata S., Nakata S., Interpro; IPR001465; Malate Synthase.

B. Interpro; IPR001465; Malate Synthase.

R. TIGRAMS; TIGR01345; Malate Synthase; 1.
R. TIGRAMS; TIGR01345; Malate Synthase; 2.
R. Complete Protecome.

C. SEQUENCE 721 AA; 78058 MW; 65376311A7E1BFDF CRC64;
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             Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
''OLB_TaxID=381;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.9%; Score 2416; DB 16;
64.4%; Pred. No. 1.4e-131;
live 86; Mismatches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 64.4%;
Matches 467; Conservative
  Malate synthase G.
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Professor FROM N.A.

REQUENCE FROM N.A.

MEDLINE=21608551; PubMed=11743194; Miller N., Blanchard M.,

Goodner B., Hinkle G., Gattung S., Miller N., Halling C., Mullin L.,

A Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,

Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,

Nollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,

Relangan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,

A Genome sequence of the plant pathogen and biotechnology agent

Agrobacterium tumefaciens C58.";

REMBL, AE008979; AA441078.1;

REMBL, AE0089971, AAK85871.1;
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68 QAQIDKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSGVDAEITTTAGPQLVVP
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                                       RVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDELQAQ
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01-DEC-2001 (TEBMBLrel. 19, Last sequence update)
01-MAR-2003 (TEBMBLrel. 23, Last annotation update)
Malate synthase G.
MASG.
Rhizobium leguminosarum (biovar viciae).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium.
NCBI_TaxID=387;
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Garcia de los Santos A., Hynes M.F.;
Garcia de los Santos A., Hynes M.F.;
"Malate synthase gene from Rhizobium leguminosarum.";
submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AX059637; AAL17965.1;
InterPro; IPR0014655.1;
InterPro; IPR006553; Malate synthase.
InterPro; IPR006553; Malate synthas.
FFG1274; Malate synthase; 1.
IIGREAMS; ITGR01345; malate synthase; 2.
IIGREAMS; TGG01345; malate synthase; 3.
SEQUENCE 723 AA; 79677 MW; ĀE879906CFD64444 CRC64;
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Matches 464, Conservative
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STRAIN=1021;
MEDLINE=21396507; PubMed=11481430;
Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Probable malate synthase G protein (EC 4.1.3.2).
GLCB OR R00062 OR SMC02581.
Brizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiacee;
Rhizobiacee; Sinorhizobium.
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Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.; "Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021.", Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882 (2001).
BMBL, AL59182; CAC41449.1; --
InterPro; IPR00465; Malate_synthase.
InterPro; IPR004653 Malate_synths.
Pfam; PP01774; Malate_synthase; 1
TIGRFAMs, TIGROL145; malate_synthg:
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38.8%; Score 2351.5; DB 16; Lengt
Best Local Similarity 62.9%; Pred. No. 7.6e-128;
Matches 455; Conservative 94; Mismatches 169; Indels
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SEQUENCE 723 AA; 78853
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Brucellaceae; Brucella.
NCBI_TaxID=29459;
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                                                                         Score 2318; DB 16;
Pred. No. 6.8e-126;
97; Mismatches 174;
            728
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InterPro; IPR006253; Malate_synthG.
Pfam; PF01274; Malate synthase; I
IIGRFAMs; TIGR01345; malate_syn_G; 1.
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STRAIN=16M / ATCC 23456 / Biotype 1;
MEDLINE=20020109; PubMed=11756688;
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nes 444; Conservative
        PRELIMINARY;
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Q8YIR3 / Q8YIR3 / 01-MAR-2002 (01-MAR-2002                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72
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SPTAATLHATHYHKIDVAAVQEKLKSRPRAKLDDILSVPVAVRPNWTPDDIQHEIDNNAQ 606
                                       SILGYVVRWVDQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRHGVITSADVRASLE 670
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                                                           RMAPLVDRQNAGDVAYRPMAPNFDDSIAFLAAQELILSGAQQPNGYTEFILHRRRREFK
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MEDLINE=2247741; PubMed=12271122;

REDLINE=22247741; PubMed=12271122;

Paulsen I.T., Seehadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,

Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,

Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,

Nelson W.C., Ayodelji B., Kraul M., Shetty J., Malek J., Van Aken S.E.

Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,

Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;

"The Brucella suis genome reveals fundamental similarities between animal and plant pathogens and symbionts.";

EMBL, AB014458; AAN30550.1;

EMBL, AB014458; AAN30550.1;
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Last annotation update)
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NCBL_TaxID=29461;
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443; Conserv
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Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
Uskoo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
Usuda Y., Sugimoto S.;
"The entire genomic sequence of Corynebacterium efficiens YS-314.";
Smbilli (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AP005221; BAC190411;
Lyase, Complete proteome.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=152794;
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Last annotation update)
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61.5%; Pred. No. 2.9e-123;
tive 90; Mismatches 182;
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01-MAR-2003 (TrEMBLrel. 23, L
Malate synthase (EC 4.1.3.2).
MASZ OR CE2231.
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GPQLVVPVLNARFALNAANARWGSLYDALYGTDVIPETDGAEKGPTYNKVRGDKVIAYAR 180
                                                                       173 DFLDHTFPLTSGSHHEALNYAIMDKQLVVTLESGKMTRLKDETQFVGYQGSQGDFSVILL
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                                                                                                                                                                                                                                                                                                                                                                                                          300 GLNKGDLAAAVDKDGTAFLRVLNRDRNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDAIVD
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
NCBI_TaxID=217992,
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MEDLINE=22388234; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch Rasko D., Buckles E.L. Liou S.-R., Boutin A., Hackett J., Smyhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome
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Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).

EMBL. AE016766, AAN82151.1;

Lyass; Complete protecme.

SEQUENCE 723 AA; 80440 MW; AAF740ESFE038F6F CRC64;
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SEQUENCE FROM N.A.

SEQUENCE TROM N.A.

SEQUENCE 125 / JCM 913;

MEDLINE=20512582; PubMed=11058132;

A Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,

Ruli F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,

Ruli F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,

Ruli F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,

Ruli F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,

Nucleic Resonance sequence of the alkaliphilic bacterium Bacillus

Ruli Alodurans and genomic sequence comparison with Bacillus subtilis.";

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Nucleic Acids Res. 28:4317,4331(2000).

Ruli Alodurans and genomic sequence somparison with Bacillus subtilis.";

Ruli Alodurans and genomic sequence somparison with Bacillus subtilis.";

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Matches
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Q9KB03
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MEDLINE=21128732; PubMed=11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Holavies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                               44663 MW; 4A3BA44D1CEEFE06 CRC64;
                                                                                                                                                                                                    "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
EMBL; AL583925; CAC31839.1; -.
Leproma, ML2323; -.
InterPro; IPR001048; Aa Kinase.
InterPro; IPR001341; Aspartate_kinase.
Pfam; PF0066; aakinase; 1.
Pfam; PF00696; aakinase; 1.
FIGRPAMS; TIGR00657; asp kinases; 1.
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25.5%; Score 1545.5; DB
Best Local Similarity 80.4%; Pred. No. 1.7e-81;
Matches 319; Conservative 18; Mismatches 43
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Complete protecms
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KSTPWIKAYERNNVLSGLFCGLRGKAQIGKGMWAMPDLMADMYSQKGDQLRAGANTAWVP
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                                                                                                                                                                                                            DEWHRSNPGPVKDKAAYKSFLRELGYLVPQPDHVTVETTGIDSEITSQAGPQLVVPAMNA
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                                                                                                                                                                                                                                                                                                                                  GSFGDATGFTVQDGQLVVALPD-KSTGLANPGQFAGYTGAAESPTSVLLINHGLHIEILI
                                                       Gaps
                                                       15;
                DB 16; Length 723;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                       Indels
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Last sequence update)
Last annotation update)
                                                       173;
              Query Match
35.8%; Score 2168.5; DB 16
Best Local Similarity 58.4%; Pred. No. 3.1e-117;
Matches 422; Conservative 113; Mismatches 173;
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ASK OR ML2323.
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DB 16; Length 421;

17;

43; Indels

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                                                                                                  ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA
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                              VQKYGGSSVADADRIRRVAERIVQTKKQGNDIVVVVSAMGDTTDDLLDLAQQVCPEPPAR
                                                                                                                                                                                                        LEEGRVVLVAGFQGVSQDTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP
749 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPR
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Aspartate kinase alpha subunit (EC 2.7.2.4) (Aspartokinase)
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989 IKDVPMEDPILIGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRRRQHRHGAAE---- 1043
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WEDLINE-99453302; PubMed=10521665;
Zhang W., Jiang W., Zhao G., Yang Y., Chiao J.;
The Sequence analysts and expression of the aspartokinase and aspartate
T semialdehyde dehydrogenase operon from rifamycin SV-producing /
T amycolatopsis mediterranel.";
T amycolatopsis mediterranel.";
T amycolatopsis mediterranel.";
T c. CATALYHIC ACTIVITY: ATP + L-ASPARTATE = ADP + 4-PHOSPHO-L-
ASPARTATE.

- CATALYHIC ACTIVITY: ATP + L-ASPARTOKINASE FAMILY.

- SPARTATE.

- SIMILARITY: BELONGS TO THE ASPARTOKINASE FAMILY.

E MBL, AF134837; AAD49557.1; -

INTERPRO, IPR001941; AASPARTOKINASE.

N INTERPRO; IPR001048; ASP Kin monofn.

INTERPRO; IPR001057; Glu_Skinase.

N INTERPRO; IPR001057; Glu_Skinase.

Pram; PF01842; ACT; 2.

PRAM; PR01842; ACT; 2.

PRAM; PR01842; ACT; 2.

TIGRRAMS; TIGRO055; asp Kinases; 1.

TIGRRAMS; TIGRO055; asp Kinases; 1.

TIGRRAMS; TIGRO055; asp Kinases; 1.

TIGRRAMS; TIGRO055; asp Kinases; 1.

R MARS; TARSGERSES.

KW KINASE; TARSGERSES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 IEEIPVEQALITGVAHDRSEAKITVTGVPDHTGAAARIFRVIA------DAEIDIDM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 749 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVSAMGDTTDDLLDLAQQVCPAPPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         809 ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           929 RIVRNARKLDTVTFEEMLEMAACGAKVLMLRCVEYARRHNIPVHVRSSYSDRPGTVVVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.9%; Score 1267.5; DB 2; Length 421; llarity 65.3%; Pred. No. 2.2e-65; Conservative 53; Mismatches 61; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EC 2.7.2.
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Corymebacterium crenatum.

Bacteria, Actinobacteria; Actinobacteridae; Actinomycetales;
Corymebacterineae; Corymebacteriaceae; Corymebacterium.

NCBI_TaxID=168810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421 AA; 44393 MW; 633D9C2D023145E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Feedback-resistant aspartokinase LysC alpha subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ą
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SEQUENCE FROM N.A.
STRAIN=CD945;
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Best Local Simi
Matches 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kinase; T;
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     989 IKDVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRRRQHRHGAAE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      749 VQKYGGSSVADAERIRRVAERIVATKKQGNDVVVVVSAMGDTTDDLLDLAQQVCPAPPPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                809 ELDMLLTAGERISNALVAMAIESLGAHARSFTGSQAGVITTGTHGNAKIIDVTPGRLQTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                               "Isolation and characterization of the aspartokinase and aspartate semilalebyked dehydrogenase genes from cephamycin C-producer Streptomyces clavuligerus.";

**Rieptomyces clavuligerus.";

**Thereis (2002), University of Middle Bast Technical University, Ank:
                                                                                                                                                     C. -! CATALYTIC ACTIVITY: ATP + L-ASPARTATE = ADP + 4-PHOSPHO-L-ASPARTATE.

C. -! SIMILARIY: BELONGS TO THE ASPARTOKINASE FAMILY.

C. -! SIMILARIY: BELONGS TO THE ASPARTOKINASE FAMILY.

DR INTERPRO; IPRO01948; AA KINASE.

DR INTERPRO; IPRO01941; ASPARTOKINASE.

DR INTERPRO; IPRO01941; ASPARTOKINASE.

DR INTERPRO; IPRO01057; Glu_5kinase.

DR INTERPRO; IPRO01057; Glu_5kinase.

DR Fam; PFO01842; ACT; 2.

DR PRINTS; PRO0474; GLUSKINASE.

PRINTS; PRO0474; GLUSKINASE.

DR TICRFAMS; TICRO0655; asp_kin_monofn; 1.

DR PROSITE; PS00324; ASPARTOKINĀSE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421;
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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Pseudonocardineae; Pseudonocardiaceae, Amycolatopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
21.0%; Score 1272.5; DB 2; Length
Best Local Similarity 66.1%; Pred. No. 1.1e-65;
Matches 257; Conservative 51; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9RQ25
GPRQ25
GPRQ25
GPRQ27
GPRQ27
G1-MAY-2000 (TEMBLrel. 13, Created)
01-MAY-2000 (TEMBLrel. 13, Last sequence update)
01-MAY-2003 (TEMBLrel. 23, Last annotation update)
Aspartokinase subunit A (EC 2.7.2.4) (Aspartate kinase)
ASKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44399 MW; 08262D81045735C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1099 MRSHPGVTATFCEALAAVGVNIELISTSE 1127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 AA;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=33910;
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1039 HGAAERLQGRGRQD-RHHLHLL--PQTSGPPPWKNWTRSETRSASTQLLYDDHIGKVSLI 1095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               809 ELDMILTAGERISNALVAMAIESLGAHARSFIGSQAGVITIGIHGNAKIIDVIPGRLQTA 868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEEGRVVLVAGFOGVSODTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIFSADP 928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 MEDIPVEEAVLTGVATDKSEAKVTVLGISDKPGEAAKVFRALADAEINIDMVLQNVSSVE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             305 DGTTDITFTCPRSDGRRAMEILKKPQVQG----NW-----TNVLYDDQVGKVSLV 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64
                                                                                                                                                                                                                                                                                                                                                                                                                                                               27; Gaps
Liu Y., Ding J., Wang J.;
"Cloning and sequence analysis of aspartokinase genes from Corynebacterium crenatum.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + L-ASPARTATE = ADP + 4-PHOSPHO-L-
                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                     58; Indels
                                                                                    ASPARATATE

ASPARATATE

ASPARATATE

1- SIMILARITY: BELCONGS TO THE ASPARTCKINASE FAMILY.

EMBL; AF414084; AALO7807.1; -.

InterPro; IPR0012912; ACT.

InterPro; IPR0012912; ACT.

InterPro; IPR0012913; ASPARTATE Exinase.

InterPro; IPR0012914; Aspartate Exinase.

InterPro; IPR0012915; ACT.

InterPro; IPR001291; ASPARIORES; 1.

ITGRFAMS; TIGR00657; asp kinases; 1.

ITGRFAMS; TIGR00656; asp kin monofn; 1.

PROSITE; PS001294; ASPARTOKINĀSE; 1.

Kinase; Transferase.

Kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                421 AA; 44738 MW; 473A19409C0215E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                20.3%; Score 1232.5; DB 2 64.3%; Pred. No. 2.3e-63; tive 55; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGMRSHPGVTATFCEALAAVGVNIELISTSE 1127
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Best Local Similarity 64.3%
Matches 252; Conservative
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Search completed: November 21, 2003, 16:08:15 Job time : 60.6698 secs

M. tuberculosis im Mycobacterium tube Mycobacterium tube M tuberculosis re M tuberculosis fus M tuberculosis fus M tuberculosis fus Mycobacterium 39 k Mycobacterium 19 k Mycobacterium tube M tuberculosis 38 Mycobacterium tube Mycobacterium t

Scoring table:

Searched:

Sequence:

Minimum DB Maximum DB

Database

Result

2 6 4 5 9 6 7 8 6

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OM protein

Run on:

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3..8
/label= Histidine tag
/note= "Nickel chelating region used for purifying
the fusion protein"
9..74
/label= Ra3_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TbF15; antigen; vaccine; tuberculosis; AIDS; His tag; Ra3; 38KD;
38-1; FL TbH4; acquired immunodeficiency disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= 38-1_region
525..983
/label= FL_TbH4_region
                                                                                                                                                                                                                                                                               AAE29719
AAU74590
AAE17583
AAM50733
AAR30090
                                                                                                                                                                                                                                                                                                                                                                     AAW32445
AAW32377
AAW81681
                                                                                                                                                                                                                                                                                                                                                                                                                          AAW64319
AAY38119
AAY38982
AAW81706
AAW64339
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ABU05988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU01901 standard; Protein; 983 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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WO200124820-A1
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Binding-site
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                                                                                                              November 21, 2003, 15:50:31 ; Search time 59.515 Seconds (without alignments) 2621.664 Million cell updates/sec
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1:_/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.
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Compugen Ltd
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Copyright (c) 1993 - 2003
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Listing first 45 summaries
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ANEVEAPMADPPTDVPITPCELTAAKNAAQQLVLSADNMREYLAAGAKERQRLATSLRNA
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                                                               601 AKAYGEVDEEAATALDNDGEGTVQAESAGAVGGDSSAELTDTPRVATAGEPNFMDLKEAA
                                                                                                      RKLETGDOGASLAHFADGWNTFNLTLOGDVKRFRGFDNWEGDAATACEASLDQORQWILH
                                                                                                                           MAKLSAAMAKQAQYVAQLHVWARREHPTYEDIVGLERLYAENPSARDQILPVYAEYQQRS
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                                             AKAYGEVDEEAATALDNDGEGTVQAESAGAVGGDSSAELTDTPRVATAGEPNFMDLKEAA
                                                                                                                                                                MAKLSAAMAKQAQYVAQLHVWARREHPTYEDIVGLERLYAENPSARDQILPVYAEYQQRS
                                                                                                                                                                                                                                                                                                         841 APMVPPTGSPGGLPADTAAQLTSAGREAALSGDVAVKAASLGGGGGGGVPSAPLGSAI
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Twardzik DR, Vedvick TS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tuberculosis fusion protein TbF-2
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96US-0730510.
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Reed SG, Skeiky YAW,
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N-PSDB; AAV64567.
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99US-0158425.
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07-OCT-1999;
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                                                                                                                                      Gaps
protein is used in a method for inducing protective immunity agai tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of TB
                                                                                                                                      116;
                                                                                                                                      Indels
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                                                                                                      53.2%; Score 2700; DB 19;
66.6%; Pred. No. 2.9e-158;
ive 27; Mismatches 153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This polypeptide comprises a fusion protein, designated TDF-2, composed of Mycobacterium tuberculosis antigens TDRa3 (see AAW64295), 38 kDa antigens (see AAW64322) and DDRP (see AAW64322). It was produced by PGC amplification (see AAV4450-57) of the appropriate antigen DNA sequences, cloning into an expression vector, and expression in E. coli. TDF-2 can be used for serodiagnosis of tuberculosis. The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAW64291-W64379) comprising antigenic or immunogenic portions of M. tuberculosis antigens, or fuelon proteins, DNA sequences encoding such polypeptides, recombinant expression vectors and host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient.
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infection
                                                                                                                                                                                                                                                                              infection; diagnosis; 38 kDa antigen; TbRa3; DPEP;
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Twardzik DR, Vedvick TS;
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and diagnosis of tuberculosis
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96US-0729622.
                                      standard; Protein;
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N-PSDB; AAV55801.
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Tb38-1; TbF-2.
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                                           ISFLDQASQRGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTPANQAISMIDGPAPDGY
                                                           ISFLDQASQRGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTPANQAISMIDGPAPDGY
                                                                              PIINYEYAIVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAVVKLSDALI
                                                                                             PIINYEYAIVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAVVKLSDALI
                                                                                                                 ATI SSAEMKTDAATLAQEAGNFERI SGDLKTQI DQVESTAGSLQGQWRGAAGTAAQAAVV
                                                                                                                                                                                                       PPAPATPVAPPPPAANTPNAQPGDPNAAPPPPADPNAPPPVIAPNAPQPVR-----
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DPEP; diagnosis; therapy;
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                                                                                                                                                                                                        This sequence represents a recombinant Mycobacterium tuberculosis tetra-antigen fusion protein, termed TDF-2, composed of the antigens TDR3, 39KD, TD38-1 and DPBP. The fusion protein is expressed in host cells using a vector carrying a polymucleotide (see AAZ20198) comprising the 4 coding sequences. The invention provides fusion proteins (see AAX2059-71) containing at least 2 M. tuberculosis antigens. The new fusion proteins and polymucleotides encoding them are useful as vaccines for preventing tuberculosis (claimed), for diagnosis (via in vitro assays or intradermal skin tests for detection of anti-M. tuberculosis antibodies), monitoring of detection of anti-M. tuberculosis antibodies), monitoring of effective immunogens than mixtures of the individual protein
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                                                                           New fusion proteins useful for diagnosis, prevention tuberculosis
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66.6%; Pred. No. 2.9e-158;
ive 27; Mismatches 153;
                                                                                                                                                            Claim 1; Fig 5G-J; 83pp; English.
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Best Local Similarity 66.6
Matches 591; Conservative
WPI; 1999-601610/51
N-PSDB; AAZ20198.
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GS 4	aim 37; Page 271-273; 299pp; English. In the present invention describes polypeptides comprising an interest in well and tuberculosis antigen (Ag). Also describes and fusion protein containing M. tuberculosis tuberculosis Ag's, DNAs encoding them, derived fusion protein can be used in pharmaceutical vaccines to generate a protective or therapeutic immune tuberculosis and as reagents in skin tests for diagnosis tuberculosis. Ag can induce proliferation of, or cytckine sk'r, T, B or natural killer cells and/or macrophages in berculosis-immune subjects. AA219249 to AA219460 and AA931 (Y39225 are used in the exemplification of the present invequence 802 AA; Match 53.2%; Score 2700; DB 20; Length 80; Local Similarity 66.6%; Pred, No. 2, 9e-158;

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                                                                                                                 61 KLEVSFKMRPAQPR-GSKPPSGSPETGAGGTVATTPASSPVTLAETGGTLLYPLFNLWG
                                                                                                                                                                 PAFHERYPNVTITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKGLMNIALAISA
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ANAPDAGPPORWFVVW-----LGTANNPVDKGAAKALAESIRPLVAPPPA---P
                                             420 ATISSAEMKTDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVV
                                                                                                   480 RFQEAANKQKQELDBISTNIRQAGVQYSRADEEQQQALSSQMGFV--PTTAASPPSTAAA
                                                                                                                                         541 ANEVEAPMADPPTDVPITPCELTAAKNAAQQLVLSADNMREYLAAGAKERQRLATSLRNA
                                                                                                                                                                                                                                  -----IDNPVGGFSFALPAGWVESDAAHFDYGSALLS-----KTTGDPPFP
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                                                                                                                                                                                                      501 AKAYGEVDEEAATALDNDGEGTVQAESAGAVGGDS-----SAELTDTPRVATAGEPNF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes novel recombinant antigens and their encodin
nucleic acids derived from Mycobacterium tuberculosis. The novel
polypeptides are useful for detecting M. tuberculosis infection in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antigen; diagnosis; detection; infection; antibody; immunisation;
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                                                                                                                                                                     538 PPAPATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPPVIAPNAPQPVR-
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Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 10; Page 316-318; 323pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag) Also described are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's. DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion tuberculosis-immune subjects, AAX19299 to AAX19460 and AAX39083 to AAX39225 are used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                        New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions
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                                                                                                                                                                                                                                                                 Houghton R;
, Vedvick TS;
   diagnosis; immunisation; vaccine; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.2%; Score 2700; DB 20;
66.6%; Pred. No. 2.9e-158;
iive 27; Mismatches 153;
                                                                                                                                                                                                                                                                 Hendrickson RC, Hc
YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 205-208; 299pp; English
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Lodes MJ, Reed SG, Skeiky
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                                                              tuberculosis.
                  immune response; skin test
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Best Local Similarity
Matches 591; Conserv
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   immunotherapy;
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biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed current vaccination strategies do not provide 100% immunity.
                                                                                                                                Indels 116;
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; Pred. No. 2.9e-158;
27; Mismatches 153;
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                                                                                                    antibody; immunisation;
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Reed SG, Skeiky YAW, Twardzik DR,
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                                                                                                      detection; infection;
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                                                                                                                                                                                                                                                                                                                                                                                                    antigenic
                                                                            tuberculosis fusion protein TbF-2
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                                                                                                                                                                                                                                                   98US-0072596
98US-0024753
                                                                                                                                                                                                                                                                                                                                                                                                    polypeptide comprising
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                                                 ATISSAEMKTDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVV
                                                                  RFQEAANKQKQELDEISTNIRQAGVQYSRADEEQQQALSSQMGFTQSQTVTVDQQEILNR
                                                                              541 ANEVEAPMADPPTDVPITPCELTAAKNAAQQLVLSADNMREYLAAGAKERQRLATSLRNA
                                                                                                                                                    ------IDNPVGGFSFALPAGWVESDAAHFDYGSALLS----KTTGDPPFP
                                                                                                                                                                     ------MDLKEAARKLETGDQGASLAHFADGWNTFNLTLQGDVKRFRGFD
                                                                                                                                                                                     GQPPPVANDTRIVLGRLDQKLYASAEATDSKAAA------RLGSDMGEF--YM
                                                                                                                                                                                                      NWEGDAATACEASLDQQRQWILHMAKLSAAMAKQAQYVAQLHVWARREHPTYEDIVGLER
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PIINYEYAIVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAVVKLSDALI
                                 ATISSAEMKTDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVV
                                                                                                                                     AKAYGEVDEBAATALDNDGEGTVQAESAGAVGGDS-----SAELTDTPRVATAGEPNF-
                                                                                                                                                                                                                      PYPGTRINOETVSLD------ANGVSGSASYYEVKFSDPSKPNGQIWTGVIGSPA
                                                                                                                    PPAPATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPPVIAPNAPOPVR-----
                                                                                                                                                                                                                                                                                                                                                                                                           TbF-2.
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                                                                                                                                                                                                                                                                                                                                                                                                   ubberculosis; Mycobacterium tuberculosis; immunogen; vaccine; TbRa3-38kD-Tb38-1-DPEP;
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97US-0942578.
98US-0025197.
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98US-0223040.
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SKEIKY Y A.
DILLON D C.
ALDERSON M.
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                                                                                                                                                                                                                                                                                                                                                                                                   Fusion protein; t
tuberculostatic;
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01-OCT-1997;
18-FEB-1998;
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30-DEC-1998;
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The invention relates to a purified polypeptide which induces an immune response of Mycobacterium tuberculosis. Polypeptides of the invention are useful for diagnosing, treating or preventing M. tuberculosis infection, particularly tuberculosis infection. In particular, the polypeptides are useful as a vaccine formulation with an adjuvant to afford long-term protection in animals against the development of tuberculosis. The protein coding sequence may be used to encode a protein product for use as an immunogen to induce and/or enhance an immune response to M. tuberculosis. This sequence represents an M. tuberculosis fusion protein of the invention.

Note: The specification states that this polypeptide is encoded by the polynucleotide shown in ABK14132.
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New fusion proteins of Mycobacterium tuberculosis antigens, usef
diagnosing, treating or preventing M. tuberculosis infection,
particularly as vaccine for treating or preventing tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 116;
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; Pred. No. 2.9e-158;
27; Mismatches 153;
                                                                                                         5G-J; 62pp; English
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Best Local Similarity 66.6'
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                                                                                                      Claim 1; Fig
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631 GOPPPVANDTRIVLGRLDOKLYASABATDSKAAA-------RLGSDMGEF--YM 675

WPI; 2002-171134/22

181 764 241 824 301 884 361

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362 GGGGGGVPSAPLGSAIGGAESVRPAGAGDIAGLGQGRAGGGAALGGGGMGMPMGAAHQGQ 421
                     122 VATAGEPNFMDLKEAARKLETGDQGASLAHFADGNNTFNLTLQGDVKRFRGFDNWEGDAA
                                                                                      TACEASLDQQRQWILHMAKLSAAMAKQAQYVAQLHVWARREHPTYEDIVGLERLYAENPS
                                                                                                                                ARDQILPVYAEYQQRSEKVLTEYNNKAALEPVNPPKPPPAIKIDPPPPPQEQGLIPGFLM
                                                                                                                                                               ARDQILPVYAEYQQRSEKVLTEYNNKAALEPVNPPKPPPAIKIDPPPPQEQGLIPGFLM
                                                                                                                                                                                                 PPSDGSGVTPGTGMPAAPMVPPTGSPGGLPADTAAQLTSAGREAAALSGDVAVKAASLG
                                                                                                                                                                                                                               302 PPSDGSGVTPGTGMPAAPMVPPTGSPGGCLPADTAAQLTSAGREAALSGDVAVKAASLG
                                                                                                                                                                                                                                                                  GGGGGGVPSAPLGSAIGGAESVRPAGAGDIAGLGQGRAGGGAALGGGGMGMPMGAAHQGQ
                                                                  TACEASLDQQRQWILHMAKLSAAMAKQAQYVAQLHVWARREHPTYEDIVGLERLYAENPS
VATAGEPNFMDLKEAARKLETGDQGASLAHFADGWNTFNLTLQGDVKRFRGFDNWEGDAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This polypeptide is the predicted amino acid sequence of Mycobacterium tuberculosis antigen TPH4-XPI. The sequence was deduced from a composite sequence (see AAV44440) of overlapping DNA clones TbH4 and XPI. TbH4 (see also AAW64319) was isolated from a M. tuberculosis strain H37Rv expression library and XPI from a M. tuberculosis Exchan expression library. Recombinant XPI protein was prepared. It stimulates cell proliferation and interferongamma production in T cells isolated from M. tuberculosis-immune donors. The invention relates to methods for diagnosing tuberculosis. It provides polypeptides (see AAW64291-W64379)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated Mycobacterium tuberculosis polypeptides and DNA - user to develop products for the detection of M. tuberculosis infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tuberculosis; infection; diagnosis; antigen; TbH-4; XP1
                                                                                                                                                                                                                                                                                                                                                        GGAKSKGSQQEDEALYTEDRAWTEAVIGNRRRQDSKESK 460
                                                                                                                                                                                                                                                                                                                                   GGAKSKGSQQEDEALYTEDRAWTEAVIGNRRRQDSKESK 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R, Lodes MJ;
Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis antigen TbH-4-XP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tuberculosis strain H37Rv.
tuberculosis strain Erdman.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Page 189-191; 250pp; English.
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96US-0729622.
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Bood SG. Skeiky YAW,
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Mycobacterium
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                                                                                                     | : |: || || || ANAPDAGPPORNFUVW-------LGTANNPVDKGAAKALAESIRPLVAPPPA---P 770
                                                                                  LYAENPSARDQILPVYAEYQQRSEKVLTEYNN-----KAALEPVNP-PKPPPAIKIDP 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                   NWEGDAATACEASLDQQRQWILHMAKLSAAMAKQAQYVAQLHVWARREHPTYEDIVGLER 757
                                                 676 PYPGTRINQETVSLD-----ANGVSGSASYYEVKFSDPSKPNGQIWTGVIGSPA 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method inducing protective immunity against tuberculosis (TB). This sequence be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TQSQTVTVDQQEIINRANEVEAPMADPPTDVPITPCELTAAKNAAQQLVLSADNMREYLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  Tuberculosis, immunogenic; soluble, antigen, protective immunity, TB; vaccine, pharmaceutical; infection; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
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                                                                                                                                                   810 PPPPQRQGLIPGFLMPPSDGSGVTPGTGMPAAPMVPPTGSPGGLPA 856
                                                                                                                                                                                   771 APAPAEPA-----PAPAGEVAP------TPTTPTPQRTLPA 802
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Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;
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46.8%; Score 2375; DB 19;
Best Local Similarity 100.0%; Pred. No. 1.6e-138;
Matches 459; Conservative 0; Mismatches 0;
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96US-0730510
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11-OCT-1996;
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                                                                                                                                                     Gaps
comprising antigenic or immunogenic portions of M. tuberculosis antigens, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonucleotide probes and primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tuberculosis, M. tuberculosis, antigen, immunogen, diagnosis, immunisation; vaccine, infection;
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                                                                                                                          Length
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                                                                                                                       Score 2375; DB 19;
Pred. No. 1.6e-138;
0; Mismatches 0;
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                                                                                                                                    Best Local Similarity 100.0%; P:
Matches 459; Conservative 0;
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                                                                                                                       46.8%;
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98US-0025197
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                                                                                                                                                                                      The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's. DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion tuberculosis-immune subjects. AZ19249 to AAZ19460 and AAX3983 to AAX39225 are used in the exemplification of the present invention.
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                                                                                                     New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions
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                                                                                                                                                                                                                                                                                                                                                                                                                                     46.8%; Score 2375; DB 20;
100.0%; Pred. No. 1.6e-138;
iive 0; Mismatches 0;
Campos-Neto A, Dillon DC, Hendrickson RC, Ho
Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                          Example 3; Page 174-175; 299pp; English
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Antigen; diagnosis; detection; infection; antibody; immunisation;

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AAY39225 standard; Protein; 652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                         This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 TOSOTVTVDOQEILNRANEVEAPMADPPTDVPITPCELTAAKNAAQQLVLSADNMREYLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VATAGEPNFMDLKEAARKLETGDQGASLAHFADGWNTFNLTLQGDVKRFRGFDNWEGDAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGGGGVPSAPLGSAIGGAESVRPAGAGDIAGLGQCRAGGGAALGGGGGMMPMGAAHQGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                         525 TQSQTVTVDQQEILNRANEVEAPMADPPTDVPITPCELTAAKNAAQQLVLSADNWREYLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     585 AGAKERQRLATSLRNAAKAYGEVDEBAATALDNDGEGTVQAESAGAVGGDSSAELTDTPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VATAGEPNFMDLKEAARKLETGDQGASLAHFADGWNTFNLTLQGDVKRFRGFDNWEGDAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARDQILPVYAEYQQRSEKVLTEYNNKAALEPVNPPKPPPAIKIDPPPPPQEQGLIPGFLM
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                            antigenic portions of M. tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                            Length 460;
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                                                                                                                                                                          Houghton R;
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                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
46.8%; Score 2375; DB 20;
Best Local Similarity 100.0%; Pred. No. 1.6e-138;
Matches 459; Conservative 0; Mismatches 0;
                                                                                                                                                                        Campos-Neto A, Dillon DC, Hendrickson RC, Hc
Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                   Example 3; Page 219-220; 323pp; English.
                                                                                           99WO-US03265
                                                                                                                 98US-0072596
98US-0024753
                                                                                                                                                                                                                                             New polypeptide comprising
                       Mycobacterium tuberculosis
                                                                                                                                                                                                            WPI; 1999-527416/44
                                                                                                                                                   (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                     460 AA;
 vaccine; immunity
                                                                                                                                                                                                                        N-PSDB; AAZ19138.
                                             WO9942118-A2
                                                                                           17-FEB-1999;
                                                                                                                 05-MAY-1998;
18-FEB-1998;
                                                                    26-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes polypeptides comprising an immunogenic are vaccines and fusion tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's, DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions of vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T. B or natural killer cells and/or marcophages in tuberculosis-immune subjects. AZI9249 to AAZI9460 and AAXI99083 to AAXI93225 are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGHHHHHHVIDIIGTSFTSWEQAABAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions
                                                                                                                  s; M. tuberculosis; antigen; immunogen;
immunisation; vaccine; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 652;
                                                         M. tuberculosis fusion protein TbF-8 amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Houghton R;
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48.5%; Pred. No. 3.2e-105;
tive 26; Mismatches 132;
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YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 37; Page 274-276; 299pp; English.
                                                                                                                      Mycobacterium tuberculosis; M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0072967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Campos-Neto A, Dillon DC,
Lodes MJ, Reed SG, Skeiky
                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US03268
                                                                                                                                                                                  immune response; skin test.
                                                                                                                                                                                                                                            Synthetic.
Mycobacterium tuberculosis.
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Best Local Similarity 48.5%
Matches 441; Conservative
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05-NOV-1999
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                                           N-PSDB; AAZ19248
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      GDTFLFTQYLSKODPEGWGKSPGFGTTVDFPAVPGALGENGNGGMVTGCAETPGCVAYIG
                                           ISFLDQASQRGLGEAQLGNSSGNFLLPDAQSIQAAAGFASKTPANQAISMIDGPAPDGY
                                                                       PIINYEYAIVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAVVKLSDALI
                                                                                                                                                                                                                                                       BFYMPYPGTRINQETVSLDANGVSGSASYYEV-----KFSDPSKPNGQIWTGV
                                                             PIINYEYAIVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAVVKLSDALI
                                                                                                                                                                      ANEVEAPMADPPTDVPITPCELTAAKNAAQOLVLSADN----MREYLAAGAKERQ----
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                         ISFLDQASQRGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTPANQAISMIDGPAPDGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antigen; diagnosis; detection; infection; antibody; immunisation;
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                                                                                                                 ATISSGG------GSGGGSGGSGGSVPTTAASPPSTA-
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18-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDTFLFTQYLSKQDPEGWGKSPGFGTTVDFPAVPGALGENGNGGMVTGCAETPGCVAYIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATISSAEMKTDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 KLEVSFKMRPAQPRCGSKPPSGSPETGAGAGTVATTPASSPVTLAETGSTLLYPLFNLWG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234 ISFLDQASQRGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTPANQAISMIDGPAPDGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIINYEYAIVNNRÇKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAVVKLSDALI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---RLATSLRNAAKAYGEVDEEAATALDND--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                              nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in blological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                                                                                                                                                                           tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 310;
                                                                                                                                                                                                                                                                                         invention describes novel recombinant antigens and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 652;
                           TS;
   Houghton R;
Vedvick
                                                                                                                                                                        Σ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.3%; Score 1839; DB 20;
48.5%; Pred. No. 3.2e-105;
ive 26; Mismatches 132;
                                                                                                                                                                        New polypeptide comprising antigenic portions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      397 PPPPAA-----ANTPNAOPG-----
                           DR,
Campos-Neto A, Dillon DC, Hendrickson RC,
Lodes MJ, Reed SG, Skeiky YAW, Twardzik
                                                                                                                                                                                                                              Example 10; Page 320-321; 323pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 48.5
Les 441; Conservative
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---KFSDPSKPNGQIWTGV

	Search completed: November 21, 2003, 16:03:20 Job time : 63.515 secs	earch com ob time :
-	644 PIPORTLPA 652	qa
	848 GSPGGDPA 856	λο.
	617	qq
	788 NNKAALEPVNPPKPPPAIKIDPPPPPQEQGLIPGFLMPPSDGSGVTPGTGMPAAPMVPPT 847	٠.
	601	Op QD
	728 MAKQAQYVAQLHVWARREHPTYEDIVGLERLYAENPSARDQILPVYAEYQQRSEKVLTEY 787	
	570 IGSPAANAPDAGPPQRWFVVWLGTANNPVDK	qq
	668 QGASLAHFADGWNTFNLTLQGDVKRFRGFDNWEGDAATACEASLDQQRQWILHMAKLSAA 727	λō

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Perfect score:

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Scoring table:

Searched:

2, Appli 117, App 117, App 112, App 112, App 121, App 379, Appl 73, Appl 73, Appl 74, Appl 74, Appl 77, Appl 77, Appl

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KLEVSFKMRPAQPRCGSKPPSGSPETGAGAGTVATTPASSPVTLAETGSTLLYPLFNLWG 120
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Sequence 4953, Ap
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Patent No. 6350456
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Patent No. 6350456

APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: OCMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
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CORRESSONDENCES: 241
CORRESSONDENCES: 241
CORPERSION AND ACTION OCOUNDIA CENter, 701 Fifth Avenue
CITY: Seattle
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STREET: Mashington
COUNTRY: USA
ZIP: Mashington
COUNTRY: USA
ZIP: BM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIN Release #1.0, Version #1.30
CURRENTING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENTING SYSTEM: DC-DOS/NS-DOS
SOFTWARE: O7-APR-1998
FILING DATE: 07-APR-1998
FILING DATE: 07-APR-1998
FILING DATE: Maki, David J.
REGISTRATION NUMBER: 210121.457
REGISTRATION NUMBER: 210121.457
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Best Local Similarity 66.6%; Pred. No. Se-187;
Matches 591; Conservative 27; Mismatches 153; Indels 116; Gaps
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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   amino acid
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US-09-056-556-214
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5072
1 MGHHHHHHVIDIIGTSPTSW......RAWTEAVIGNRRRQDSKESK 983
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1. /cgr2_6/ptodata/1/iaa/5A_COMB.pep:*

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3. /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4. /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5. /cgn2_6/ptodata/1/iaa/PcrUS_COMB.pep:*

5. /cgn2_6/ptodata/1/iaa/PcrUS_COMB.pep:*

6. /cgn2_6/ptodata/1/iaa/PcrUS_COMB.pep:*
                           GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
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US-09-072-596-184
US-09-072-596-370
US-08-818-111-148
US-08-818-111-148
US-09-056-556-155
US-09-056-556-148
US-09-072-596-148
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TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 209
SEQUENCE CHARACTERISTICS:
LENGTH: 802 amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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:: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
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120 119 180

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359 420 540

us-09-688-672a-54.rai

AKAYGEVDEBAATALDNDGEGTVQAESAGAVGGOSSAELTDTRAVATAGEDNP

Qy Dp	ਜ ਜ	MGHHHHHHVIDIIGTSPTSWEQAARAVORARDSVDDIRVARVIEQDWAVDSAGKITVRI 60
Qy Dp	61	KLEVSFKMRPAQPRCGSKPPSGSPETGAGAGTVATTPASSPVTLAETGSTLLYPLENLWG 120
Sy Dp	121	PAFHERYDNVTITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKGLMNIALAISA 180
<u>کې</u> ۾	181	QQVNYNLPGVSEHLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGS 240
, 6,	241	GDTPLFTQYLSKQDPGGMGKSPGFGTTVDFPAVPGALGENGNGGMVTGCAETPGCVAYIG 300
Q.Y D.b	301	ISFLDQASQRGLGEAQLGNSSGNFLLPDAQSIQAAAAGPASKTPANQAISMIDGPAPDGY 360
- 20 40	361	PIINYEYAIVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHPQPLPPAVVKLSDALI 420
% q	421	atissaemktdaatlaqeagnferisgdlktqidqvestagslqqqwrgaagtaaqaavv 480
oy Db	481	RFOBAANKOKOELDEISTNIRQAGVQYSRADEBOQOALSSOMGFTQSOTVTVDQOEILNR 540
& a	541 538	ANEVEAPMADPPTDVPITPCELTAAKNAAQQLVLSADNWREYLAAGAKERQRLATSLRNA 600
<i>ે</i> લ	601	AKAYGEVDEBAATALDNDGEGTVQAESAGAVGGDSSAELTDTPRVATAGEPNF- 653
ð á	n c	
a ò	698	VLGKLDQRLIASAEAIDSKAAAKLGSDWGEFIM O SLDQQRQWILHMAKLSAAMAKQAQYVAQLHVWARREHPIYEDIVGLER 7
Db	919	A
Qy Db	758	LYAENPSARDQILFUYAEYQQRSEKULTEYNNKAALEPUNP-PKPPPAIKIDP 809
Qy Db	810	PPPPQEQGLIPGFLMPPSDGSGVTPGTGMPAAPMVPPTGSPGGGLPA 856
RESULT 4 US-09-05(Sequent) Setent GENERA APPP APPP APPP APPP APPP APPP APPP A	S-556. Ce 18. No. (AL IN) LICAN, LICAN, LICAN, LICAN, SER OF SER	UULT 4 09-056-556-184 dequence 184, Application US/09056556 GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Skeiky, Yasir A.W. APPLICANT: Skeiky, Yasir A.W. APPLICANT: OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241 CORRESPONDENCE ADDRESS:

TREATMI

TUBERCULOSIS

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APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: ADDRESS: 350
CORRESPONDENCES: 350
CORRESPONDENCES: 350
ADDRESSEE: SEED and Purning
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER:
31,392
REGISTRATION NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE:
(206) 622-4900
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al Similarity 100.0%; Pred. No. 7.3e-164;
459; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                          6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 179:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 460 amino acids amino acid
                                                                                                                                                                                                                                                                      STREET: 6300 Columbia
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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Best Local Similarity
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US-09-072-596-179
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                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
ATCASSIFICATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 210121.457
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SOURCE: 1060 622-4900
TELEFAX: (206) 622-4910
TELEFAX: (206) 622-631
INFORMATION FOR SEQ ID NO: 184:
SEQUENCE CHARACTERISTICS:
TENGRAL FOR SEQ ID NO: 184:
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                      1: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
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TYPE: amino acid
STRANDEDNESS:
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Matches 459; Conservative
                                                                                    Washington
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                                                              Seattle
                                                                                                          USA
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                                                                                                        COUNTRY:
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ö 704 644 764 182 TACEASLDQQRQWILHMAKLSAAMAKQAQYVAQLHVWARREHPTYEDIVGLERLYAENPS 241 242 ARDQILPVYAEYQQRSEKVLTEYNNKAALEPVNPPKPPPAIKIDPPPPPQEQGLIPGFLM 301 PPSDGSGVTPGTGMPAAPMVPPTGSPGGGLPADTAAQLTSAGREAAALSGDVAVKAASLG 884 362 GGGGGGVPSAPLGSAIGGAESVRPAGAGDIAGLGQGRAGGGALGGGGMGMPMGAAHQGQ 421 61 AGAKERQRLATSLRNAAKAYGEVDEEAATALDNDGEGTVQAESAGAVGGDSSAELTDTPR 645 VATAGEPNFMDLKEAARKLETGDQGASLAHFADGWNTFNLTLQGDVKRFRGFDNWEGDAA 122 VATAGEPNFMDLKEAARKLETGDQGASLAHFADGWNTFNLTLQGDVKRFRGFDNWEGDAA PPSDGSGVTPGTGMPAAPMVPPTGSPGGGLPADTAAQLTSAGREAAALSGDVAVKAASLG GGGGGGVPSAPLGSAIGGAESVRPAGAGDIAGLGOGRAGGGAALGGGGMGMPMGAAHOGO 525 TQSQTVTVDQQEILNRANEVEAPMADPPTDVPITPCELTAAKNAAQQLVLSADNMREYLA 2 TOSOTVIVDOQEILNRANEVEAPMADPPTDVPITPCELTAAKNAAQQLVLSADNMREYLA 585 ACAKERORLATSLRNAAKAYGEVDEEAATALDNDGEGTVQAESAGAVGGDSSAELTDTPR TACEASLDQQRQWILHMAKLSAAMAKQAQYVAQLHVWARREHPTYEDIVGLERLYAENPS 765 ARDQILPVYAEYQQRSEKVLTEYNNKAALEPVNPPKPPPAIKIDPPPPPQEQGLIPGFLM Gaps 0 Length 460; 0; Indels 302 885

Sequence 179, Application US/09072596; Patent No. 6458366; GENERAL INFORMATION:
APPLICANT: Reed, Steven G.

RESULT 5 US-09-072-596-179

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   241 GDTFLFTQYLSKQDPEGWGKSPGFGTTVDFPAVPGALGENGNGGMVTGCAETPGCVAYIG 300
                                          174 GDTFLFTQYLSKQDPEGWGKSPGFGTTVDFPAVPGALGENGNGGMVTGCAETPGCVAYIG
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                                                                                                                                                             234 ISFLDQASQRGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTPANQAISMIDGPAPDGY
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                                                                                                                                                                                                                                                                                                                                             ATISSAEMKTDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVV
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APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghten, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twandark, Daniel R.
TITLE OF INVENTION: CAMPONDED AND METITLE OF INVENTION: CAMPONDED STREET: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-818-112-153
; Sequence 153, Application US/08818112
; Patent No. 6290969
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STATE: Washing
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                                                                                                                                                                                                                                                                       APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Twedrick, Thomas S.
APPLICANT: Twedrick, Daniel R.
APPLICANT: Twentickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 310;
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STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle Columbia Center, 701 Fifth Avenue
CITY: Seattle Columbia Center, 701 Fifth Avenue
CUTY: Seattle Columbia Center, 701 Fifth Avenue
STATE: Washington
COUNTY: USA
ZIP: 98104-7092
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: BATCATON PATA:
APPLICATION PATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: US/09/072,596
FILING DATE: US/09/072,596
FILING DATE: US/09/072,596
FILING DATE: US/09/072,596
FILING DATE: US/09/072,596
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945 GGAKSKGSQQEDEALYTEDRAWTEAVIGNRRRQDSKESK 983
                                 422 GGAKSKGSQCEDEALYTEDRAWTEAVIGNRRRQDSKESK 460
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                                                                                                                                                                                            Sequence 350, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEED and BERRY LLP
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INFORMATION FOR SEQ ID NO: 350:
SEQUENCE CHARACTERISTICS:
LENGTH: 652 amino acids
TYPE: amino acids
STRANDEDNESS: single
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MOLECULE TYPE: protein
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Best Local Similarity
                                                                                                                                                                      US-09-072-596-350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-072-596-350
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MOLECULE TYPE: protein
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US-09-056-556-153
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Patent No. 6338652

GENERAL INPORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Vedvick, Thomas S.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, 140mas S.
APPLICANT: CAMPOINDS AND METHODS FOR DIAGNOSIS OF TOWNER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
CLASSIFICATION: 42-1997
CLASSIFICATION: 42-1997
ATTORNEY/AGENT INFORMATION:
NAME: Maxi, David J.
REGISTRATION NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-600
TELEPHONE: (206) 682-601
INFORMATION FOR SEQ ID NO: 153:
SEQUENCE CHARACTERISTICS:
TENERAL 374 amino acids
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Pred. No. 1.3e-124;
3; Mismatches 9;
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95.2%;
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Best Local Similarity 95.2
Matches 355; Conservative
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US-08-818-111-148
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Patent No. 6350456
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Steid, Yasir A.W.
APPLICANT: Steidy, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 374;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13.8AR-1997
CLASSIFICATION: 424
ATTONREY/AGENT INPORMATION:
NAME: MAKA, David J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.417C6
TELEFAN: (206) 682-6930
TELEFAN: (206) 682-6031
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
TEMPRATION FOR SEQ ID NO: 148:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1831; DB 4;
Pred. No. 1.3e-124;
3; Mismatches 9;
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95.2%;
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Matches 355; Conservative
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TREATM

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59 RIKLEVSFKMRPAQP-----RCGSKPPSGSPETGAGAGTVATTPASSPVTLAETGSTLL 112
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                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER EBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
CLASSIFICATION:
ATTORNEY APACEMT INFORMATION:
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 155:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TYPE: AMINO acids
TYPE: AMINO acids
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6300 Columbia Center, 701 Fifth Avenue
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Pred. No. 1.3e-124;
3; Mismatches 9;
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) Sequence 148, Application US/09072596
) Patent No. 6458366
) GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Offilon, Davin C.
APPLICANT: Offilon, Davin C.
APPLICANT: Houghton, Raymond;
APPLICANT: Houghton, Raymond;
APPLICANT: Vedvick, Thomas S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 95.2%;
Matches 355; Conservative
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                                                   Washington
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                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 YPLFNLWGPAFHERYPNVTITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKGLM 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 RIKLEVSFKMRPAQP-----RCGSKPPSGSPETGAGAGTVATTPASSPVTLAETGSTLL
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US-09-056-566-155
Sequence 155, Application US/09056556
Sequence 155, Application US/09056556
Setent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Compound C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                             COMPUTER: FIDOPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
ATTORNEY/APR-1001:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1831; DB 4;
Pred. No. 1.3e-124;
3; Mismatches 9;
                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 210121.457
REERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (206) 682-631
INFORMATION FOR SEQ ID NO: 153:
SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids
TYPE: amino acid
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Best Local Similarity 95.2
Matches 355, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-09-056-556-153
                        Washington
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                                             COUNTRY:
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113 YPLFNLWGPAFHERYPNVTITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKGLM 172
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                                      APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Wedvick, Thomas S.
APPLICANT: Wedvick, Thomas S.
APPLICANT: Wedvick, Daniel R.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Codes, Michael J.
APPLICANT: Codes, Michael J.
APPLICANT: Codes, Michael J.
APPLICANT: Codes, Michael J.
APPLICANT: Codes, Michael J.
APPLICANT: Codes, Michael J.
APPLICANT: Codes, Michael J.
APPLICANT: APPLICANT: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
36.1%; Score 1831; DB 4; Length 37
Best Local Similarity 95.2%; Pred. No. 1.3e-124;
Matches 355; Conservative 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                              701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMOMICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/072,596 FILING DATE: 05-MAY-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                       3: SEED and BERRY LLP 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                  CITY: Seattle
STATE: Washington
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                              INFORMATION
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US-09-072-596-150
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                                                                                                   TUBERCULOSIS
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6
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.1%; Score 1831; DB 4; Length 374; 95.2%; Pred. No. 1.3e-124; ive 3; Mismatches 9; Indels
                                                                                                                                                                                                      STREET: 6300 COLUMDIA CENTER, 701 Fifth Avenue
CITY: Seattle
STATE: washington
CONTRY: USA
ZIP: 98104-7092
COMPUTER: ERADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FLING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERICS:
INFORMATION FOR SEQ ID NO: 148:
                                                                                                                                                                     E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      374 amino acids
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Best Local Similarity 95.2
Matches 355; Conservative
                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and E
STREET: 6300 Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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US-09-072-596-150
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; Sequence 150, Application US/09072596 ; Patent No. 6458366

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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Baymond
APPLICANT: Houghton, Raymond
APPLICANT: Wedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112 FILING DATE: AT MAR-1997 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM-TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 89, Application US/08818112; Patent No. 6290969; GENERAL INFORMATION:
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US-08-818-112-89
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                                                                RESULT 13
US-09-118-426-5
i Sequence 5, Application US/09118426C
j Patent No. 6517839
j GENERAL INFORMATION:
APPLICANT: Modilin, Robert L.
APPLICANT: Modilin, Robert L.
TITLE OF INVENTION: T-CELL RESPONSE
FILE REFERENCE: 30435-44501
CURRENT APPLICATION NUMBER: US/09/118,426C
CURRENT APPLICATION NUMBER: US/09/118,426C
CURRENT APPLICATION NUMBER: 60/052,970
EARLIER APPLICATION NUMBER: 60/052,970
EARLIER FILING DATE: 1998-07-17
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 373
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
PUBLICATION INFORMATION:
JOURNAL: Infect. Immun.
SISSUE: 81
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Retent No. 6517839
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Modelin, Robert L.
APPLICANT: Libraty, Daniel H.
TITLE OF INVENTION: METHODS POR INDUCING INTERLEUKING-12 AND A TYPE 1/TH1
TITLE OF INVENTION: T-CELL RESPONSE
FILE REFERENCE: 30435.40501
CURRENT PILING DAMES: 1998-07-17
EARLIER APPLICATION NUMBER: 60/052,970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 KINGKVLAAMYQGTIKIWDDPQIAALNPGVNLPGTAVVPLHRSDGSGDTFLFTQYLSKQD
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362 VKLSDALIATISS 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; PAGES: 2481-
; DATE: 1989
US-09-118-426-5
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US-09-118-426-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 GTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKGLMNIALAISAQQVNYNLPGVSEHLK 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 GTGSGAGIAQAAAGIVNIGASDAYLSEGDMAAHKGLMNIALAISAQQVNYNLPGVSEHLK 121
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35.9%; Score 1820; DB 4; Length 351;
Best Local Similarity 100.0%; Pred. No. 7.4e-124;
Matches 350; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                    NAME/KEY: LIPID
LOCATION: (1)
OTHER INFORMATION: Xaa is N_ACYL DIGLYCERIDE cysteine
US-09-IB-41Se-6
EARLIER FILING DATE: 1998-07-17
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 351
TYPE: PAT
CRGANISM: Mycobacterium tuberculosis
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62 AGAKERQRLATSLRNAAKXYGEVDEBAATALDNDGEGTVQAESAGAVGGDSSAELTDTPR 121
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15.6%; Score 791; DB 3; Length 166;
Best Local Similarity 95.2%; Pred. No. 7.4e-50;
Matches 157; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 VATAGEPNFMDLKEAARKLETGDQGASLAHXGDGWNTXTLTLQGD 166
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ATTORNEY/AGENT INPORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
FELECOMMUNICATION INFORMATION:
FELEPHONE: (206) 622-4900
FELEPHONE: (206) 682-6031
FELEPHONE: C06) 682-6031
FELEPHONE: CAGO ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 annino acids
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Search completed: November 21, 2003, 16:11:43 Job time: 22.7299 secs

Sequence 40, Appl Sequence 99, Appl Sequence 90, Appl Sequence 115, Appl Sequence 639, Appl Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 73, Appl Sequence 73, Appl Sequence 73, Appl Sequence 74, Appl Sequence 77, Appl Sequence 77, Appl Sequence 77, Appl Sequence 77, Appl Sequence 77, Appl Sequence 77, Appl Sequence 78, Appl Sequence 77, Appl Sequence 69, Appl Sequence 69, Appli Sequence 69, Appli Sequence 69, Appli Sequence 69, Appli Sequence 69, Appli Sequence 69, Appli Sequence 69, Appli Sequence 69, Appli Sequence 69, Appli Sequence 69, Appli Sequence 69, Appli Sequence 69, Appli

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General 10, Application US/09287849

Sequence 10, Application US/09287849

Sequence 10, Application US/09287849

GENERAL INFORMATION:

APPLICANT: Rede, Seeven G.

APPLICANT: Dillon, Davin C.

APPLICANT: Allon, Davin C.

APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Autonio
APPLICANT: Campos-Neto, Autonio
APPLICANT: Campos-Neto, Autonio
APPLICANT: Campos-Neto, Autonio
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APPLICANT: Campos-Neto, Autonio
APPLICANT: Campos-Neto, Autonio
APPLICANT: Campos-Neto, Autonio
APPLICANT: 1999-02008

FILE REFERENCE: 1999-04-07

PRIOR APPLICATION NUMBER: US 09/026,556

PRIOR FILING DATE: 1998-04-07

PRIOR PILING DATE: 1998-04-07

PRIOR FILING DATE: 1998-04-07

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2 US-10-193-002-150
2 US-10-359-460-6
2 US-10-359-460-6
2 US-10-359-460-6
2 US-10-098-732A-39
2 US-10-098-732A-39
2 US-10-193-002-910
2 US-10-193-002-910
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ORGANISM: Artificial Sequence
         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       324
324
324
313.5
276
217.5
202.5
192
           Sequence 10, Appl
Sequence 214, App
Sequence 351, App
Sequence 209, App
Sequence 10, Appl
Sequence 119, Appl
Sequence 179, Appl
Sequence 355, Appl
Sequence 6, Appli
Sequence 6, Appli
Sequence 150, Appl
Sequence 151, Appli
Sequence 153, Appli
Sequence 153, Appli
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Sequence 153, Appli
                                                                                                                                                   November 21, 2003, 16:08:22 ; Search time 38.3392 Seconds (without alignments) 4680.740 Million cell updates/sec
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                                                                                                                                                                                                                                         US-09-688-672A-54
5072
1 MGHHHHHHVIDIIGTSPTSW......RAWTEAVIGNRRRQDSKESK 983
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1: /cgm2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgm2_6/ptodata/1/pubpaa/PCT_MBW_PUBL_pep:*

3: /cgm2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

4: /cgm2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

5: /cgm2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

6: /cgm2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

7: /cgm2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

8: /cgm2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

10: /cgm2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

11: /cgm2_6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*

10: /cgm2_6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*

11: /cgm2_6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*

12: /cgm2_6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*

13: /cgm2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

14: /cgm2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

15: /cgm2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

16: /cgm2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

17: /cgm2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

18: /cgm2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

19: /cgm2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

11: /cgm2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

12: /cgm2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

13: /cgm2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
                             GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-287-849-10

US-10-084-843-214

US-10-084-843-314

US-10-193-002-209

US-10-193-002-346

US-10-193-002-346

US-10-193-002-346

US-10-193-002-346

US-10-193-002-350

US-10-084-843-355

US-10-084-843-355

US-09-287-849-40
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US-10-084-843-155
US-10-193-002-148
                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                              666188 segs, 182559486 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                 - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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ALIGNMENTS

Score 2700; DB 9; Length 802, Pred. No. 6.1e-161;

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                                                                                                              KLEVSFKMRPAQPR-GSKPPSGSPETGAGAGTVATTPASSPVTLAETGSTLLYPLFNLWG 119
                                                                                                                                               PAFHERYPNVTITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKGLMNIALAISA 180
                                                                                                                                                                       PAFHERYPNVTITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKGLMNIALAISA 179
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                                              QQVNYNLPGVSEHLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGS
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                             1 MGHHHHHHVIDIIGTSPISWEQAAEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRI
   Gaps
 Indels 116;
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   153;
 27; Mismatches
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US-10-084-843-214
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Sequence 214, Application US/10084843
Publication No. US20030143243A1
GENERAL INFORMATION:
SPELICANT: Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond

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Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 802;
                                                                                                                                                                                                                                                                                                                                                            Version #1.30
                                                                                                                                                                            701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          %; Score 2700; DB 12;
%; Pred. No. 6.1e-161;
27; Mismatches 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Maki, David J.
REGIEGRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25.Feb-2002
CLASSIFICATION: <a href="checkbox">cunknown></a>
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 9810-4-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM FC Compatible
COMPUTER: PATEM: PC-DOS/MS-DOS
SOFTWARE: PATEMIN Release #1.0,
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TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 214:
05-10-084-843-214
                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (206) 682-6031
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66.6%;
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                                                                                                                                                                                                                  STATE: Washington
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Best Local Similarity 66.69
Matches 591; Conservative
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                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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                                                                              TITLE OF
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REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION.
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
                                                                               INFORMATION FOR SEQ ID NO: 351:
SEQUENCE CHARACTERISTICS:
JENGTH: 802 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLCGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 351:
US-10-084-843-351
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Best Local Similarity 66.6'
Matches 591, Conservative
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                                                                ATISSAEMKTDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVV 479
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                                                                                                                                                            RFQEAANKOKOELDEISTNIRQAGVOYSRADEEQQQALSSOMGFV--PTTAASPPSTAAA
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Skeiky, Yasir A.W.
Skeiky, Davin C.
Skeiky, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
Hendrickson, Ronald C.
AND DIAGNOSIS OF TUBERCULOSIS
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MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPATIEN: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                631 GOPPPVANDTRIVLGRLDOKLYASABATDSKAAA-----
                                                                                                                                                                                                                                                                                                     AKAYGEVDEEAATALDNDGEGTVOAESAGAVGGDS---
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APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: <UNKNOWN>
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ZIP: 98104-7092
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US-10-084-843-351
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GDTFLFTQYLSKQDPEGWGKSPGFGTTVDFPAVPGALGENGNGGMVTGCAETPGCVAYIG 300
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                                     QOVNYNLPGVSEHLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGS
                                                                                                                                                                                                                                                                                                                                                                                                                    ATISSAEMKTDAATLAQEAGNFERISGDLKTQIDOVESTAGSLQGQWRGAAGTAAQAAVV
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  QQVNYNL PGVSEHLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGS
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                                                                                                                                        GDTFLFTQYLSKQDPEGWGKSPGFGTTVDFPAVPGALGENGNGGWVTGCAETPGCVAYIG
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CORRESPONDENCE ADDRESS:
CARRESPONDENCE SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TUBERCULOSIS
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Houghton, Raymond
Vedvick, Thomas S.
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Publication No. US20030135026A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Skeiky, Yasir A.W. Dillon, Davin C.
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STATE: Washington
COUNTRY: USA
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US-10-193-002-346
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                                                                                                                                                                                                                                                       Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hondrickson, Ronald C.
OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 116;
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  856
                                          771 APAPAEPA------PAPAPAGEVAP------TPTTPTPQRTLPA 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISA
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
COMPUTER: ISM PC Compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION: CURKOWN>
810 PPPPQEQGLIPGFLMPPSDGSGVTPGTGMPAAPMVPPTGSPGGGLPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Maki, David J.
REGISTATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121,417C9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 209:
US-10-193-002-209
                                                                                                                                                                 Sequence 209, Application US/10193002
Publication No. US20030135026A1
GENERAL INFORMATION: APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 802 amino acids
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington
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STATE: Washing
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                                                                                                                                          US-10-193-002-209
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF
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PRIOR FILING DATE: 1997-10.01

PRIOR FILING DATE: 1997-10.01

PRIOR FILING DATE: 1997-0.01

PRIOR PEDICATION NUMBER: US 09/025,197

PRIOR PEDICATION NUMBER: US 09/02.55

PRIOR PEDICATION NUMBER: US 08/942,578

PRIOR PEDICATION NUMBER: US 09/02.55

PRIOR PEDICATION NUMBER: US 08/942,578

PRIOR PEDICATION NUMBER: US 08/942,578

PRIOR PEDICATION NUMBER: US 09/02.5197

PRIOR PEDICATION NUMBER: US 09/02.5197

PRIOR PEDICATION NUMBER: US 09/02.5197

PRIOR PEDICATION NUMBER: US 09/025,197

PRIOR PEDICATION NUMBER: US 09/025,197

PRIOR PEDICATION NUMBER: US 09/025,197

PRIOR PEDICATION NUMBER: US 09/025,197

PRIOR PEDICATION NUMBER: US 09/025,197

PRIOR PEDICATION NUMBER: US 09/025,197

PRIOR PEDICATION NUMBER: US 09/026,556

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                                                                                                                                                                                                                                                                                                       676 PYPGTRINQETUSLD-----ANGVSGSASYXEVKFSDPSKPNGQIWTGVIGSPA 724
                              601 AKAYGEVDEEAATALDNDGEGTVQAESAGAVGGDS-----SAELTDTPRVATAGEPNF-
                                                                                                                                             ------MDLKEAARKLETGDQGASLAHFADGWNTFNLTLQGDVKRFRGFD
                                                                                                                                                                                                   ----RLGSDMGEF--YM
                                                                                                                                                                                                                                                             NWEGDAATACEASLDQQRQWILHMAKLSAAMAKQAQYVAQLHVWARREHPTYEDIVGLER
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                                                                                       ----KTTGDPPFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116;
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                                                                                       ---IDNPVGGFSFALPAGWVESDAAHFDYGSALLS-
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llarity 66.6%; Pred. No. 6.1e-161;
Conservative 27; Mismatches 153;
                                                                                                                                                                                                631 GOPPPVANDTRIVLGRLDQKLYÁSAEATDSKAÁA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-359-460-10
Sequence 10, Application US/10359460
Publication No. US20030147911A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 591, Conserv
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LENGTH: 802
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               COMPUTER RADDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
OPTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION: ~Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 53.2%; Score 2700; DB 12; Best Local Similarity 66.6%; Pred. No. 6.1e-161; Matches 591; Conservative 27; Mismatches 153;
                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY, AGENT INFORMATION:
NAME: MAKI, DAVIG J.
REGISTRATION NUMBER: 31,392
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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// MOLECULE TYPE: protein
// SEQUENCE DESCRIPTION: SEQ ID NO: 346:
US-10-193-002-346
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INFORMATION FOR SEQ ID NO: 346:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 802 amino acids
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STRANDEDNESS: single
ZIP: 98104-7092
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                                                                                                                                                                                                                                                                                                                                                   NAME: Maki, David J.
REGIESTRATION NUMBER: 31,392
REPERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                             APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: <UNKNOWD>
                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: TRY PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 184:
US-10-084-843-184
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                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 460 amino acids
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                           CURRENT APPLICATION DATA:
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                       COUNTRY: USA
ZIP: 98104-7092
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US-10-193-002-179
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PAFHERYPNVIITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKGLMNIALALSA
                                                                                            QOVNYNLPGVSEHLKINGKVIAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 GDTFLFTQYLSKQDPEGWGKSPGFGTTVDFPAVPGALGENGNGGMVTGCAETPGCVAYIG
                                                                                                                                                                                               GDTFLFTQYLSKQDPEGWGKSPGFGTTVDFPAVPGALGENGNGGMVTGCAETPGCVAYIG
                                                                                                                                                                                                                                           ISFLDQASQRGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTPANQAISMIDGPAPDGY
                                                                                                                                                                                                                                                                     ISFLDQASQRGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTPANQAISMIDGPAPDGY
                                                                                                                                                                                                                                                                                                                                                                        PIINYEYAIVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAVVKLSDALI
                                                                                                                                                                                                                                                                                                                                                                                                                    ATISSAEMKTDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----IDNPVGGFSFALPAGWVESDAAHFDYGSALLS----KTTGDPPFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----MDLKEAARKLETGDQGASLAHFADGWNTFNLTLQGDVKRFRGFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  631 GQPPPVANDTRIVLGRLDQKLYASAEATDSKAAA------RLGSDMGEF--YM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LYAENPSARDQILPVYAEYQQRSEKVLTEYNN-----KAALEPVNP-PKPPPAIKIDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      725 ANAPDAGPPORWFVVW-----LGTANNPVDKGAAKALAESIRPLVAPPPA----P
                                                                   QQVNYNLPGVSEHLKLNGKVLAAMYQGT1KTWDDPQ1AALNPGVNLPGTAVVPLHRSDGS
                                                                                                                                                                                                                                                                                                                               PIINYEYAIVNNROKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAVVKLSDALI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  601 AKAYGEVDEEAATALDNDGEGTVQAESAGAVGGDS-----SAELTDTPRVATAGEPNF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       538 PPAPATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPVIAPNAPQPVR-----
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Skelky, Yasir A.W.
Davin C.
Campos-Neto, Artonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
Hendrickson, Ronald C.
OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPPPQEQGLIPGFLMPPSDGSGVTPGTGMPAAPMVPPTGSPGGGLPA
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STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
US-10-084-843-184
; Sequence 184, Application US/10084843
; Publication No. US20030143243A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
Skeiky, Yasir A.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYPGTRINGETUSLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF
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302 PPSDGSGVTPGTGMPAAPMVPPTGSPGGGLPADTAAQLTSAGREAAALSGDVAVKAASLG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                  885 GGGGGGVPSAPLGSAIGGAESVRPAGAGDIAGLGQGRAGGGAALGGGGMGMPMGAAHQGQ
                                                                                                  362 GGGGGGVPSAPLGSAIGGAESVRPAGAGDIAGLGGGRAGGGAALGGGGMGMPMGAAHQGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:

STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STREET: Mashington
COUNTRY: USA
COUNTRY: USA
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: BATTON: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084, 843
FILING DATE: S-Feb-2002
CLASSIFICATION: CURKNOWN>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                       Sequence 355, Application US/10084843

Publication No. US20030143243A1

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

Skeiky, Yasir A.W.

Campos-Neto, Antonio

Houghton, Raymond

Vedyick, Thomas S.

Twardzik, Daniel R.

Lodes, Michael J.

Hendrickson, Ronald C.

Hendrickson, Ronald C.

TILLE OF INVENTION: COMPOUNDS FOR INMUNOT
                                                                                                                                                                                     945 GGAKSKGSQQEDEALYTEDRAWTEAVIGNRRRQDSKESK 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.3%; Score 1839; DB 12;
48.5%; Pred. No. 4.4e-107;
tive 26; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEFRONE: (206) 622-4900
TELEFRAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STEANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: procein
SEQUENCE DESCRIPTION: SEQ ID NO: 355:
US-10-084-843-355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 652 amino acids TYPE: amino acid
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 35 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Best Local Similarity
Matches 441; Conserv
                                                                                                                                                                                                                                                                             RESULT 9
US-10-084-843-355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              585 AGAKERORLATSLRNAAKAYGEVDEEAATALDNDGEGTVQAESAGAVGGDSSAELTDTPR 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 AGAKERQRLATSLRNAAKAYGEVDEEAATALDNDGEGTVQAESAGAVGGDSSAELTDTPR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VATAGEPNFMDLKEAARKLETGDQGASLAHFADGWNTFNLTLQGDVKRFRGFDNWEGDAA 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 TACEASLDQQRQWILHMAKLSAAMAKQAQYVAQLHVWARREHPTYEDIVGLERLYAENPS 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      765 ARDQILPVYAEYQQRSEKVLTEYNNKAALEPVNPPKPPPAIKIDPPPPPQEQGLIPGFLM 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 ARDQILPVYAEYQQRSEKVLTEYNNKAALEPVNPPKPPPAIKIDPPPPPQEQGLIPGFLM 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPSDGSGVTPGTGMPAAPMVPPTGSPGGGLPADTAAQLTSAGREAAALSGDVAVKAASLG 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 VATAGEPNFMDLKEAARKLETGDQGASLAHFADGWNTFNLTLQGDVKRFRGFDNWEGDAA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACEASLDQQRQWILHMAKLSAAMAKQAQYVAQLHVWARREHPTYEDIVGLERLYAENPS 764
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                                                                                               Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Konald C.
TILLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS
                                                                                                                                                                                                                                                                                                                                                                                          CUNTRY: Search E
CUNTRY: USA

ZIP: 98104-7092

COMPUTER READBELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPETING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002

FILING DATE: 10-Jul-2002

CLASSIFICATION NUMBER: US/10/193,002

FILING DATE: 0-Jul-2002

CLASSIFICATION NUMBER: US/09/072,596

FILING DATE: 05-MAY-1998

ATTORNEY AGENT INFORMATION:
NAME: MARL, DAVIG J.
REGISTRATION NUMBER: 31,392

REGISTRATION NUMBER: 31,392

REGISTRATION NUMBER: 31,392

TELEFAX: (206) 622-4900

TELEFAX: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 46.8%; Score 2375; DB 12; Best Local Similarity 100.0%; Pred. No. 6.9e-141; Matches 459; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 179:
                          Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 460 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 179:
SEQUENCE CHARACTERISTICS:
  Reed, Steven G.
  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-193-002-179
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121 PAFHERYPNVTITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDWAAHKGLMNIALAISA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISFLDQASQRGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTPANQAISMIDGPAPDGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIINYEYAIVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAVVKLSDALI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGHHHHHHVIDIIGTSPTSWEQAAABAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 310;
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                               METHODS FOR DIAGNOSIS
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                                                                                                                                         ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
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REFERENCE/DOCKET NUMBER: 210121.417C9
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 350:
  Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND
TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 652 amino acids
TYPE: amino acid
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                                                                                   SEQUENCES: 350
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                                                                                   NUMBER OF SEQUENCES: 35 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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------GSKPPSGSPETGAGAGTVATTPASSPVTLAETGSTLLYPLKWG
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                                                                                      PAFHERYPNVTITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKGLMNIALAISA
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Publication No. US20030135026A1
GENERAL INFORMATION:
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonia Houghton, Raymond Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
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644 PTPQRTLPA 652
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US-10-193-002-350
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233 360

Best Local Similarity 95.2%; Pred. No. 6.6e-107; Matches 355; Conservative 3; Mismatches 9; Indels 6; Gaps	Qy 59 RIKLEVSFKMRPAQPRCGSKPPSGSPETGAGAGTVATTPASSPVTLABTGSTLL 112	QY 113 YPLFNLWGPAFHERYPNVTITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKGLM 172	QY 173 NIALAISAQQVNYNLPGVSEHLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVV 232	QY 233 PLHRSDGSGDTFLFTQYLSKQDPBGWGKSPGFGTTVDFPAVPGALGENGNGGMVTGCAET 292	QY 293 PGCVAYIGISFLDQASQRGLGBAQLGNSSGNFLLPDAQSIQAAAAGFASKTPANQAISMI 352	Oy 353 DGPAPDGYPIINYEYAIVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAV 412	Qy 413 VKLSDALIATISS 425 	Application US/09267849 Application US/09267849 RMATION: Reed, Stasir A.W. Billon, Davin C. Alderson, Mark A.W. Dillon, Davin C. Alderson, Antonio Corixa Corporation VERTION: Fusion Proteins of Mycobacterium tube VERTION: Fusion Proteins of Mycobacterium tube VERTION: Fusion Proteins NCE: 014058-009020US LICATION NUMBER: US/09/287,849 LICATION NUMBER: US/08/9112 CATION NUMBER: US/08/9112 CATION NUMBER: US/08/925,197 CATION NUMBER: US/08/925,197 CATION NUMBER: US/09/056,556 G DATE: 1998-04-07 CATION NUMBER: US/09/056,556 G DATE: 1998-12-30 CATION NUMBER: US/09/023,040	Query Match 36.1%; Score 1831; DB 9; Length 374; Best Local Similarity 95.2%; Pred. No. 6.6e-107; Matches 355; Conservative 3; Mismatches 9; Indels 6; Gaps 1;	Qy 59 RIKLEVSFKMRPAQPRCGSKPPSGSPETGAGAGTVATTPASSPVTLAETGSTLL 112
	OY 481 RFQEAANKOKGELDEISTNIRQAGVQYSRADEEQQQALSSQMGFTQSQTVTVDQQEILNR 540 DD 397 PPPPAAANTPNAQPGA11	OY 541 ANEVEAPWADPPTDVPITPCELTAAKNAAQQLVLSADNMRFYLAAGAKERQ 591	OY 592	Qy 619GEGTVQAESAGAVGGDSSAELTDTPRVATAGEPNFMDLKEAARKLETGD 667 Db 522 EFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKPNGQIWTGV 569	QY 668 QGASLAHFADGWNTFNLTLQGDVKRFRGFDNWEGDAATACEASLDQQRQWILHMAKLSAA 727	QY 728 MAKQAQYVAQLHVWARREHPTYEDIVGLERLYAENPSARDQILPVYAEYQQRSEKVLTEY 787 Db 601	QY 788 NNKAALEPVNPFKPPPAIKIDPPPPPQEQGLIPGFLMPPSDGSGUTPGTGMPAAPWVPPT 847 Db 617	PAPELICANT: INCRMENTION: APPLICANTION WHERE US OF PRINKE 199-00 TITLE OF INVENTION WHERE: US OS OS OS OS OS OF OS OF ON WHERE IN SPELICANT: APPLICANT: Canica Mark APPLICANT: Steiky, Yasir A.W. APPLICANT: Steiky, Yasir A.W. APPLICANT: Steiky, Yasir A.W. APPLICANT: Steiky, Yasir A.W. APPLICANT: Orderson, Antonio Mark APPLICANT: Canica Corporation TITLE OF INVENTION: Ension Protiens of Mycobacterium tuberculosis Antigens TITLE OF INVENTION WARE: US OS OS OS OS OS OS OS OS OS OS OS OS OS	; FEMIUKE: ; OTHER INFORMATION: Description of Artificial Sequence:tri-fusion US-09-287-849-6	Query Match 36.1%; Score 1831; DB 9; Length 374;

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352
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                                                                                                                                                                                       . 9
                                                                                                                                               Length 374;
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Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardisk, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOI
                                                                                                                                                                                       Indels
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COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: <a href="https://documents.com/brown">UNATOR: 108/10/084</a>,843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        701 Fifth Avenue
                                                                                                                                          Score 1831; DB 12;
Pred. No. 6.6e-107;
3; Mismatches 9;
                      TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 153:
US-10-084-843-153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-084-843-155; Sequence 155, Application US/10084843; Publication No. US20030143243A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
    LENGTH: 374 amino acids
                                                                                                                                          36.1%;
nilarity 95.2%;
Conservative 3
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                                                                                                                                                                   Similarity
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Matches
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                                                               YPLFNLWGPAFHERYPNVTITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKGLM 172
                                                                                              62 YPLFNLWGPAFHERYPNVTITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKGLM 121
                                                                                                                                               NIALAISAQQVNYNLPGVSEHLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVV 232
                                                                                                                                                                                       122 NIALAISAQQVNYNLPGVSEHLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVV 181
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PLHRSDGSGDTFLFTOYLSKODPEGWGKSPGFGTTVDFPAVPGALGENGNGGMVTGCAET
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Vecvic.,
Twardzik, Daniel A.
Lodes, Michael J.
Hendrickson, Ronald C.
Hendrickson, COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA

ZIP: 98104-705
ZOMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Maki, David J.
REGISTATION NUMBER: 31,392
REFRENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 153, Application US/10084843; Publication No. US20030143243A1
GENERAL INFORMATION:
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos Neto, Antonio Houghton, Raymond Vedvick, Thomas S.
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US-10-084-843-153
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62 YPLFNLWGPAFHERYPNVTITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKGLM 121
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                                 COMPUTER READBELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION CATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1831; DB 12;
Pred. No. 6.6e-107;
3; Mismatches 9;
                                                                                                                                                                                                                                                                             APPLICATION DATE: US/09/072,596
ATTORNEY/AGENT INPORMATION:
NAME: Maki, David J. 392
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
FORMATION POR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 148:
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Best Local Similarity 95.2%;
Matches 355; Conservative
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KIRLHTILLAVLTAAPLLLAAAGGGSKPPSGSPETGAGAGTVATTPASSPVTLAETGSTLL 61
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Skeiky, Yasir A.W.
Campon, Davin C.
Campon. Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 374;
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ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
           APPLICATION DATE: US/09/072,967
FILING DATE: 05-MAY-1998
FILING DATE: 05-MAY-1998
ATORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION INFORMATION:
FEGEROFICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPANCE: (206) 622-4900
TELEPANC: (206) 622-4900
TELEPANC: (206) 622-4900
TELEPANC: ATORNEY: ATORNEY:
SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 155:
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 36.1%; Score 1831; DB 12; Best Local Similarity 95.2%; Pred. No. 6.6e-107; Matches 355; Conservative 3; Mismatches 9;
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Publication No. US20030135026A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 350
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PRIOR APPLICATION DATA
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Indels

Length 374;

172

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292 241

232 181 412

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us-09-688-672a-54.rpr

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November 21, 2003, 15:57:31 ; Search time 20.507 Seconds (without alignments) 4609.825 Million cell updates/sec
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5072
1 MGHHHHHVIDIIGTSPTSW......RAWTBAVIGNRRQDSKESK 983
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	othetic	a	hypothetical prote	phosphate-binding	ABC transporter ph	able phospha	ABC phosphate tran	a)	a)		a	phosphate-binding	6	periplasmic phosph	apo	phosphate-binding	-bindin	hypothetical prote	phosphate-binding	PstS component of			a)	Φ	Ψ	phosphate-binding	periplasmic phosph	hypothetical prote	
SUMMARIES	ΩΙ		F70584	H70802	AG2377	G82595	H72756	AD1920	H75611	4	AI0499	H91211	H86057	BYECPR	AB0956	D75081	F64426	C70473	C90194	C87183	B87171	D70584	F70833	S74876	H70583	I64120	539852	D97110	H96597	A86840
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hypothetical prote	probable serine-th	phosphate ABC tran	phosphate ABC tran	probable large gly	hypothetical prote	conserved hypothet	hypothetical prote	3C3.18c protein -	hypothetical prote	phosphate ABC tran	tail length tape m	female sterile hom	CDA peptide synthe	hypothetical prote	hypothetical prote
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202.5 4	202 4	197.5 3		194 3		187.5			184	184	183.5	183 3	182.5	181	179.5

ALIGNMENTS

9 & 9 9 &	362 GGGGGVPSAPLGSALGGAESVRPAGAGDIAGLGQGRAGGGAALGGGGWGMPMGAAHQGQ 421 945 GGAKSKGSQQEDEALYTEDRAWTEAVIGNRRQDSKESK 983 	Qy S9 RIKLEVSFKWRPAQPRCGSKPPSGSPBTGAGAGTVATTPASSPVTLAETGSTLL 112 b :
RESULT 2 P70584 Phosphate Nyhternate Nyhternate C,Species C,Date: 1 C,Acternate R,Cole,Si R,Cole	() (1) (4) (5) (7) (8) (8) (9) (9) (9) (9) (9) (9) (9) (9) (9) (9	Db 62 YPLFNLWGPAFHERYPNVTITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDWAAHKGLM 121 QY 173 NIALAISAQQVNYNLPGVSEHLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVV 232 122 NIALAISAQQVNYNLPGVSEHLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVV 181 QY 233 PLHRSDGSGDTFLFTQYLSKQDPGWGKSPGFGTTVDFPAVPCALGENGGAVTGCAET 292 Db 182 PLHRSDGSGDTFLFTQYLSKQDPGGWGKSPGFGTTVDFPAVPCALGENGGAVTGCAET 241 QY 293 FGCVAYGISFLDQASORGLGBAGGKSPGFGTTVDFPAVPCALGENGGAVTGCAET 241 Db 242 PGCVAYGISFLDQASORGLGBAGGKSPGFGTTVDFPAVPCALGENGGAVTGCAET 241 QY 293 GGVAYIGISFLDQASORGLGBAGLGNSSGNFLLPDAQSIQAAAAGFASKTPANQAISMI 301 QY 353 DGPAPDGYPIINYEYAIVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAV 412 QY 413 VKLSDALIATISS 425 Db 362 VKLSDALIATISS 374
ATTELLY ATTELLY ATTELLY ANACCESS ANACCE	tuberculosis gene cluster encoding proteins of a phosphate tran MUID:97075926; PMID:8918249 80046; NID:9149987; PIDN:AAA25374.1; PID:9149988 lete nucleic acid sequence nor the complete translation are show lated the initiation codon GTG for residue 1 as Met E.B. 488, 1989 applied of antigenic domains of protein antigen b, a 38,000-molec applied of antigenic domains of protein antigen b, a 38,000-molec applied of antigenic domains of protein antigen b, a 38,000-molec applied by MUID:89307568; PMID:2545626 80; MUID:89307568; PMID:2545626 81, Lathigra, R.; Quiocho, F.A. 81958, 1994 81, MUID:94124544; PMID:8294447	rotein Rv3874 - Mycobacterium tubercul obacterium tuberculosis -1998 #sequence_revision 17-Jul-1998 # 70802 Brosch, R.; Parkhill, J.; Garnier, T.; Davies, R.; Devlin, K.; Feltwell, T.; A.; Rogers, J.; Rutter, S.; Seeger, K. 7-S44, 1998 res, R.; Sulston, J.E.; Taylor, K.; Whering the biology of Mycobacterium tumber: A70500; MUID:98295987; PMID:9634 70802 iminary; nucleic acid sequence not shoe: DNA coccis strain H37Rv
A, Molecule A, Molecule A, Andersen, Gen, Mic A, Title: Mic A, Reference A, Accession A, Molecule A, Residues: A, Residues	A,Rociecule type: protein A,Rociecule type: protein B,Radersen, A.B.; Ljungqvist, L.; Olsen, M. J. Gean. Microbiol. 136, 477-480, 1990 A,Fittle: Evidence that protein antigen b of Mycobacterium tuberculosis is involved in ph. A,Rocession: A45820, MUID:90362031, PMID:2118164 A,Rocession: A45820 A,Rociesion: A48820 A,Rociecule type: protein A,Residues: 'X'.27-28'X',30-34'XX',37 <and2> A,Rociecule type: confirmed presence of normal signal and absence of lipoprotein attachment A,Gonetics: A,Gonetics: A,Gonetics: A,Gonetics:</and2>	Ouery Match Query Match Best Local Similarity 100.0%; Pred. No. 55e-17; Length 100; Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 426 ABMKTDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEA 485 Db 2 ABMKTDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEA 61 Qy 486 ANKQKQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 524
C, Superfamily: C, Keywords: su C, Keywords: su F, 1-25/Domain: F, 26-374/Produ Query Match Best Local S. Matches 355	C.Superfamily: phosphate-repressible phosphate-binding protein C.Keywords: surface antigen C.Keywords: surface antigen F;1-25/Domain: signal sequence #status predicted <sig> F;26-374/Product: phosphate specific transporter S #status experimental <wat> Query Match Best Local Similarity 95.2%; Pred. No. 1.98-80; Matches 355; Conservative 3; Mismatches 9; Indels 6; Gaps 1;</wat></sig>	RESULT 4 AG2377 phosphate-binding periplasmic protein of phosphate ABC transporter all4575 [imported] - h phosphate-binding periplasmic protein of phosphate ABC transporter all4575 [imported] - h phosphate: Nostoc sp. PCC 7120 A,Note: Nostoc sp. strain PCC 7120 C,Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 C,Accession: AG3377 C,Accession: AG3377 R,Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

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C'Species: Xylella fastidiosa
C'Species: Xylella fastidiosa
C'Species: Xylella fastidiosa
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C'Species: Sep-2000
C'Species: Sep-2000
C'ACCESSION: GB2595
R'Sanonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A2515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Reference number: A2515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Residues: l-364 <SIN
A;Residues: l-364 <SIN
A;Residues: l-364 <SIN
A;Cross-references: GB.AE004028; GB:AE003849; NID:g9107266; PIDN:AAF84940.1; GSPDB:GNO1
A;Experimental source: strain 9a5c
A;Experimental source: strain 9a5c
A;Experimental source: strain 9a5c
B;Simpson, A.J.G.; Renach, E.C.; Arruda, P.; Abreu, F.A.; Carraro, D.M.; Carrer, H
B;Simpson, A.J.G.; Renach, C.; El-Dorry, H.; Ferdicani, A.P.; Ferreira, A.J.S.
Bueno, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, B.J.S.; Franca, S.C.; Franco, M.C.; Fronco, M.C.; Fronco, M.C.; Fronco, M.C.; Marchins, E.M.F.; Madeira, A.M.B.N.; Madeira, A.M.B.N.; Madeira, A.M.B.N.; Madeira, A.M.B.N.; Machins, A.M.B.N.; Machins, A.M.B.N.; Machins, A.M.B.N.; Machins, A.M.B.N.; Machins, A.M.B.N.; Machins, A.M.B.N.; Machins, A.M.B.N.; Machins, A.M.B.N.; Machins, A.M.B.N.; Machins, A.M.B.N.; Machins, A.M.B.N.; Machins, A.M.B.N.; Machins, A.M.B.N.; Machins, A.M.B.N.; Machins, A.M.B.N.; Machins, A.M.B.N.; Machins, A.M.B.N.; Machins, A.M.B.N.; Machins, A.M.B.N.; Machins, A.M.B.N.; Machins, A.M.B.N.; Machins, A.M.B.N.; Machins, A.M.B.N.; Machins, A.M.B.N.; Machins, A.M.B.N.; Machins, A.M.B.N.; Machins, A.M.B.N.; Ma
                                    Ana
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AG2377
A;Status: preliminary
A;Residues: preliminary
A;Residues: 1-392 «VUR»
A;Cross-references: GB:BA000019; PIDN:BAB76274.1; PID:g17133711; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics: A;Gene: al14575
C;Superfamily: phosphate-repressible phosphate-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184
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                                                                                                                                                                                                                                                                                                                                                                                                        29;
                                                                                                                                                                                                                                                                                                                                                     Length 392;
                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                9.5%; Score 482.5; DB 2;
33.7%; Pred. No. 4.1e-16;
live 64; Mismatches 151;
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takahayasi, Y.; Hino, Y.; Horikawa, H.; Tanaka, T.; Kudoh, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Vamazaki, J.; K. DNA, Res. G. 83-101, 1999

A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrt A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable phosphate-binding periplasmic protein APE0045 - Aeropyrum pernix (strain K1)
10;
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                                                                                                                                                                                                                                                                                                                                                             79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Species: Aeropyrum pernix
C.Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                             21 GCKPSNDNQSTGVSQDGNSTTPPSAEQTKSVKISGAGASFIYPLISQWSADYNAATGN-K
                                                                                                                                                                                                                                                                                                                                                                                                                                             SKVSAE-WKQKVGEGTSVQW---PGGVGGKGNEGVASYVQQIKGSIGYVELAY---ALQN
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                                                                                                                                                                                                                                                                                                                                                                                                                1TAQGTGSGAGIAQAAAGTVN1GASDAYLSEGDMAAHKGLMN1ALA1SAQQVNXNLPGVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252 KWSYTALQNAAGQWVQPSAESFAAAASNADBWSNAKDFNLVITNATGEA--AWPITATNFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESSGGSG----PAQ--VVLQGEGSTFIYPQIQAWSEEIKKTYPWITINYNPTGSGAGGS
                                                                                                                                                                                                                                                                                                          76 GSKPPSGSPETGAGAGTVATTPASS----PVTLAETGSTLLYPLFNLWGPAFHERYPNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAVVKLSDALIAT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 373;
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C;Superfamily: phosphate-repressible phosphate-binding protein
                                                                                                                                                                                                         9.1%; Score 463; DB 2; Length 36 larity 32.8%; Pred. No. 3.2e-15; Conservative 67; Mismatches 151; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: strain Kl
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Matches 112; Conservative
                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 116; Conserv
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A,Molecule type: DNA
A,Residues: 1-373 <KAW>
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S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A.Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A.Reference number: A75250; MUID:20036896; PMID:10567266
A.Acefession: H75611
A.Status: preliminary
A.Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 LYS-----KMFSEYKASNVNYQSVGSGGGKQILERTVDFAGSDNPMTDAQLGSAPGTLLH 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 IALAISAQQVNYNLPGVSEHLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVP 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 PLCGTSPVFGSLDAPLTKPRHTRRKKTLLGLSALVMISTAAAQGAITGA--GASFPYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 VPTAIGAVVPAYNLPGVTKPLNFDGPTLANIYLGKIKTWGDPAIAKLNPGVTIPPLPITV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     234 LHRSDGSGDTFLFTQYLSKQDPEGWGKSPGFGTTVDFPAVPGALGENGNGGMVTGCAETP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.8%; Score 445; DB 2; Length 403;
31.5%; Pred. No. 2.6e-14;
ive 60; Mismatches 157; Indels
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118; Conserv
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A;Gene: DRA0157
A;Map position: 2
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Best Local S:
Matches 118
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H75611
phosphate ABC transporter, periplasmic phosphate-binding protein - Deinococcus radiodura
phosphate ABC transporter, radiodurans
C,Species: Deinococcus radiodurans
C;Becies: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: H75611
R;Milte, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247
                                                                                                                      GNFLLPDAQSIQAAAAGFASKTP-----ANQAISMIDGPAPDGYPIINYEYAIVNNRQ 374
                                                                                                                                                                                                                                                                                                         264 DVFLKPSPEGAQAAASGAVQNLPDSPDDDWSTGYDAIIYAPGKDSYPITSWSFLLFYKQY 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:BA000019; PIDN:BAB72868.1; PID:g17130257; GSPDB:GN00179
A;Experimental source: strain PCC 7120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGSGDTFLFTQYLSKQDPEGWGK 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261 SPGFGTTVDFPAVPGALGENGNGGMVTGCAETPGCVAYIGISFLDQASQRGLGEAQLGNS 320
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                                                                    FGTTVDFP--AVPGALGENGNGGMVTGCAETPGCVAYIGISFLDQASQRGLGBAQLGNSS 321
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                                                                                                                                                                                                                                                                                                                                                                                                                  KDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAVVKLSDALIATIS 424
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---PETGAGAGT---VATTPASSPVTLAETGSTLLYP

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S.
A.Reference number: S74322, MUID:97061201; PMID:8905231
A.Reference number: S7422, MUID:97061201; PMID:8905231
A.Status: No.24423
A.Status: no.2161c acid sequence not shown; translation not shown
A.Residues: 1-383 <KRAN>
A.Residues: 1-383 <KRAN>
A.Residues: 1-383 <KRAN>
A.Rote: references: EMBL:D64001; GB:AB001339; NID:g1001102; PIDN:BAA10341.1; PID:g1001197
A.Rote: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C.Genetics:
A.Gene: pstS-1
C.Superfamily: phosphate-repressible phosphate-binding protein
phosphate-binding periplasmic protein pstS-1 - Synechocystis sp. (strain PCC 6803)

N.Alernate names: protein s110680

C,Alernate names: protein s110680

A,Variety: PCC 6803

A,Variety: PCC 6803

C,Date: 10.-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000

C,Accession: S74423

R;Kaneko, T.; Sato, S.; Kotami, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

R;Kaneko, T.; Sato, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tanaka, A.; Tan
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Best Local Similarity
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phosphate-binding periplasmic protein PstS [imported] - Escherichia coli (strain O157:H7, C;Species: Escherichia coli (cjate: 18-Jul-2001 #text_change 03-Aug-2001 C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 C;Accession: H91211 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. D)NA Res. 8, 11-22, 2001 A;Reference number sequence of enterohemorrhagic Escherichia coli O157:H7 and genor A;Reference number: A99629; MUID:21156211; PMID:11258796
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A;Residues: 1-346 <STO>
A;Cross-references: GB:AE005174; NID:g12518575; PIDN:AAG58924.1; GSPDB:GN00145; 'Skxperimental source: strain O157:H?, substrain EDL933
C;Ganetics:
A;Gene: pstS
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A,Molecule type: DNA
A,Residues: 1-346 <HAY>
A,Cross-references: GB:BA000007, PIDN:BAB38087.1, PID:gl3364139, GSPDB:GN00154
A,Experimental source: strain O157:H7, substrain RIMD 0509952
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C;Superfamily: phosphate-repressible phosphate-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
8.3%; Score 419; DB 2; Length 34
Best Local Similarity 32.5%; Pred. No. 3.7e-13;
Matches 109; Conservative 56; Mismatches 144; Indels
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| | | | | ::: : | | | | : FDWGYTHGAKQA--NELDYATLPAEVVE 327
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                                                                                  CGSKPPSG-SPETGAGAGTVATT--PASSPVTLAETGSTLLYPLFNLWGPAFHERYPNVT 131
                                                                                                                                                                                                                                                           190
                                                                                                                                                                                                                                                                                                             150 -EGLKLSQEALAGIMLGNITKWNDPKLVADNPDLTLPDRPITVVHRSDGSGTTAVFTWNL 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKQDPEGWGKSPGFGTTVDFPAVPGA-LGENGNGGMVTGCAETPGCVAYIGISFLDQASQ 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAMSPE-FKETIGDGKTVEWPTSKGKFIGGKGNEGVTAGIQONEGAIGYVEYGY---AIN 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTPANQAISMIDGPAPDGYPIINYEYAI 369
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                                                                                                                                                                                                                                                           ITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKG-LMNIALAISAQQVNYNLPGV
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8.7%; Score 440; DB 2; Length 34:
Best Local Similarity 33.4%; Pred. No. 3.7e-14;
Matches 110; Conservative 60; Mismatches 141; Indels
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69;
    Conservative
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periplasmic phosphate-binding protein [imported] - Salmonella enterica subsp. enterica scrovar Typhi (Species: Salmonella enterica subsp. enterica serovar Typhi (Species: Salmonella enterica subsp. enterica serovar Typhi (Species: Salmonella typhi (Species: Salmonella typhi (Species: Salmonella typhi (Species: O'-Nov-2001 #text_change 18-Nov-2002 (Species: O'-Nov-2001 #text_change 18-Nov-2002 (Species: Species: Nov-2001 #text_change 18-Nov-2002 (Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Spe
                                                                                 A/Gene: pstS; phoS

A/Map position: 84 min

C; Superfamily: phosphate-repressible phosphate-binding protein

C; Keywords: phosphate transport

F;1-25/Domain: signal sequence #status predicted <SIG>

F;26-346/Product: phosphate-repressible phosphate-binding protein #status experimental </br>
F;26-346/Product: phosphate repressible phosphate (Thr, Ser, Asp, Arg, Ser, Thr) #status experimental </br>
        C;Comment: This protein is a component of the inducible, high-affinity, phosphate-specifi
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261 SPGFGTTVDFPAVPGALGENGNGGMVTGCAETPGCVAYIGISFLDQASQRGLGEAQLGNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGNFLLPDAQSIQAAAAGFA-SKTPANQAISMIDGPAPDGYPIINYEYAIVNNRQKDAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----SPVTLAETGSTLLYPLFNLWGPAFHERYPNVTITAQGTGSGA
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                                                                                                                                                                                                                                                                                                                                                                                                          8.1%; Score 413; DB 1; Length 34: 32.2%; Pred. No. 7.2e-13; ive 56; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: STY3326
C;Superfamily: phosphate-repressible phosphate-binding protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            380 AQTLQAFLHWAITDGNKASFLDQVHFQPLPPAVVK 414
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32.6%; Pred. No. 9e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 32.2
Matches 108; Conservative
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R; Luecke, H.; Quiocho, F.A.

R; Luecke, H.; Quiocho, F.A.

R; Luecke, H.; Quiocho, F.A.

A; Title: High specificity of a phosphate transport protein determined by hydrogen bonds. A; Reference number: A30645; MUID:91015319; PMID:2215649

A; Contents: annotation; X-ray crystallography, 1.7 angstroms
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                                                                                                                                                                                                                                               TVATTPAS------SPVTLAETGSTLLYPLFNLWGPAFHERYPNVTITAQGTGSGA 141
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                                                                                                                                                                       Gaps
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C; Superfamily: phosphate-repressible phosphate-binding protein
                                                                                 ; Score 419; DB 2; Length 34; Pred. No. 3.7e-13; 56; Mismatches 144; Indels
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                                                                        8.3%;
                                                                                                                                                          Matches 109; Conservative
                                                                                                                            Similarity
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                                                                                     Query Match
Best Local
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phosphate abc transporter, periplasmic phosphate-binding protein (phox) PAB2365 - Pyrocd C; Species: Pyrococcus abyss:
C; Species: Pyrococcus abyss:
C; Species: O'-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C; Accession: D75081
R; anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A; Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru A; Rèference number: A75001
A; Réference number: A75001
A; Réference number: A75001
A; Réference number: B7801
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: SB: AJ248286; GB: AL096836; NID: G5458366; PIDN: CAB49953.1; PID: G545846
A; Experimental source: strain Orsay
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: phosphate-repressible phosphate-binding protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 VTITAQGTGSGAGIAQAAAGTVNIGASD-----AYLSEGDMAAHKGLMNIALAISA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 COVNYNLPGVSEHLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGS 240
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250 TELSF---AIEENLKVAALENKAGKFVKPNEETIKAAVANVKAFIPDPTEGYKEDLKQLL 306
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                                                                                                                                       261 SPGFGTTVDFPAVPGALGENGNGGMVTGCAETPGCVAYIGISFLDQASQRGLGEAQLGNS 320
                                                                                                                                                                                                                321 SGNFLLPDAQSIQAAAAGFA-SKTPANQAISMIDGPAPDGYPIINYEYAIVNNRQKDAAT 379
LAAMYOGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGSGDTFLFTQYLSKQDPEGWGK 260
                                                                                                                                                                                                                                                     238 DGKPVSPTEESFSNAAKGADWSKTFAQ---DLINQKGDDVWPITSTTFILVHKAQKKPEQ 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64;
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8.0%; Score 406; DB 2; Length 383;
Best Local Similarity 29.0%; Pred. No. 1.8e-12;
Matches 113; Conservative 64; Mismatches 149; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299 IGISFLDQASQRGLGBAQLGNSSGNFLLPDAQSIQAAAAGFASKTP-
                                                                                                                                                                                                                                                                                                                     380 AQTLOAFLHWAITDGNKASFLDQVHFQPLPPAVV 413
                                                                                                                                                                                                                                                                                                                                                    409 PPAVVKLSDALIATISSAEMKTDAATLAQE 438
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Search completed: November 21, 2003, 16:09:57 Job time: 21.507 secs

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Mon Nov 24 15:02:03 2003

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GenCore version 5.1.6
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November 21, 2003, 15:51:11 ; Search time 11.5909 Seconds (without alignments) 3988.226 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-09-688-672A-54 5072 1 MGHHHHHVIDIIGTSPTSW......RAWTEAVIGNRRRQDSKESK 983 Title: Perfect score: Seguence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 segs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Q933k8	15712 mycobact		xylella fa	rhiz	escherichi	Q9chj4 pasteurella	P45192 haemophilus	Q9kk89 mycobacteri	Q9cbe5 mycobacteri						P46338 bacillus su		P03736 bacteriopha					E	P35482 pseudomonas	Q90501 eptatretus	Д	Q09624 caenorhabdi	P07207 drosophila	×	Q9rt44 deinococcus	P39061 mus musculu	ratt	Q61282 mus musculu
SUMMARIES		ДE	MB48 MYCTU	PST1 MYCTU	CF10 MYCTU	PSTS_XYLFA	PSTS_RHILO	PSTS_ECOLI	PSTS_PASMU	PSTS HAEIN	PST3_MYCAV	PST3_MYCLE	PST2 MYCTU	PST3 MYCTU	RAA3_CHLRE	SEPA_EMENI	CF10_MYCLE	YQGG_BACSU	FSH_DROME	VMTH_LAMBD	TEGU_HSV11	VNUA_PRVKA	SBCC_RHOCA	NCR2_HUMAN	IF2_MYCLE	PPBL_PSEAE	TBFA_EPTST	CSP_FLACE	YS89 CAEEL	NOTC_DROME	BCSC_XANAC	SBCC_DEIRA	CA1H_MOUSE	MAPA_RAT	PGCA_MOUSE
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HFC1_MESAU ELS_RAT	CBP_MOUSE PGCA_HUMAN	CSP_PLACG	AK12_HUMAN	IF2 MYCTU	PHC1_MOUSE	ELS MOUSE	TPM4 DROME	ELS BOVIN	Y456_CHLTR
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ALIGNMENTS

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TIGR; MT0961; -.
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MIRDLINES-89307568, PubMed=2545626;
Andersen A. B., Hansen B.B.;
"Structure and mapping of antigenic domains of protein antigen b,
"Structure and mapping of Antigenic Mycobacterium tuberculosis.";
Infect. Immun. 57:2481-2488 (1989).
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P15712, 0.05868;
01-APR-1990 (Rel. 14, Last sequence update)
01-APR-2003 (Rel. 41, Last annotation update)
28-FBS-2003 (Rel. 41, Last annotation update)
Phosphate-binding protein 19 precursor (PBP-1) (PstS-1) (Protein antigen B) (PatS-1) (Protein PSTS1 OR PHOSI OR RV0934 OR MT0961 OR MTCY08D9.05C.
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Pred. No. 1.1e-98;
  not removed.
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            entities requires a license agreement ((or send an email to license@isb-sib.ch)
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                                            EMBL, AY029285, AAK31576.1, -.
EMBL, AL022120; CAA17973.1; -.
EMBL, AE007191, AAK48364.1; -.
PIR; G70803; G70803.
TIGR, MT3996; -.
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                                                                                                    Tuberculist; Rv3881c; -.
Antigen; Complete proteome.
DOMAIN 306 428
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Matches 459; Conserv
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FNBL outstation the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Pleischmann R.D., Alland D., Eisen J.A., Haft D., Hickey E.,
Peterson J. DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
MEDLINE 9839597; PubMed=9634230;

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Gas S., Bary C.E. III. Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Comor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd & Hornsby T., Jagels K., Krogh A., Mchean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Encomplete genome sequence.";

Complete genome sequence.";
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Tuberculist; Rv0934, -.
InterPro; IPR006059; SBP_bac_1.
Pfam, PF01547; SBP_bac_1; 1.
PROSITE; PS00013; PROKAR, LIPOPROTEIN; 1.
Phosphate transport; Transport; Membrane; Lipoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: Required for binding-protein-mediated phosphate
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N-ACYL DIGLYCERIDE (POTENTIAL).
6334968191FF38AA CRC64;
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EMBL; AE006981; AAK45208.1; -.
PIR; F70584; F70584.
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374 AA; 38243 MW;
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                                                                                                                                                                                                                    DGPAPDGYPIINYEYAIVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAV 361
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Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W.,
PGCVAYIGISFLDQASQRGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTPANQAISMI
                                                                                                                              PGCVAYIGISFLDQASQRGLGEAQLGNSSGNFLLPDAQSIQAAAGFASKTPANQAISMI
                                                                                                                                                                                    DGPAPDGYPIINYEYAIVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
10 kDa culture filtrate antigen cfpl0 (Secreted antigenic protein
MTSA-10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A Mycobacterium tuberculosis operon encoding ESAT-6 and a novel low-molecular-mass culture filtrate protein (CFP-10)."; Microbiology 144:3195-3203 (1998).
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"Rv3874 (mtsa-10) gene of a clinical isolate of Mycobacterium
tuberculosis from India.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE ESAT6 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis.
Bacteria, Actinobacteria; Actinobacteridae, Actinomycetales, Corynebacterineae, Mycobacterinaee, Mycobacterinaee, Mycobacterinae, NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Berthet F.-X., Rasmussen P.B., Rosenkrands I., Andersen P.,
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                     413 VKLSDALIATISS 425
                                                                                                                                                                                                                                                                                                                          362 VKLSDALIATISS 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          426 AEMKTDAATLAQEAGNFERISGDIKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AEMKTDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGGWRGAAGTAAQAAVVRFQEA
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Pred. No. 9.7e-16;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phosphate-binding periplasmic protein precursor (PBP).
Xylella fastidiosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 AA; 10663 MW; EBCAE6A996C5489D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        524
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                                                                                                                                                                                                                                                                                       EMBL, AF004671; AAC83445.1; -.
EMBL, AL022120; CAAL7966.1; -.
EMBL, AE007130; AAX48356.1; -.
EMBL, AF419854; AAL14999.1; -.
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INIT MET 0 0 0
SEQUENCE 99 AA, 10663 MW
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                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; H70802; H70802.
TIGR; MT3988; -.
Tuberculist; Rv3874; -.
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Best Local
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09PBK3;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSKPPSGSPETGAGAGTVATTPASS----PVTLAETGSTLLYFLFNLWGPAFHERYPNVT 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 E-HLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGSGDTFLFTQYL 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLGEAQLGNSSGNFLLPDAQSIQAAA--AGFASKTPANQAISMIDGPAPDGYPIINYEYA 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             252 KMSYTALONAAGOWVQPSAESFAAASNADWSNAKDFNLVITNATGEA--AWPITATNFI 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCKPSNDNQSTGVSQDGNSTTPPSAEQTKSVKISGAGASFIYPLISQWSADYNAATGN-K 79
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38736 MW; 8609CFAA1S9D4277 CRC64;
                                                                       "The genome sequence of the plant pathogen Xylella fastidiosa.";
Nature 406:151-159(2000).
de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H. Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L., Zago M.A., Zatz M., Meidanis J., Setubal J.C.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
                                                                                                                                                -!- FUNCTION: REQUIRED FOR BINDING-PROTEIN-MEDIATED PHOSPHATE TRANSPORT (BY SIMILARITY).
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4.1e-14;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Phosphate-binding periplasmic protein precursor (PBP).
PSTS OR MIL3723.
Rhizobium loti (Mesorhizobium loti).
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.1%; Score 463; DB 1; Length 36.
32.8%; Pred. No. 4.1e-14;
Live 67; Mismatches 151; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPRO06059; SBP_bac_1.
PERM; PRO1547; SBP_bac_1, DRO1547; SBP_BAC_1, DRO1547; PROSITE, PROKAR LIPOPROTEIN, 1.
PROSITE: PROMOPORT; Transport; Periplasmic; Signal;
                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Periplasmic (Potential).
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Best Local Similarity 32.89
Matches 116; Conservative
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364
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098FL2;
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DDT 28
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SEQUENCE FROM N.A.
STRAIN=MAPF3010999;
MEDLINE=21082930; PubMed=11214968;
MEDLINE=21082930; PubMed=11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Matanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Kishida Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., Nimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., Nimpo S., Sugimoto M., Tompolate genome structure of the nitrogen-fixing symbiotic bacterium DNA Res. 7:331-338(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTPASSPVTLAETGSTLLYPLFNLWGPAFHERYPNVTITAQGTGSGAGIAQAAAGTVNIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 ASDAYLSEGDMAAHKGLMNIALAISAQQVNYNLPGVSE-HLKLNGKVLAAMYQGTIKTWD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
PHOSPHATE-BINDING PERIPLASMIC PROTEIN.
2710D1BC0417574D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
                                                                                                                                                                                                                                                                                                              Res. 7:331-338(2000).
FUNCTION: REQUIRED FOR BINDING-PROTEIN-MEDIATED PHOSPHATE TRANSPORT (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51; Mismatches 149; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 346 AA.

BCOLI
BCOLI
BCOLI
P06128; P76744;
01-07AN-1988 (Rel. 06, Created)
01-17AN-1988 (Rel. 06, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phosphate-binding periplasmic protein precursor (PBP).
BSTS OR PHOS OR B3778 OR SF3727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AP003002; BAB50555.1; -.
HSSP: P06128; 1IXH.
INTERPRO; IPR06059; SBP_bac_1.
Pfam: PP01547; SBP_bac_1; 1.
Phosphate transport; Transport; Periplasmic; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Periplasmic (Potential).
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Pred. No. 2.7e-13;
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Matches 112; Conservative
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SPECIES=E.coli;
MEDLINE=84135579; PubMed=6321434;
MEDLINE=84135579; PubMed=6321434;
Surin B.P., Jans D.A., Fimmel A.L., Shaw D.C., Cox G.B., Rosenberg H.;
"Structural gene for the phosphate-repressible phosphate-binding
protein of Escherichia coli has its own promoter: complete nucleotide
sequence of the phoS gene.";
J. Bacteriol. 157:772-778 (1984).
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MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Xan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=E.coli, STRAIN=K12 / EMG2,
MEDLINE=97443975; PubMed=9298646;
Link A.J., Robison K., Church G.M.;
Comparing the predicted and observed properties of proteins encoded
in the genome of Eschericina coli K-12.";
Electrophoresis 18:1259-1313(1997).
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MEDLINE=97372887; PubMed=9228942;
Wang Z., Luecke H., Yao N., Quiocho F.A.;
"A low energy short hydrogen bond in very high resolution structures of protein receptor-phosphate complexes.";
Nat. Struct. Biol. 4:519-522(1997).
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MEDLINE=84135599; PubMed=6365894;
MEDLINE=84135599; PubMed=6365894;
Magota K., Otsuji M., Miki T., Horiuchi T., Teunasawa S., Kondo J.,
Sakiyama F., Amemura M., Morita T., Shinagawa H., Nakata A.;
"Nucleotide sequence of the phoS gene, the structural gene for the phosphate-binding protein of Escherichia coli.";
Dacteriol. 157:909-917(1984).
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SPECIESE=COOL; STRAIN=K12 / MG1655;
MEDLINE=93315143; PubMed=7686882;
Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.;
Burland Sequence and analysis of 136 kilobases of the Escherichia coli
genome: organizational symmetry around the origin of replication.";
Genomics 16:551-561(1999).
                   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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MEDLINE=98337779; PubNed=9671506;
Hishberg M., Henrick K., Haire L.L., Vasisht N., Brune M.,
Corrie J.E., Webb M.R.;
"Crystal structure of phosphate binding protein labeled with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (1.89 ANGSTROMS) OF MUTANT ASN-81
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
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MEDLINE=91015319; PubMed=2215649;
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Nature 347:402-406(1990).
                                                              NCBI_TaxID=562, 623;
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SEQUENCE FROM N.A.
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  Shigella flexneri
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coumarin fluorophore, a probe for inorganic phosphate.";
Biochemistry 37:10381-1038(1998).
-!- FUNCTION: THIS IS ONE OF THE PROTEINS REQUIRED FOR BINDING-PROTEIN
-MEDIATED PHOSPHATE TRANSPORT.
                                                                                                                                                                                                                                                                                                              EcoGene; EG10714; psts.
InterPro; IPR005673; Peri-phosph.
InterPro; IPR006059; SBP_bac_1.
Pfam; PF01547; SBP_bac_1.
IGRPAMS; TIGR00975; 3ā0107803; 1.
Phosphate transport; Transport; Periplasmic; Signal; 3D-structure;
                                                                                                                                                                                                                                                                                                                                                                                  PHOSPHATE-BINDING PERIPLASMIC PROTEIN
                                 -!- SUBCELLULAR LOCATION: Periplasmic.
-!- INDUCTION: BY PHOSPHATE DEPRIVATION AND SUBJECT TO POSITIVE CONTROL BY THE PHOB GENE PRODUCT AND TO NEGATIVE CONTROL BY PHOR GENE PRODUCT AND TO NEGATIVE CONTROL BY PHOR GENE PRODUCT
                                                                  -!- SIMILARITY: BELONGS TO THE PSTS FAMILY.
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L10328; AAA62079.1; -.
AE000449; AAC76751.1; -.
AE015380; AAN45173.1; -.
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PDB, 1DBP, 15-OCT-94.
PDB, 1DQU7, 11-JUL-96.
PDB, 1QU7, 11-JUL-96.
PDB, 1QU7, 11-JUL-96.
PDB, 1QU7, 11-JUL-96.
PDB, 1QU1, 11-JUL-96.
PDB, 1XK9, 04-FEB-98.
PDB, 1XX1, 22-OCT-97.
PDB, 1AX1, 22-OCT-97.
PDB, 1AX6, 23-MAR-99.
PDB, 1AX6, 14-OCT-98.
PDB, 1AX6, 14-OCT-98.
PDB, 1AX5, 14-OCT-98.
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STRAIN=RA (FW20 / ATCC 51907;
STRAIN=RA (FW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Karlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L. I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                    POTENTIAL.
PHOSPHATE-BINDING PERIPLASMIC PROTEIN.
6378650112CF9161 CRC64;
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Pasteurellaceae; Haemophilus.
FUNCTION: REQUIRED FOR BINDING-PROTEIN-MEDIATED PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                  344;
                                                                                                                                                                                                                                                                                                                                                                                 59; Mismatches 159; Indels
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Phosphate-binding periplasmic protein precursor (PBP)
PSTS OR HI1383.
                                                                                                                                                                                                                       P06128; 1IXH.
PF01547; SBP_bac_1; 1.
nate transport; Transport; Periplasmic; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       391 ITDGNKASFLDQVHFQPLPPAVVKLSDALIAT-ISSAEMKT
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             TRANSPORT (BY SIMILARITY).
SUBCELLULAR LOCATION: Periplasmic (Potential).
SIMILARITY: BELONGS TO THE PSTS FAMILY.
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Pred. No. 7.4e-12;
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01-NOV-1995 (Rel. 32, Last seqn
28-FEB-2003 (Rel. 41, Last anno
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Matches 108; Conserv
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P45192;
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Best Local 9
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STRAIN=Pm70;
MEDILINE=21145866; PubMed=11248100;
MEDILINE=21145866; PubMed=11248100;
MEDILINE=21145866; PubMed=11248100;
MCOMPLete genomic sequence of Pasteurella multocida Pm70.";
Proc., Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
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Pasteurellaceae; Pasteurella.
NCBI_TaxID=747;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
PSTS OR PM0436
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56; Mismatches 145;
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les 108; Conservative
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   Pasteurella multocida.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 SFMAAASHAKWHEKAGMGVILTNETGEKSWPITAASFILLNKYSDNPETTKNVLAFFDWA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89
                                                                                          Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 TLGTLPFAQANSITGAGASFPYPIYAKWA-SLYEKETGNKVNYOSIGSGGGOOOIIAKTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 NIGASDAYLSEGDMAAHKGLMNIALAISAQQVNYNLPGVSE-HLKLNGKVLAAMYQGTIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 DFGASDDPMKSBLLQQHQ-LVQFPAVIGGIVPVVNLPEIKPGKLKLSGKLLAEIFLGKIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      271 PAVPGALGENGNGGMVTGCAETPGCVAYIGISFLDQASQRGLGEAQLGNSSGNFLLPDAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 TVATTPASSPVTLAETGSTLLYPLFNLWGPAFHERYPNVTITAQGTGSGAGIAQAAAGTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 TWDDPQIAALNPGVNLPGTAVVPLHRSDGSGDTFLFTQYLSKQDPEGWGKSPGFGTTVDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187 LTGQGGKGNEGVASYVRQMKYSIGYVEYA-----YAKQNQLAWISLQNQAGQFVQPSNE
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Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                                    PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.6%; Score 384; DB 1; Length 334; Best Local Similarity 30.5%; Pred. No. 1.2e-10; Matches 104; Conservative 55; Mismatches 162; Indels 3
                                                                                                                                                                                                                                                                                                                                            t
                                                                                                                                                                                                                  1 19 POTENTIAL.
20 334 PHOSPHATE-BINDING PERIPLA.
334 AA; 36665 MW; FFC44EE853FE6B62 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        391 ITDGNKASFLDQVHPQPLPPAVVKLSDALIATISSAEMKTD 431
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InterPro; IPR006059; SBP bac_1.
Pfam, PF01547; SBP bac_1; Pfam, PF01547; SBP bac_1; TGRPAM; TIGRO975; 3a0107803; 1.
Phosphate transport; Transport; Periplasmic; Signal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U32818; AAC23028.1; ALT_FRAME.
HSSP; P06128; 11XH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 41, Created)
                                                                                                                                   Science 269:496-512(1995).
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                                                                                                                                                                            CONCEPTUAL TRANSLATION.
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                                                                     Jenter G.C.;
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28-FEB-2003
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PST3_MYCAV
ID PST3_M3
AC Q9KK89;
DT 28-FEB-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTPANQAIS-----MID-----GPAP 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 AOKLNWAKIITSAG----PDAVAİSADSVG----KTIAGAKİSGQGNDLVLDTLSFYKPTQ 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304 AGSYPIVLATYEIVCSKYPDPQVGTAVKAFLQSTVGAGQNG--LADNGYIPIPDAFKSRL 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 GTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHK-----GLMNIALAISAQQVNYNLPGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DAAADGAWGKGAG-----KTFKGGVGEGAKGNDGTSAAIKATEGSITYNEWSF---AQ
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                                                                                                                                                                                                                                                                                                                                                      STRAIN=96945;
Carroll JO., Wallace R.C., Keane J., Arbeit R.D.;
Carroll JO., Wallace R.C., Keane J., Arbeit R.D.;
Carroll JO., Wallace R.C., Keane J., Arbeit R.D.;
Carroll JO.,
Submitted (MRR-1999) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: Required for binding-protein-mediated phosphate
transport (By similarity)
-!- SUBCELLUAR LOCATION: Attached to the membrane by a lipid anchor
-!- SIMILARITY: BELONGS TO THE PSTS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pfam; PF01547; SBP bac 1; 1.
PROSTITE; PS001013; PROKĀR_LIPOPROTEIN; 1.
Phosphate transport; Transport; Membrane; Lipoprotein; Signal. SIGNAL 1 22 POTENTIAL.
CHAIN 23 369 PHOSPHATE-EINDING PROTEIN 3.
TIPID 23 NACYL DIGLYCERIDE (POTENTIAL).
TIPID 23 A7725 MW; CBOEAOACIOF463EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 369;
                                                                                                                                                                                Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phosphate-binding protein 3 precursor (PBP-3) (PstS-3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.7%; Score 339.5; DB 1;
31.0%; Pred. No. 1.2e-08;
iive 46; Mismatches 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF137360; AAF74819.1; -. HSSP; P06128; 1A54.
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                                                                                                                                                      Mycobacterium avium
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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Content J., Three different putative phosphate transport receptors are encoded by "Three different putative phosphate transport receptors are encoded by the Mycobacterium tuberculosis genome and are present at the surface of Mycobacterium bovis BCG.";
J. Bacteriol. 179:2900-2906(1996).
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Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Emolaeva M.D., Salzberg S.L.,
Deloher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                    302 SFLDQASQRGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTPAN------QAI
                                                                                                                                 SMIDGPAPDGYPIINYEYAIVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAINHJARY;

MEDINES-89255887;

PREARMED TRANSPORTED TO COLUTCHER C., Harris Gordon S.T., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Bardock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Deviln K., Feltwell T., Gentles S., Hamin N., Holroyd S. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

Pleciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Required for binding-protein-mediated phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lefevre P., Braibant M., de Wit L., Kalai M., Roeper D.,
Groetzinger J., Delville J.-P., Peirs P., Ooms J., Huygen K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                   005870; P96905;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phosphate-binding protein 2 precursor (PBP-2)
PSTS2 OR WY0932C OR WT0959 OR WTCY08D9.07.
                                                                                                                                                                                                                                                                                                                                       370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Erdmann;
MEDLINE=97284492; PubMed=9139906;
                                                                                                                                                                                                          410 PAVVKLSDALIATISSA 426
                                                                                                                                                                                                                                           -----DSFKSRLSTA 364
                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Content J.;
Submitted (JAN-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 NVTITAQCTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHK----GLMNIALAISAQQV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GQTLNYTANGSGAGVSEFNGNQTDFGGSDSPLSRKEYAAAEQRCGSQAWNLPVVFGPIAI 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 NYNLPGVSEHLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGSGDT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 FLFTQYLSKQDPEGWGKSPGFGTTVDFPAVPGALGE--NGNGGMVTGCAETPGCVAYIGI 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74
                                                                                                                                                                                                                                                                                                MEDLINE=21128732; PubMed=11234002;
Cole S.T., Eglameier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGSKPPSGSPETGAGAGTVATTPASSPV-----TLAETGSTLLYPLFNLWGPAFHERYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 409:1007-1011(2001).
-!- FUNCTION: Required for binding-protein-mediated phosphate transport (By similarity).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; INFOGO659; SBP_bac_1.
Pfam; PF01547; SBP_bac_1; 1.
PROSITE; PS00013; FROKAR_LIPOPROTEIN; 1.
Phosphate transport; Transport; Membrane; Lipoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.6%; Score 335.5; DB 1; Length 369; 28.9%; Pred. No. 1.9e-08;
                                                                                                                                                                            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corymebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHATE-BINDING PROTEIN 3.
N-ACYL DIGLYCERIDE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phosphate-binding protein 3 precursor (PBP-3) (PstS-3)
PSTS2 OR PHOS2 OR ML2095.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 21 POTENTIAL.
22 369 PHOSPHATE-EINDING PROTEIN
22 22 N-ACYL DIGLYCERIDB (POTENT
369 AA; 37733 MW, 697DECEC6AB4B9AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Massive gene decay in the leprosy bacillus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE PSTS FAMILY.
                                         369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AL583924; CAC31050.1; -.
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                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; B87171; B87171.
HSSP; P06128; 11XH.
Leproma; ML2095; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome.
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                         MYCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75
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Bishai W.;
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    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 KGVST-LNLDGPTTAKIFNGTITVWNDPQ1QALNSGTDLPPTPISVIFRSDKSGTSDNFQ 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGSKPPSGSPETGAGAGTVATTPASSPVTLAETGSTLLYPLFNLWGPAFHERYPNVTITA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 NANGSGAGVTQFLNNETDFAGSDVPLNPSTGQPDRSAERCGSPAWDLPTVFGPIAITYNI 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGVSEHLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGSGDTFLFT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QYLSKQDPEGWGKSPGFGTTVDFPAVPGALGENGNGGMVTGCAETPGCVAYIGISFLDQA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SORGIGEAQLGNSSGNFILPDAQSIQAAAGFASKTPANQAI-----SMIDGP 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APDGYPIINYBYAIVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAV-VK 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135 QGTGSGAGIAQAAAGTVNIGASDAYLS----EGDMAAHK---GLMNIALAISAQQVNYNL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251 VGKQLNWAQIITSAG----PDPVAITTESVG---KTIAGAKIMGQGNDLVLDTSSFYRPT 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 304 QPGSYPIVLATYEIVCSKXYPDATIGTAVRAFMQAAIGPGQEG--LDQYGSIPLPKSFQAK 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 CGGGTNSSS--SGAG-GISGSVHCGGKKELHSSGSTAQENAMEQFVYAYVRSCPGYTLDY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Antigen Ag88).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                      INDUCTION: ACCUMULATION OF PROTEIN IS ENHANCED UNDER PHOSPHATE STARVATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41;
                                                                                                                                                                                                                                                                                                                                                                                                     Tuberculist; Rv0932c; -.
InterPro; IPR06059; SBP bac_1.
Ffam; PF01547; SBP_bac_1; 1.
PRO$TIE; PS00013; PRO$AR, LIPOPROTEIN; 1.
Phosphate transport; Transport; Membrane; Lipoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
PHOSPHATE-BINDING PROTEIN 2.
N-ACYL DIGLYCERIDE (POTENTIAL).
97F5116CEE9B3B5C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.5%; Score 330.5; DB 1; Length 3
31.1%; Pred. No. 3.1e-08;
tive 44; Mismatches 168; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PST3_MYCTU STANDARD; PRT; 370 AA.
086343; Q50794;
086543; Q50796;
141, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phosphate-binding protein 3 precursor (PBP-3)
PSTS3 OR PMOS2 OR RV0928 OR MT0955 OR MTCY21C12.22.
Mycobacterium tuberculosis.
                                                    SIARVATION.
SIMILARITY: BELONGS TO THE PSTS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 22 PO
23 370 PH(
23 23 N-;
370 AA; 37864 MW;
                                                                                                                                                                                                                                                                          EMBL, Z48056; CAA88137.1; -.
EMBL, Z95209; CAB08486.1; -.
EMBL, AB006581; AAK45206.1; -.
PIR, D70584; D70584.
HSSP; P06128; IIXH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAAAVNA 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSDALIA 421
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Best Local
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PST3 MYCTU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., Boefoy R., Godson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encoded by
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"Three different putative phosphate transport receptors are encoded the Mycobacterium tuberculosis genome and are present at the surface of Mycobacterium bovis BCG.",
J. Bacteriol. 179:2900-2906(1997).
-:- FUNCTION: Required for binding-protein-mediated phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                   MEDLINE=97000022; PubMed=8843165;
Braibant M., Lefevre P., de Wit L., Ooms J., Peirs P., Huygen K., Wattiez R., Content J.;
"Identification of a second Mycobacterium tuberculosis gene cluster encoding proteins of an ABC phosphate transporter.";
FEBS Lett. 394:206-212(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Gas S., Bary C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Comor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., Mclean J., Moule S., Murphy L., Cliver S., Seberne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitchead S., Barrell B.G.;
Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Erdmann;
MEDLINE=97284492; PubMed=9139906;
Lefevre P., Braibant M., de Wit L., Kalai M., Roeper D.,
Groetzinger J., Delville J.-P., Peirs P., Ooms J., Huygen K.,
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FICORDIE).
-!- INDUCTION: By phosphate starvation.
-!- SIMILARITY: BELONGS TO THE PSTS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AE006981; AAK45202.1; ALT_INIT.
BTR; H70883; H70583.
HSSP; P06128; IIXH.
                                                                                                                                                              SEQUENCE FROM N.A., AND INDUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tuberculist, Rv0928, -.
InterPro, IPR006059, SBP bac_1.
Pfam, PF01547, SBP_bac_1, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z95209; CAB08488.1; -. EMBL; Z48057; CAA88138.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHARACTERIZATION.
                                                                                 NCBI_TaxID=1773;
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between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            564 AAKNAAQQLVLSADNMREYLAAGAKERQRLATSLRNAA-KAYGEVDEEA--ATALDNDGE 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----SNAKKTSDAAVSLPV-----GQQPAAEQPHVPTAPGGPSQTG 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAAPQIGATKPAATAKTIPQRPRGSDADAGSRAQSQYGFGDPPGGGALKGAVDAASDAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 GTVATTPASSPVTLAETGSTLLYPLFNLWGPAFHERYPNVTITAQGTGSGAGIAQAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----QASQRGLGEAQ----LGNSSGNFL-LPDAQSIQAAAAGFASKTPANQAISMIDGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----ÓGPVOSÓPGRRÓEPAASATK---ÍHVADGLPARPVOPAVSATDLOTDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RD-----TPSLSAVAGPVTLSGSSSSSGRNSSSNSNTSTSSTSNGVTITSNVGVNGASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----DLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQKQELDEISTNIRQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLGRTIQGRIARLQAAREALRAARHARVGAAMQPPPV-----QARPVQGQSGQVPQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAGKITYRIKLEVSFKMRPAQPR-----AGSK------PPSGSPETG-----AGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVAAASPA--PAGISDQLSTPACP-----PEREPQ---AGKPRASGRAPAPGVGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 VNIGASDAYLSEGDMAAHKGLMNIALAISAQQVNYNLPGVSEHLKLNGKVLAAMYQGTIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 QDVGGGSGACAPAPDESHMGL-----THRDQGHDERIS-----QTAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TWDDPQIAA -- LINPGVNLPGTAVVP-----LHRSDGSGDTFLFTQYLSKQDPEGWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280 AWKAGAVAAPPAAPTPSPPGLAAAPTRLASSALGTHSSDGD-------MRRAVP---G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              383 QERLMAARRAVVIMQWNTHLGRRGRSFAPLPIGGMSIAISAASSSISSASSSSSMNDG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260 KSPGFGTTVDFPAVPGAL-----GBNGNGGMVTGCAETPGCV---AYIGISFLD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      478 ASAVAAQAPSSAMPTAAMAATWGSATIGSAATLPTAAVVSSAAAEGTQPSGLLLAGGRPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVQYSRADEEQQQALSSQMGFTQSQTVTVDQQEILNRANEVEAPMADPPTDVPITPCELT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1783;
                                                                                                                                          mRNA processing; mRNA splicing.
CHLOROPLAST (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                          40F6206BA6EBDCDB CRC64;
                                                                                                                                                                  TRANS-SPLICING FACTOR RAA3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 203.5; DB Pred, No. 0.081;
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ALA-RICH.
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GIN-RICH.
ARG-RICH.
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POLY-ALA.
POLY-PRO.
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POLY-GLY.
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EMBL; AF310674; AAG39999.1; -.
Chloroplast; Transit peptide; m
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                                                                                                                                                                                                                       11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TMANIVISAGGD--PVAITIDSVGQTIAGATISGVGNDLVLDTDSFYRPKRPGSYPIVLA 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     313 GEAQLGNSSGNFLLFDAQSIQAAAAGFASKT---PANQAISMIDG----PAPDGYPIINY 365
                                                                                                                                                                                                                                                                                  98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      be required which it
                                                                                                                                                                                                                                                                                                                                    GAGIAQAAAGTVNIGASDAYLSEGDMAAHK-----GLMNIALAISAQQVNYNLPGVSEHL
                                                                                                                                                                                                                                                                                                                                                                             KLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGSGDTFLFTQYLSKQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206 NGAWGKGAG-----KSFQGGVGEGARGNDGTSAAAKNTPGSITYNEWSF---AQAQHL
                                                                                                                                                                                                                                                   TGAGAGTVATTPASSPV-----TLAETGSTLLYPLFNLWGPAFHERYPNVTITAQGTGS
                                                                                                                                                                                                                                                                                  TGGGA---TTGQASAKVDCGGKKTLKASGSTAQANAMTRFVNVFEQACPGQTLNYTANGS
                                                                                                                                                                                                                                                                                                                                                                                                                                          255 PEGWGKSPGFGTTVDFPAVPGALGE--NGNGGMVTGCAETPGCVAYIGISFLDQASQRGL
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  precursor RNA to exon 1 and the tscA RNA.
SUBCELLULAR LOCATION: Chloroplast stroma.
DOMAIN: The N-terminal 453 amino acids are dispensable, while
C-terminal 630 amino acids are required for function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Required for trans-splicing of exons 1 and 2 of the chloroplast encoded psaA mRNA (a group II intron). May be requirer stability of the chloroplast RNA-protein complex in which is found.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlamydomonas reinhardtii.
Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae, Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in chloroplast
                                                                                                                                                                                                                     38;
                Phosphate transport; Transport; Membrane; Lipoprotein; Signal
                                                            PHOSPHATE-BINDING PROTEIN 3.
N-ACYL DIGLYCERIDE (POTEWIAL).
AAA - PSG (IN STRAIN BEDWAN).
Q -> A (IN STRAIN ERDWAN).
MISSING (IN STRAIN ERDWAN).
QH -> HD (IN STRAIN ERDWAN).
W; 7D557829A9A118E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND CHARACTERIZATION.
STRAIN=13C / CC-125;
STRAIN=13C / CC-125;
MEDLINE=21181833; PubMed=11285239;
Rivier C., Goldschmidt-Clermont M., Rochaix J.-D.;
"Identification of an RNA-protein complex involved in chlorog group II intron trans-splicing in Chlamydomonas reinhardthi:"EMBO J. 20:1765-1773 (2001)
                                                                                                                                                                                        Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EYAIVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLP 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYBIVCSKYPDSQVGTAVKAFLQSTIGAGO--SGLGDNGYIPIP 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: Part of a 1700 kDa complex that includes the
                                                                                                                                                                                                     Pred. No. 1.7e-07;
39; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Trans-splicing factor Raa3, chloroplast precursor.
                                                                                                                                                                                        ; DB 1;
1.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1783 AA
                                                                                                                                                                                        Score 314;
   PROKAR LIPOPROTEIN; 1
                                                 POTENTIAL.
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                                                                                                                                                         37953 MW;
                                                                                                                                                                                                   30.8%;
                                Antigen; Complete proteome.
SIGNAL 1 22
                                                                                                                                                                                   Query Match
Best Local Similarity 30.8'
Matches 106; Conservative
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                                                   370<sub>1</sub>
23
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370 AA;
   PS00013;
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Q9FEC4;
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   PROSITE;
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COMFLICT
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                                                                                                                                                                                                                                     842
                                                                                                                                                           PQLAAVVAGYAAAGH----RHEPLLEALAGVALAKAGGAGGIGGGAAGAVPRGQAASELK 845
                                                                                                                                                                                    RDQI-----BPVYAEYQQRSEKV-----BTEYNNKAALEPVNPPKPP----- 802
GTVQAESAGAVGGDSSA----ELTDTPRVATAGEPNFMDLKBAARKLETGDQGASLAHFA 676
                                                                                                           ------LLGRLSRYQPAGRDDGPAVLAPHARYSPAAYQAAAAAAAAQPQLLLAPLSL 789
                                                                                                                                                                                                                                                          LWAYATLEQLPAAAPTPPPPPASAAASTAPRAAESRPAAAPAPABATATR--TPLLTAP 963
                                                                                                                                                                                                                                                                                    GREAALLSGDVAVKAASLG 884
                                                                                                                                                                                                                                                                                                                                                          GRGEGTASGAVYVAAAGGYAMLQSGGAG---GGGMGQA-GGAGRGGAGAGAAALPLVVA 1077
                                                                                                                                                                                                                                                                                                                                    940
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RSRLTFRAACVFLTALARLGYRGGAVTRLAAALAVWLARQLNTGAVTPRAKWKGTWLAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97361829; PubMed=9218790;
Harris S.D., Hamer L., Sharpless K.E., Hamer J.E.;
"The Aspergillus nidulans sepA gene encodes an FH1/2 protein involved
in cytokinesis and the maintenance of cellular polarity.";
EMBO J. 16:3474-3483(1997).
                                                                                                                                    -----LERLYAENPSA
                                                                                                                                                                                                                                    -----PGFLMPPSDGSGVTPGTGMPAAP
                                                                                       DGWNTFNLTLQGDVKRFRGFDNWEGDAA-----TACEASLDQQRQWILHMAKL
                                                                                                                                                                                                                                                                                                                                   GGGGGGVPSAPLGSAIGGAESVRPAGAGDIAGLGQGRAGGGAALGGGGGMG---MPMGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTRAMOLECULAR GBD-DAD BINDING WHE DISRUPTING THE GBD-DAD INTERACTION
                                                                                                                                                                                                                                                                                                                                                                                                              DEPA EMBNI STANDARD; PRT; 1790 AA.

P78621; 000760;
T 16-OCT-2001 (Rel. 40, Created)
T 28-PEB-2003 (Rel. 41, Last annotation update)
E CYTOXINESIS protein sepA (FH1/2 protein) (Forced expression inhibition of growth A).

E Bericella nidulans (Aspergillus nidulans).
E EMARYOLA; FIGA.

SEPA OR FIGA.

SENAROLA; FIGA:
C BLUCCHIALS; ASCOMYCOTA; PEZIZOMYCOTINA; Burctionaycetes; C BLUCCHIALS; Trichocomaceae; Emericella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 559-1790 FROM N.A., AND FUNCTION.
STRAIN=FGSC 26;
MRDLIN=952296; PubMed=7713416;
Marboul J.F., Adams T.H.;
"identification of developmental regulatory genes in Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nidulans by overexpression.";
Genetics 139:537-547(1995).
-!- FUNCTION: INVOLVED IN CYTOKINESIS. OVEREXPRESSION RESULTS IN
                                                             GTVRAPTDTAAPAASPAATAPALASTPFATPAAAP----LPEPPEVVAARD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY)
SIMILARITY: Contains 1 GTPase-binding (GBD) domain.
SIMILARITY: Contains 1 Formin homology 1 (FH1) domain.
SIMILARITY: Contains 1 Formin homology 2 (FH2) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REVISIONS TO 143-153; 207; 1071-1109 AND 1644.
Hamer L., Harris S.D., Sharpless K.E., Hamer J.E.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                     SAAMAKQAQYVAQLHVWARREHPTYEDIVG------
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RHO-GTP ACTIVATES THE DFRS BY
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P--GFGTTVDFPAV------PGALGE-NGNGGMVTGCAETPGCVAYIGIS-FLDQASQR
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larity 19.4%; Pred. No. 0.36;
Conservative 145; Mismatches 430; Indels 38
-:- SIMILARITY: Contains 1 Formin homology 3 (FH3) domain.
-:- SIMILARITY: Contains 1 DRF autoregulatory (DAD) domain.
-:- SIMILARITY: BELONGS TO THE FORMIN HOMOLOGY FAMILY. BNI1
SUBFAMILY:
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                                                                                                                                                                                                                                                                              EMBL, U83659, AAB63335.3; -.
EMBL, L36341, AA533306.1; ALT_SEQ.
InterPro; IPR003104; FH2.
Ffam, PF02181; FH2; 1.
SMART; SM00498; FH2; 1.
Cell division; Colled coll.
EMAIN
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DLKTQID---QVESTAGSLQGQWRGAAGTA----AQAAVVRFQEAANKQKQELDEIST
                                                                                                                                                                                                                                                                                      HİRAQFISCGIKRLLSKMEGFQYEVIDKQIEHFRENE--AIDYEDLLQRESSSTKDSIEG
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                                                                                                                                                                                            NIR----QAGVQ--YSRADEEQQQALSSQM-GFTQSQTVTVDQQEILNR-----ANEVEA
                                                                                                                                                                                                                                                                                                                                                                                         547 PMADPPTDVPITPCELTAA------KNAAQQLVLSADN-------
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Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
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10 kDa culture filtrate antigen cfp10 homolog.
MLOSGO OR MLCB628.13C.
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STRAIN=IN;
MEDLINE=21128732; Pubmed=11234002;
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16-OCT-2001 (Rel. 40, Last anno
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3.6%; Score 184; DB 1; Length 99;
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                                                             "Massive gene decay in the leprosy bacillus.";
                                                                                  Nature 409:1007-1011(2001).
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OM protein - protein search, using sw model Run on:

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US-09-688-672A-54 5072 1 MGHHHHHHUIDIIGTSFTSW......RAWTEAVIGNRRRQDSKESK 983 Title: Perfect score: Sequence:

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830525 segs, 258052604 residues Searched:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Q49590 mycobacteri	Q49589 mycobacteri	Q8paf7 xanthomonas	Q8ynj0 anabaena sp		Ogyq56 aeropyrum p		Q8u247 pyrococcus	Q49675 mycobacteri	Q9ryz6 deinococcus	Q55199 synechocyst	Q8z9s9 yersinia pe	Q8pm55 xanthomonas	Q56833 xanthomonas	Q8ky90 edwardsiell	Q9am16 edwardsiell
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ALIGNMENTS

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Duplication of genese encoding the immunodominant 38 kDa antigen Mycobacterium intracellulare.";
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro, IPR006059; SBP bac 1.
Pfam; PF01547; SBP bac 1; 1.
SEQUENCE 374 AA; 37998 MW; 45796D4E9F6F513D CRC64;
                                                                                                                                                                                                                                               01, Last sequence update)
23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;; Score 1412; DB 2;
;; Pred. No. 7.2e-64;
33; Mismatches 49;
                                                                                                                                                                                                               374 AA
                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                          STRAIN=ATCC 35761;
MEDLINE=97055782; PubMed=8900068;
                                                                                                                                                                                                                      Q49589;
01-NOV-1996 (TrEMBLrel. 01, Crea
01-NOV-1996 (TrEMBLrel. 01, Last
01-MAR-2003 (TrEMBLrel. 23, Last
Psts subunit of ABC transporter.
PSTS1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.8%;
76.5%;
                                                                                                                                                                                                                                                                                          Mycobacterium intracellulare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 76.5%
Marches 267; Conservative
                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1767;
                                                                                                                                  371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      255
                    139
                                                                                      311
                                                                                                             259
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 523913 / NCPPB 528;

MEDLINE=20202145; PubMed=12024217;

RA

da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA

Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA

Camarotte G., Cannavan F. M., Bertolini M.C., Camargo L.B.A.,

RA

Camarotte G., Cannavan F. M., Bertolini M.C., Canargo L.B.A.,

RA

Caral J.B., Ferrela A.B., Rerela D.P.,

RA

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA

Rotal J.B., Maddanis J., Madelra A.M., Miyaki C.Y., Moon D.H.,

RA

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

Recita L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

Recita L.M., Riadima J.P.,

Ratindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

Setubal J.C., Kitajima J.P.,

Ratindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

Ratindade dos Santos M., Truffi D., Tsai S.M., White P.F.,

Ratindade dos Santos M., Truffi D., Tsai S.M., White P.F.,

Ratindade dos Santos M., Truffi D., Tsai S.M., White P.F.,

Ratindade dos Santos M., Truffi D., Tsai S.M., White P.F.,

Ratindade dos Santos M., Truffi D., Tsai S.M., White P.F.,

Ratindade dos Santos M. Truffi D., Tsai S.M., White P.F.,

Ratindade dos Santos M. Truffi D., Tsai S.M., White P.F.,

Ratindade dos Santos M. Truffi D., Tsai S.M., White P.F.,

Ratindade dos Santos M. Truffi D., Tsai S.M., White P.F.,

Ratindade dos Santos M. Truffi D., Tsai S.M., White P.F.,

Ratindade dos Santos M. Truffi D., Tsai S.M., White P.F.,

Ratindade dos Santos M. Truffi D., Tsai S.M., White P.F.,

Ratindade dos Santos M. Truffi D., Tsai S.M., White P.F.,

Ratindade dos Santos M. Truffi D., Tsai S.M., White P.F.,

Ratindade dos Santos M. Truffi D., Tsai S.M., White P.F.,

Ratindade dos Santos M. Truffi D., Tsai S.M., White P.F.,

Ratindade dos Santos M. Truffi D., Tsai S.M., White P.F.,

Ratindade dos Santos M. T.M. Truffi D., Tsai S.M., White P.F.,

Ratindade dos Santos M. T.M. Truffi D., T .20 GPAFHERYPNVTITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKGLMNIALAIS 179 SADYNAATGN-KVNYQSIGSGGGIAQIKAGTVDFGSSDKPLDSAEL-QQAGLGQFPSAIG 125 67 299 AWPITATNFMLMHKQPKDAARSKATLDPFKWALENGQAQA--SELHYVPLPPELVKQIEA 356 .80 AQQVNYNEPGVSE-HLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSD 126 GVVPVVNIEGMAPGKLRLTGALLGDIFLGKVTWWNDAAIAAANPGVTLPATKINLVHRSD IGISFLDQASQRGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTPANQAISMIDGPAPD 359 GYPIINYEYAIVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAVVKLSDA 60 IKLEVSFKMRPAQPRCGSKPPSGSPETGAGAGTVATTPASSPVTLAETGSTLLYPLFNLW LSĽTIALALAACSP--GKDAQSGDPAQG-GANAGAAAGESKSAEIAGAGASFIYPĽVSKŴ GSGDTFLFTQYLSKQDPEGWGKSPGFGTTVDFPAVPGALGENGNGGMVTGCAETPGCVAY GSGTTFNFSNYLSKVSPE-WKTKVGEGTSVQW---PGGVGGKGNEGVASYVQQIKGSIGY Gaps Xanthomonas campestris (pv. campestris). Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; 15; DB 16; Length 363; 161; Indels 363 AA; 37606 MW; F26D1C51BD149D4A CRC64; Created)
Last sequence update)
Last annotation update) ch 9.5%; Score 483.5; DB 16 11 Similarity 32.5%; Pred, No. 6.8e-17; 117; Conservative 67; Mismatches 161. 01-OCT-2002 (TrEMBLrel. 22, Last sequence I-MAR-2003 (TrEMBLrel. 23, Last annotation ABC transporter phosphate binding protein. PSTS OR XCC1527. 363 PRT; Bacteria; Proteobacteria; Gamm Xanthomonadaceae; Xanthomonas. PRELIMINARY;

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Xanthomonadaceae; Xanthomonas
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Q9YG56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOASORGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTPANQAISMIDGPAPDG---YP 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 362 IINYEYAIVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAVVKLSDALIA 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RYPNVTITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDM-AAHKGLMNIALAISAQQVN 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGOOGSDNTATODGSSGTAKDATASSPAKLDLGGNVSLTGAGASFPAPLYASWFTDLNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 VFTKHLAAVSPE-WKSKVGEGKSVSWPV---GVGGKGNEGVTAQIKQTQGAIGYIEYGY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --AKONNISYATLENKAGKFVKYNDESASQTLA--AIQLPENLRAFV---PDPDGDGSYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGSKPPSGSPETGAG-AGTVATTPASSP-----VTLAETGSTLLYPLFNLWGPAFHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YNLPGVSEHLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGSGDTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Proteobacteria; Gammaproteobacteria, Xanthomonadales;
                                                                                                                                                                                                                                                                                                                      Kaneko I., Nakamura Y., Wolk C.P., Kuritz I., Sasamoto S.,
Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
Yasuda M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 16; Length 392;
                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120."; DNA Res. 8:205-213(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 9.5%; Score 482.5; DB 16; Length Local Similarity 33.7%; Pred. No. 8.5e-17; nes 124; Conservative 64; Mismatches 151; Indels
                                                                                                                                                                                              Anabaena sp. (strain PCC 7120).
Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc
                                                               01-MAR-2002 (TrEMBirel. 20, Created)
01-MAR-2002 (TrEMBirel. 20, Last sequence update)
01-MAR-2003 (TrEMBirel. 23, Last annotation update)
Phosphate-binding periplasmic protein of phosphate ABC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    392 AA; 41343 MW; FF28D266FB59C950 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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                        392 AA
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01-0CT-2002 (TrEMBLrel. 22, Last sequence
01-MAR-2003 (TrEMBLrel. 23, Last annotatio
ABC transporter phosphate binding protein.
PSTS OR XAC1577.
Xanthomonas axonopodis (pv. citri).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                           PRT;
                                                                                                                                                                                                                                                                                                      MEDLINE=21595285; PubMed=11759840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AP003596; BAB76274.1; -.
InterProv. IPR006659; SBP bac_1.
Pfam; PF01547; SBP_bac_1; 1.
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOISPEYK 380
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                                                                                                                                                                                                                                    NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                             FROM N.A.
                                             QBYNJO;
01-MAR-2002
                                                                                                                                                     transporter
ALL4575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  305
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                                                                                                                                                                                                                                                                               SEQUENCE
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RC STRAIN=306 / ATCC 13902 / XV 101;

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA dayogio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA damarotte G., Cannavan F., Cardozo J., Chambergo F., Clapina L.P.,
RA Caraelli R.M. B., Coutinho. L.L., Cursino-Santos J.F., El-Dorry H.,
RA Formighieri B.F., Franco M.C., Greggio C.C., Gruber A., T.
RA Formighieri B.F., Franco M.C., Greggio C.C., Gruber A., R., Machado M.A., Machia A.M.B.N., Martinez Rossi N.M.,
RA Martins B.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Morelia L.M., Novo M.T.M., Okura V.K., Olivaria M.C., Oliveira V.R.,
RA Spinola L.A.F., Rossi A., Sena J.A.D., Silva C., Ge Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,
RA Sceubal J.C., Kitajima J.P.;
RA "Comparison of the genomes of two Xanthomonas pathogens with differing three frontes and the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of
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23, Last annotation update)
phosphate-binding periplasmic protein.
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01-NOV-1999 (TrEMBLrel. 12, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
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EMBL, ABO11790; AAM36445.1; -1.
InterPro; IPR006059; SBP_bac_1.
Pfam; PF01547; SBP_bac_1.
Complete proteome.
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                                                                                                                                                           Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Julino X., Takahashi M., Sekine M., Baba S. I., Ankai A., Kosugi Bosoyama A., Fukui S., Nagai Y., Nishijiama K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota X., Nakamura Y., Nomura N., Sako Y., Kikuchi H.; Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix Kl.";
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MEDLINE=21995285; PubMed=11759840;
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             324 NDRDKABAIKKFIEWINTEGOTKIIEGYI---PIPDEIRQINMKAVEMIS 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.1%; Score 460.5; DB 17; Length 373; 32.0%; Pred. No. 1e-15; tive 65; Mismatches 150; Indels 23;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
ABC phosphate transport system phosphate-binding periplasmic
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Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
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HSSP; P06128; 1IXG.
Interbro; IPR006059; BB-bac_1.
Interbro; IPR006051; SBP-dom1.
Pfam; PP01547; SBP-bac_1; 1.
PROSITE; PS01037; SBP_BACTERIAL_1; 1.
                                                                                                                                     MEDLINE=99310339; PubMed=10382966;
                             Desulfurococcaceae; Aeropyrum
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                                           NCBI_TaxID=56636;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGNFLLPDAQSIQAAAAGFASKTPANQAISMIDGPAPDGYPIINYEYAIVNNRQKDAATA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 RGEFVAPSLOSANAALS--AVSFPDNFRVFV--GDPGQGYPIVGLTWMMVYRQYADAAKS 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 GIAQAAAGTVNIGASDAYLSEGDMAAHK-GLMNIALAISAQQVNYNLPGVSEHLKLNGKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261 SPGFGTTVDFPAVPGALGENGNGGMVTGCAETPGCVAXIGISFLDQASQRGLGEAQLGNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGSPETGAGAGTVATTPASSPVTLAETGSTLLYPLFNL--WGPAFHERYPNVTITAQGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 LAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGSGDTFLFTQYLSKQDPEGWGK
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Archaea; Euryarchaecta; Thermococci; Thermococcales; Thermococcaceae;
RA Yasuda M., Tabata S.;

RT Yasuda M., Tabata S.;

RT 'Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";

RI DNA Res. 81.205-213 (2001).

DR EMBL; AP003584; BAB72868.1; -..

DR InterPro; IPR06059; SBP_bac_1.

R Fonsty; SBP_bac_1: 1.

R Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                              20;
                                                                                                                                      nitrogen-fixing
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Weiss R.B., Dunn D.M., Robb P.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; ABCI0212; AAABI127.1, -..
InterPro; IPR06659; SBP_bac_1.
Pfam; PF01547; SBP_bac_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.0%; Score 456; DB 16; Length 3
13.0%; Pred. No. 1.6e-15;
ve 69; Mismatches 142; Indels
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Last sequence update)
Last annotation update)
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32.1%; Pred. No. 1.7e-15;
tive 58; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phosphate-binding periplasmic protein (pbp)
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                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 33.0%;
Matches 114; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2003 (TrEMBLrel. 23,
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SEQUENCE FROM N.A. STRAIN=R1;
294 IDGP 297
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                                                                                                                                                                                                                                                                                         Fraser C.M.;
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                                                    Q9RYZ6
                               RESULT 10
Q9RYZ6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGCVAYIGISFLDQASQRGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTP-ANQAISM 351
                                          249
                                                                                                   SCHOQBAFLKGLTDIGRTDPPVXESTWKKFLETGDQP----LQPPIVVGAVVVHNIPN 132
                                                        LSKODPEGWGKSPGFGTTVDFPA--VPGALGENGNGGWVTGCAETPGCVAYIGISFLDQA 307
                                                                                                                                               248 IEENLKIVALKONALGONFVKPTEETIKAANAAPKAPIPDPAEGYKEDIRQLLNAPGENSYP 307
SGAGIAQAAAGTVNIGASD-----AYLSEGDMAAHKGLMNIALAISAQQVNYNLPG 189
                                                                                                                                  SQRGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTP----ANQAISMIDGPAPDGYP 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94
                                                                                                                                                                            IINYEYAIV----NNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAVVKL 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152 NIGASDAYLSEGDMA-AHK----GLMNIALAISAQQVNYNLPGVSEHLKLNGKVLAAMYQ
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                                          VSEHLKLINGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGSGDTFLFTQY
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                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=96084954; PubMed=7489918;
Doukhan L., Predich M., Nair G., Dussurget O., Mandic-Mulec I.,
Cole S.T., Smith D.R., Smith I.;
"Genomic crganization of the mycobacterial sigma gene cluster.";
Gene 165:67-70(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86;
                                                                                                                                                                                                                                                       049675 PRELIMINARY; PRT; 336 AA.
049675;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
PabB.
Mycobacterium leprae.
Mycobacterium leprae.
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TAXID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 8.9%; Score 452; DB 2; Length 33
Best Local Similarity 40.1%; Pred. No. 2.4e-15;
Matches 122; Conservative 22; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Robison K.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U00012; AAA85925.1; -.
SEQUENCE 336 AA; 35916 MW; OCE7CABDB3CBD99F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270 GAIGYVELVY----AKONKLSFGAVKNRAGKFILADNGPASNAALGVV--IPADTRVSLTN 324
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White O., Blsen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makazrova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Phosphate ABC transporter, periplasmic phosphate-binding protein.
DRA0157.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                      Deinococcus radiodurans.
Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales; Deinococcaceae; Deinococcus.
NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -403 AA; 42060 MW; 38DC61C6E7D290D0 CRC64;
403 AA
   PRT;
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InterPro; IPRO6059; SBP_bac_1.
Pfam; PF01547; SBP_bac_1; 1.
Complete proteome.
SEQUENCE -403 AA; 42060 MW;
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EMBL; AE001862; AAF12207.1;
HSSP; P06128; 1IXG.
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   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTPANQAISMIDGPAPDGYPIINYEYAI 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  265 NNLTMASLQNKDGQFVVPTDENASATLA--AVELPENLREFITNPAGADSYPIVTYTWML 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209 AAMSPE-FKETIGDGKTVEWPTSKGKFIGGKGNEGVTAGIQQNEGAIGYVEYGY---AIN 264
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MEDLINE=97061201; PubMed=8905231;
MEDLINE=97061201; PubMed=8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hisosubi T., Mateuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75 CGSKPPSG-SPETGAGAGTVATT--PASSPVTLAETGSTLLYPLFNLWGPAFHERYPNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 CGGGGGGGDTAQTGGGDATTTTAADAFASKVSLTGAGASFPAPLYQGWFVALNQAVPNLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191 SEHLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGSGDTFLFTQYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 ITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKG-LMNIALAISAQQVNYNLPGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire ganome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
EMBL; D64001; BAA10341.1; --
HSSP; P06128; 2ABH.
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=96127529; PubMed=8590279;
MEDLINE=96127529; PubMed=8590279;
Sugiura A., Sato S., Kotani H., Sazuka T., Miyajima N.,
Sugiura M., Tabata S.,
"Sequence analysis of the genome of the unicellular cyanobacterium
Sequence analysis of the genome of the unicellular in the 1 Mb
region from map positions 64% to 92% of the genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 383;
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                                                                                                                                                                                                                                 Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1A1E2CE2EDCFBFFC CRC64;
                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Phosphate-binding periplasmic protein precursor (PBP)
PSTS OR SLL0680.
                                                                                                                                  Bacteria; Cyanobacteria; Chroococcales; Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. 8.8%; Score 444; DB 16;
Similarity 31.5%; Pred. No. 7.3e-15;
08; Conservative 69; Mismatches 152;
   383 AA.
                                                                                                               Synechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR006059; SBP bac 1.
Pfam; PF01547; SBP bac 1; 1.
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SEQUENCE 383 AA;
                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                 STRAIN=PCC 6803;
Tabata S.;
                                                                                                                                                NCBI_TaxID=1148;
                           01-NOV-1996
01-NOV-1996
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 ANTVDFGASDAPLTDEKLAT-EGLFQFPTVIGGVVLAVNIPGIKSGELTLDGKTLGDIYL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                327 PDAQSIQAAAAGFA-SKTPANQAISMIDGPAPDGYPIINYEYAIVNNRQKDAATAQTLQA 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 PTEHSFSSAAKGVDWSKSFAQ---DLINQKGDDVWPITSTITILVHKEQKNAANGTEVLK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 AATLSMTAVSAFAAASLIGAGATFPAPVYAKWADSYQKEIGN-KINYQGIGSSGGVKQII 71
                                                                                                                                                                                                                                                                                                                                             MEDLINE=21470413; PubMed=11586360; ParkIN=20092 (Archit) d., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., ParkInil J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Brentice M.B., Sebainia M., James K.D., Churcher C., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Genome sequence of Yersinia pestis, the causative agent of plague.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGTVATTPAS -- SPVTLAETGSTLLYPLFNLWGPAFHERYPNVTITAQGTGSGAGIAQAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GIIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGSGDTFLFTQYLSKQDPEGWGKSPGFGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 GTVKKWNDPALVKLNPGVKLPDQNIAVVRRADGSGTSFVFTSYLAKVNAE-WKEKVGAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TVDFPAVPGALGENGNGGMVTGCAETPGCVAYIGISFLDQASQRGLGEAQLGNSSGNFLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-KIM5 / Biovar Mediaevalis;
MEDLINE=22137863; PubMed=12142430;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss
Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
Petherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.
                                                                                                                                                                                                                                 Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Yersinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
                                                                  01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative phosphate-binding periplasmic protein (Periplasmic phosphate-binding protein).
PSTS OR YPO4117 OR Y4131.
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J. Bacteriol. 184:4601-4611(2002).

EMBL, A4411460, CAC93566.1;

InterPro, IPR006059; SBP_bac_1.

Pfam, PF01547; SBP_bac_1; 1.

Pfam, PF01547; SBP_bac_1; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 346 AA; 36710 MW; 0C9B4FCF55D3C181 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
8.7%; Score 440; DB 16;
Best Local Similarity 33.4%; Pred. No. 1e-14;
Matches 110; Conservative 60; Mismatches 141;
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                             346
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                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                              Yersinia pestis.
                                                                                                                                                                                                                                                                                  NCBI_TaxID=632;
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REQUENCE FROM N.A.

SEQUENCE 702 13902 / XV 101;

RA DEDINES-202145; PubMed=2024217;

RA Ga Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Clapina L.P.,

RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Clapina L.P.,

RA Camarotte G., Cannavan F., Ferraina R.C., Camargo L.P.,

RA Camarotte G., Ferraina A.C.S., Ferraina R.C., Granary H.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Ferro M.I.T.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Formighieri E.F., Franco M.C., Madeira A.M.B.W., Mayaki C.Y., Moon D.H.,

RA Martins E.C., Machado M.A., Madeira A.M.B.W., Mayaki C.Y., Moon D.H.,

RA Martins E.C., Machado M.A., Sana J.A.D., Silva C., Gesuza R.F.,

RA Sphnola L.A.F., Takita M.A., Tamura R.B., Teixaira B.C., Tezza R.I.D.,

RA Stubal J.C., Kitajima J.P.;

RY Trindade dos Santos M., Truffi D., Teai S.M., White F.F.,

RY Trindade L.A.F., Takita M.A., Tamura R.B., Minte F.F.,

RY Comparison of the genomes of two Xanthomonas pathogens with differing RT host specificities ".

RMES, AB011790; AAM36446.1; -.

BREAPPORT SPRONGS73; Perri-phosph.

RY TIRREPRO, IPRONGS9; SaDPac_1; 1.

RY TIRREPRO, IPRONGS9; 3a0107603; 1.

RY TIRREPRO, TERROSANS, 1.

RY TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRREPROMES TIRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YNLPGVSE-HLKLNGKVLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGSGDT 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 PLFTQYLSKQDPEGWGKSPGFGTTVDFPAVPGALGENGNGGMVTGCAETPGCVAYIGISF 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 ERYPNVTITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKGLMNIALAISAQQVN 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 FNFTNYLSKVNPD-WKGKVGEGTAVQWPT---GIGGKGNEGVAAYVKQIKGGIGYVELSY 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 SFKMRPAQPRCGSKPPSGSPETGAGAGTVATTPASSPVTLAETGSTLLYPLFNLWGPAFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 SFKTRLA-------VGVLAASLALCAQAADVTGA--GASFIXPVMSKWS-ADY
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                                                                                                                                                                                                Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.6%; Score 438; DB 16; Length 339; 32.1%; Pred. No. 1.2e-14; ive 60; Mismatches 153; Indels 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35623 MW; 90E16808A4A710B1 CRC64;
                                                                             (TrEMBLrel. 22, Created)
(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                       339 AA.
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                                                                                                                                                                                                Bacteria; Proteobacteria; Gamm
Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                       Xanthomonas axonopodis (pv.
                                                                                                                                     Phosphate binding protein. PHOX OR XAC1578.
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                                       PRELIMINARY;
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SEQUENCE 339 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 ENFTNYLSKVNPD-WKSKVGEGTAVQWPT---GIGGKGNEGVAAYVKQIKGGIGYVELSY 221
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Hopkins C.M., White F.F., Heaton L.A., Guikema J.A., Leach J.E.;
Hopkins C.M., White F.F., Heaton L.A., Guikema J.A., Leach J.E.;
Hopkins C.M., White F.F., Heaton L.A., Guikema J.A., Leach J.E.;
Hopkins C.M., White F.F., Heaton L.A., Guikema J.A., Leach J.E.;

A homolog of an Escherichia coli phosphate-binding protein gene from DNA Seq. 5:299-305 (1995).

EMBL, X81478; CAS7231.1; -.
HISSP, POGLOSS, CASR7231.1; -.
InterPro; IPRO6659; SBP bac_1.
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                                                                                                                                                                                                                                                      Xanthomonas oryzae.
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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SROUENCE FROM N.A.
Tan Y.P., Leung K.Y.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Enterobacteriaceae, Edwardsiella.
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                                                                      01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2003 (TrEMBLrel. 23, Phosphate binding protein.
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Matches 115; Conserv
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32; Gaps 14;
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                                                                                                                                                                                                         145 QAAAGTVNIGASDAYLSEGDMAAHKGLMNIALAISAQQVNYNLPGV-SEHLKLNGKVLAA 203
                                                                                                                                                                                                                              69 QIIANIYUDFGASDAPLSDEKLAA-DGLFQFPTVIGGVVMAVNLPGVKSGELTLDGETLGD 127
                                                                                                                                                                                                                                                                                204 MYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGSGDTFLFTQYLSKQDPEGWGKSPG 263
                                                                                                                                                                                                                                                                                                     264 FGTTVDFPAVPGALGENGNGGMVTGCAETPGCVAYIGISFLDQASQRGLGEAQLGNSSGN 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 AVSPTEVSFSNAAKGADWSRSFAQDL-TNQA-----GDNVWPITSTTFILVHKASTKP 292
                                                                                                                                                         Length 346;
                                                     Query Match 8.5%; Score 431; DB 2; Length 346. Best Local Similarity 35.7%; Pred. No. 2.9e-14; Matches 121; Conservative 50; Mismatches 136; Indels
EMBL; AF248495; AAM45393.1; -. SEQUENCE 346 AA; 36264 MW; 9DA3670A6684B821 CRC64;
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Search completed: November 21, 2003, 16:08:17 Job time : 50.3698 secs

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1 MEHHHHHTAASDNFQLSQGG.....RAPVEADAGGGQKVLVRNVV 539
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                               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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(first entry)

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                                                                                                                                                                                                          The sequence represents Mycobacterium tuberculosis fusion protein, TDRA12-HTCC#1 and includes a His tag at the N-terminus to aid purification. Compositions comprising at least 2 heterologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially humans) against infection by Mycobacteria. The compositions contain at least 2 heterologous antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease if equently affecting patients with acquired immunodeficiency disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQ
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                                                                Lodes ML;
                                                                                                                              infections in mammals using fusion of heterologous antigens -
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                                                                Dillon DC,
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100.0%; Pred. No. 1.2e-219;
cive 0; Mismatches 0;
                                                                PD,
                                                                McNeil1
                                                              Houghton RL,
                                                                                                                              Vaccinating against Mycobacteria proteins comprising combinations
                                                                                                                                                                           Claim 17; Fig 8; 168pp; English
 99US-0158425
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                             (CORI-) CORIXA CORP.
                                                                                             WPI; 2001-290576/30
                                                              Reed S,
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                                                                                                                                                                                                                                                                                                                                                                                         543 AA;
 07-OCT-1999;
                                                                                                                            Vaccinating
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                                                              Skeiky Y,
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AAW73765 standard; Protein; 392 AA

AAW73765;

RESULT 2
AAW73765
ID AAW7
XX
AX
AC AAW7

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This sequence represents an immunogenic portion of a Mycobacterium tuberculosis antigen of the invention. The polypeptides are useful for immunotherapy to treat or prevent tuberculosis (especially in humans), e.g. they can be included with an acceptable carrier in pharmaceutical compositions or included in vaccines, and administered to induce protective immunity in a patient against M. tuberculosis. Tuberculosis a chronic, infectious disease generally caused by M. tuberculosis is a chronic, infectious disease generally results in serious complications and death. Pasion proteins containing the antigen, or DNA molecules can similarly be included with an acceptable carrier in pharmaceutical compositions or in vaccines and administered as above. The polypeptides are also useful for diagnosis of tuberculosis, by contacting dermal cells with at least one polypeptide and detecting an immune response (especially induration) on the patient's skin. Inhibiting the spread of tuberculosis requires vaccination and accurate diagnosis, since antibiotic therapy may not be effective due to the existence of an asymptomatic but contagious stage and to patient non-compliance. The polypeptides overcome concerns of safety and efficacy of current vaccination with live bacteria (usually Bacillus Calmette-Guerin) and clack of sensitivity and specificity of existing diagnostic techniques.
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                                                                          Antigen; M.tuberculosis protein; immunotherapy; tuberculosis; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polypeptide comprising immunogenic Mycobacterium tuberculosis antigen - useful for immunisation against M. tuberculosis infection to treat or prevent tuberculosis, and in diagnosis of tuberculosis
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                                       M. tuberculosis antigen clone hTcc#1 protein sequence
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; Mismatches 1;
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                                                                                                                                    Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents an immunogenic portion of a Mycobacterium tuberculosis antigen of the invention. The polypeptides are useful for immunotherapy to treat or prevent tuberculosis (especially in humans), e.g. they can be included with an acceptable carrier in pharmaceutical compositions or included with an acceptable carrier in pharmaceutical protective immunity in a patient against M. tuberculosis. Tuberculosis a chronic, infectious disease generally caused by M. tuberculosis is a chronic, infectious disease generally results in serious complications and death. Fusion proteins containing the antigen, or DNA molecules can similarly be included with an acceptable carrier in pharmaceutical compositions or in vaccines and administered as above. The plarmaceutical compositions or in vaccines and administered as above. The pharmaceutical compositions or in vaccines and administered as above. The pharmaceutical compositions or in vaccines and administered as above. The phypeptides are also useful for diagnosis of tuberculosis, by contacting dermal cells with at least one polypeptide and detecting an immune response (especially induration) on the patient 's skin. Inhibiting the spread of tuberculosis requires vaccination and accurate diagnosis, since antiblocit therapy may not be effective due to the existence of an asymptomatic but contagious stage and to patient non-compliance. The polypeptides overcome concerns of safety and efficacy of current vaccination with live bacteria (usually Bacillus Calmette-Guerin) and contaction with live bacteria (usually Bacillus Calmette-Guerin) and contaction with live bacteria (usually Bacillus Calmette-Guerin) and contaction with live bacteria (usually Bacillus Calmette-Guerin) and contaction with live bacteria (usually Bacillus Calmette-Guerin) and contaction with live bacteria (usually Bacillus Calmete-Guerin) and contaction with live bacteria (usually Bacillus Calmete-Guerin) and contaction with live bacteria (usually Bacillus Calmete-Guerin) and contaction with live bacte
  447
                                                 GATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAA 300
                                                                                                               507
                                                                                                                                               Antigen; M.tuberculosis protein; immunotherapy; tuberculosis; diagnosis;
  GATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAA
                                                                                                            STRQALRPRADGPVGAAAEQVGGQSQLVSAQGSQGMGGPVGMGGMHPSSGASKGTTTKKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated Mycobacterium tuberculosis antigens - used to develop products for the prevention, treatment and diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M. tuberculosis antigen clone hTcc#1 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Skeiky YAW;
                                                                                                                                                                                                                        SEGAAAGTEDAERAPVEADAGGGQKVLVRNVV 539
                                                                                                                                                                                                                                                              SEGAAAGTEDAERAPVEADAGGGQKVLVRNVV 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dillon DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 88-89; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   AAW73655 standard; Protein; 392 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Campos-Neto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-US10514.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAX01143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alderson MR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-MAR-1999
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IID AAW 73655

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                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 An isolated polypeptide comprising a Mycobacterium antigen, e.g., from Mycobacterium tuberculosis, useful in a vaccine for enhancing an immune response to and inhibiting development of a Mycobacterium infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 GATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRQALRPRADGPVGAAAEQVGGQSQLVSAQGSQGMGGPVGMGGMHPSSGASKGTTTKKY
                                                                                                                                                                                                                          DKYAGKNRNHVNFFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDLT
                                                                                                                                                                                                                                                                                         YIPVVGHALSAAFQAPFCAGAMAVVGGALAYLVVKTLINATQLLKLLAKLAELVAAAIAD
                                                                                                                                                                                                                                                                                                                                  121 YIPVVGHALSAAFQAPFCAGAMAVVGGALAYLVVKTLINATQLLKLLAKLAELVAAAIAD
                                                                                                                                                                                                                                                                                                                                                                                                                                181 IISDVADIIKGTLGEVWEFITNALNGLKELWDKLTGWVTGLFSRGWSNLESFFAGVPGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRQALRPRADGPVGAAAAEQVGGQSQLVSAQGSQGMGGPVGMGGMHPSSGASKGTTTKKY
                                                                                                148 MSRAFIIDPŢISAIDGLYDLLGIGIPNQGGILYSSLEYFEKALEELAAAFPGDGWLGSAA
                                                                                                                                         1 MSRAFIIDPTISAIDGLYDLLGIGIPNQGGILYSSLEYFEKALEELAAAFPGDGWLGSAA
                                                                                                                                                                                           208 DKYAGKNRNHVNFFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDLT
                                                                                                                                                                                                                                                                                                                                                                                     IISDVADIIKGILGEVWEFITNALNGLKELWDKLTGWVTGLFSRGWSNLESFFAGVPGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAA
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tuberculosis, Mycobacterium infection, gene therapy, anti bacterial, immunostimulant, clone hTcc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to the isolation of Mycobacterium tuberculosis antigen polypeptides (e.g. Tb224) and the nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polypeptide encoded by Mycobacterium tuberculosis clone hTcc#1.
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                                                Indels
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Score 1963; DB 20;
Pred. No. 3e-155;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEGAAAGTEDAERAPVEADAGGGQKVLVRNVV 539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 156-157; 161pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ovendale P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU08226 standard; Protein; 392 AA
71.78;
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08-AUG-2000; 2000US-0223828.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Skeiky Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                  Conservative
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N-PSDB; AAS12487.
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  Query Match
Best Local Similarity
Matches 391; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200162893-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-DEC-2001
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                                                                                                                                                                                                                                            61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361
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AAU08226
ID AAU0
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4059 /label= Peptide_4 /note= "Used for T-cell epitope mapping"	5372 /label= Peptide_5 /note= "Used for T-cell epitope mapping"	6685 /label= Peptide 6 /note= "Used for T-cell epitope mapping"	7998 /label= Peptide_7 /note= "Used for T-cell epitope mapping" 92 111	/label= Peptide_8 /note= "Used for T-cell epitope mapping" 105124	/label= Peptide_9 /note= "Used for T-cell epitope mapping"	11813 / Jabel= Peptide_10 Incre= "Used for T-cell epitope mapping" 131150	<pre>/label= Peptide 11 /note= "Used for T-cell epitope mapping" 144fd</pre>	/label= Peptide_12 /note= "Used for T-cell epitope mapping"	12	170189 /label= Peptide 14 /note= "Used for T-cell epitope mapping" 18320	/label= Peptide 15	19615 Jabel= Peptide 16 Inote= "Used for T-cell epitope mapping"	pitope	, i	adont d		/note= "Used for T-cell epitope mapping" 261280	/label= Peptide 21 /note= "Used for T-cell epitope mapping" 274 .294	/label= Peptide_22 /note= "Used for T-cell epitope mapping") 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,	/note= "Used for T-cell epitope mapping" 313332 /label pentide 25	/note= "used for T-cell epitope mapping" 325344	/label= Peptide 26 /note= "Used for T-cell epitope mapping" 339.,38	<pre>/label= Peptide_27 /note= "Used for T-cell epitope mapping" 352371</pre>
Peptide	Peptide	Peptide	Peptide Pentide	Pentide) q	Peptide Peptide	Peptide	(T	B Cd H	Peptide Peptide	4	reptide	Peptide	Peptide	Peptide	Peptide	Peptide	Pentide	1	Peptide	Peptide	Peptide	Peptide	Peptide	Peptide
encoding them. The invention describes compounds and mediagnosis of tuberculosis or for inducing protective in tuberculosis. The compounds comprise at least one immun	CC of one or more Mycobacterium proteins and nucleic acid molecules CC encoding such polypeptides. The Mycobacterium proteins and nucleic acid CC molecules encoding them can be used in diagnostic kits for the detection	compounds of the invent. Mycobacterium proteins		Sequence 392 AA; Query Match 71.7%; Score 1963; DE	Similarity 99.7%; Pred. No. 3e-155;	OY 148 MSRAFIIDPTISAIDGLYDLLGIGIPNQGGILYSSIBYFEKALEELAAAFPGDGWLGSAA 207 	208 DKYAGKURNHVNFFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLBFVRPVAVDLT	Db 61 DKYAGKURNHVNFFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDLT 120 OV 968 VIDKVGUBIGBABOADBGAGAMAKKGGATAVINKERTINKERTIKETARTAKTARTAN 391	121 YIPVVGHALSAAFQAPFCAGAMAVVGGALAYLVKTLINITQLKLIAKLAELVAAAIAD	QY 328 IISDVADIIKGILGEVWEFITNALNGLKELWDKLTGWVTGLFSRGWSNLESFFAGVPGLT 387 Db 181 11SDVADIIKGTLGEVWEFITNALNGLKELWDKLTGWVTGLFSRGWSNLESFFAGVPGLT 240		241	OY 448 STROALRPRADGPVGAAAEQVGGGGGLVSAQGSGGVGGPVGAGGHIPSSGASKGTTTKKY 507 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	CY 508 SEGAAAGTEDAERAPVEADAGGGKVLVRNVV 539	Db 361 SEGAAAGTEDAERAPVEADAGGGKVLVRNVV 392	SULT 5 U01882		AC AAU01882; XX DT 29-AUG-2001 (first entrv)	M. tuberculosis anti	XX XW HTCC#1; Mtb40; antigen, vaccine, tuberculosis; AIDS; XW accuired immunodeficiency disease.		Key Location/Qualifiers Peptide 120		Peptide 1433 /label= Peptide 2 /note= "Used for T-cell epitope mapping"	= Peptide_3 "Used for T-cell epitope mapping"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IISDVADIIKGILGEVWEFITNALNGLKELWDKLTGWVTGLFSRGWSNLESFFAGVPGLT 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSRAFIIDPTISAIDGLYDLLGIGIPNQGGILYSSLEYFEKALEELAAAFPGDGWLGSAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence represents Mycobacterium tuberculosis HTCC#1 (also known as Mtb40), an M. tuberculosis antigen. Compositions comprising at least 2 heterologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially humans) against infection by Mycobacteria. The compositions contain at least 2 heterologous antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease frequently affecting patients with acquired immunodeficiency disease, AlDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAA
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Pred. No. 3e-155;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                            Vaccinating against Mycobacteria infections in mammals using proteins comprising combinations of heterologous antigens
/label= Peptide_28
/note= "Used for T-cell epitope mapping"
365.384
/label= Peptide_29
/note= "Used for T-cell epitope mapping"
373.392
/label= Peptide_30
/note= "Used for T-cell epitope mapping"
                                                                                                                                                                                                                                                                                                                  Dillon DC,
                                                                                                                                                                                                                                                                                                                  McNeill PD,
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                                                                                                                                                                                                                                                                                                                  Houghton RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Fig 6; 168pp; English
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Best Local Similarity 99.7%;
Matches 391; Conservative (
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99US-0158425
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                                                                                                                                                                                                                                                                                 (CORI-) CORIXA CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 392 AA;
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N-PSDB; AAS03773.
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07-OCT-1999;
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This invention relates to a novel method for identifying essential genes for survival or virulence of mycobacteria species. The method comprises aligning the genomic sequence of a first mycobacterium species on a genomic sequence of a second mycobacterium species and selecting a polymucleotide sequence that is highly conserved in both genomes with no counterparts in other bacterial genomic sequences and that corresponds to an essential gene for the survival or virulence of mycobacterium species. The method of the invention is useful for detecting M. tuberculosis or M. leprae infection. The method reduces the number of potential new targets and protective antigens for new drugs and vaccine compositions to treat and prevent mycobacterial diseases, particularly tuberculosis and leprosy. The present sequence represents a marker protein from Mycobacterium tuberculosis, and Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DKYAGKNRHVNFFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDLT 120
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                                                                                                                                                                                                                                                                                                                           Mycobacterioses; survival; virulence; protective antigen; vaccine; mycobacterial disease; tuberculosis; leprosy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying and selecting genes for survival or virulence of mycobacteria by a comparative genomic analysis of the sequences Mycobacterium tuberculosis and M. leprae -
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99.7%; Pred. No. 3e-155;
live 0; Mismatches 1;
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                                                                     392
                                                              ABU05959 standard; Protein;
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Mycobacterium leprae.
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                                                       447
                                                                                                               300
                                                                                                                                                                         507
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181 IISDVADIIKGTLGEVWEFITNALNGLKELWDKLTGWVTGLFSRGWSNLESFFAGVPGLT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    recombinant nucleic acid molecule comprising a Leishmania TSA, M15 or 6H polynucleotide, useful as vaccine to elicit protective unity against pathogenic microorganisms e.g. Leishmania and
                                                                                                        241 GATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAA
                                                                                                                                                                                                                     301 STRQALRPRADGPVGAAABQVGGQSQLVSAQGSQGMGGPVGMGGMHPSSGASKGTTTKKY
                                                       GATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAA
                                                                                                                                                                      STROALRPRADGPVGAAABQVGGQSQLVSAQGSQGMGGPVGMGGMHPSSGASKGTTTKKY
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Pred. No. 3e-155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE29714 standard; Protein; 392 AA
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Gaps

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Query Match
Best Local Similarity 99.7%;
Matches 391; Conservative

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387
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207
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                        1 MSRAFIIDPTISAIDGLYDLLGIGIPNQGGLYSSLEYFEKALEELAAAFPGDGWLGSAA
                                                                               YIPVVGHALSAAFQAPFCAGAMAVVGGALAYLVVKTLINATQLLKLLAKLABLVAAAIAD
                                                                                                                                                       121 YIPVVGHALSAAFQAPFCAGAMAVVGGALAYLVVKTLINATQLLKLLAKLABLVAAAIAD
                                                                                                                                                                                                                                                                      STRQALRPRADGPVGAAAEQVGGQSQLVSAQGSQGMGGPVGMGGMHPSSGASKGTTTKKY
                                                                                                                                                                                                                                                                                                                                       STRQALRPRADGPVGAAAEQVGGGSQLVSAQGSQGMGGPVGMCGMHPSSGASKGTTTKKY
                                                             DKYAGKNRNHVNFFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDLT
                                                                                                                                                                                      IISDVADIIKGILGEVWEFITNALNGLKELWDKLTGWVTGLFSRGWSNLESFFAGVPGLT
                                                                                                                                                                                                                  IISDVADIIKGTLGEVWEFITNALNGLKELWDKLTGWVTGLFSRGWSNLESFFAGVPGLT
                                                                                                                                                                                                                                                  GATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fusion protein, antigen; serological sensitivity, immune response; tuberculosis; infection; vaccine; MTB40; HTCC #1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MTB39 antigen and MTB32A antigen from useful for eliciting immune response in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium species MTB40 (HTCC #1) protein.
                                                                                                                                                                                                                                                                                                                                                                             SEGAAAGTEDAERAPVEADAGGGQKVLVRNVV 539
                                                                                                                                                                                                                                                                                                                                                                                                         SEGAAAGTEDAERAPVEADAGGGOKVLVRNVV 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE17578 standard; Protein; 392 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; Page 120; 136pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reed S, Alderson M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0597796.
2001US-265737P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Composition comprising Mycobacterium species,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-147798/19.
N-PSDB; AAD28349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium sp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      skeiky Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE17578;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treatment of tuberculosis infection. Sequences of the invention are useful for eliciting an immune response in a mammal, e.g., human, immunised with BGG. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the polymucleotides are useful as diagnostic tools in patients infected with Mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as immunogens to generate or elicit a protective immune response in a patient and for raising anti-M. tuberculosis antibodies in a non-human animal. Sequences of the invention are also used as vaccines. MTB32A fusion proteins of the invention are useful as in vivo diagnostic agents for incradermal skin test. The present sequence is Mycobacterium species MTB40 (HTCC #1) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YIPVVGHALSAAFQAPFCAGAMAVVGGALAYLVVKTLINATQLLKLLAKLAELVAAAIAD 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 YIPVVGHALSAAFQAPFCAGAMAVVGGALAYLVVKTLINATQLLKLLAKLABLVAAAIAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAA 300
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                                                                                                                                                                                                                                                                                                                                                            148 MSRAFIIDPTISAIDGLYDLLGIGIPNQGGILYSSLEYFEKALEELAAAFPGDGWLGSAA
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/label= Histidine tag
/note= "Nickel chelating region used to aid
purification of the protein"
169..180
/note= "These residues are deleted to form t
HTCC#1(TM-1) protein sequence"
                                                                                                                                                                                                                                                                                                                               1; Indels
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                                                                                                                                                                                                                                                                                            Score 1963; DB 23
Pred. No. 3e-155;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acquired immunodeficiency disease; His Tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 SEGAAAGTEDAERAPVEADAGGGOKVLVRNVV
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99.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                              392 AA;
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Best Local Simil
Matches 391, C
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Binding-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 YIPVVGHALSAAFQAPFCAGAMAVVGGALKLAYLVVKTLINAKLTQLLKLLAKLAELVAA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence is Mycobacterium tuberculosis HTCC#1(TM-1)
representing HTCC#1 (an M. tuberculosis antigen) lacking the first
transmembrane domain and includes a His tag at the N-terminus to aid
purification. Compositions comprising at least 2 heterologous antigens,
as a fusion protein, and vectors expressing the fusion proteins are used
as a fusion protein, and vectors expressing the fusion proteins are used
as a fusion protein by Mycobacteria. The compositions contain at least 2
against infection by Mycobacteria. The compositions contain at least 2
individuals infected with tuberculosis, a disease frequently affecting
patients with acquired immunodeficiency disease, AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249 PGLTGATSGLSQVTGLFGAAGLSASSGLAAADSLASSASLPALAGIGGGSGFGGLFSLAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 DKYAGKNRNHVNFFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YIPVVGHALSAAFQAPFCAGAMAVVGGA--LAYLVVKTLINA--TQLLKLLAKLAELVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148 MSRAFIIDPTISAIDGLYDLLGIGIPNQGGILYSSLEYFEKALEELAAAFPGDGWLGSAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 AIADIISDVADIIKGTLGEVWEFITNALNGLKELWDKLTGWVTGLFSRGWSNLESFFAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       384 PGLTGATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             444 VHAASTRQALRPRADGPVGAAAEQVGGQSQLVSAQGSQGMGGPVGMGCMHPSSGASKGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                            fusion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 408;
                                                                                                                                                                                                                                                                                                                                                       Vaccinating against Mycobacteria infections in mammals using proteins comprising combinations of heterologous antigens
                                                                                                                                                                                                                                                                    DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Pred. No. 2.1e-153;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                504 TKKYSEGAAAGTEDAERAPVEADAGGGOKVLVRNVV
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                                                                                                                                                                                                                                                                  McNeill PD,
                                     /note= "In frame STOP codon"
                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Fig 9a; 168pp; English.
                                                                                                                                                                                                                                                                  Houghton RL,
                    /label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 98.7%;
Matches 391; Conservative
                                                                                                                                          2000WO-US28095
                                                                                                                                                                            99US-0158338
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                                                                                                                                                                                                                                 (CORI-) CORIXA CORP
Misc-difference 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              408 AA;
                                                                                                                                                                                                                                                                                                                       N-PSDB; AAS03777
                                                                       WO200124820-A1
                                                                                                                                        10-OCT-2000;
                                                                                                                                                                            07-OCT-1999;
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RESULT 10 AAU01887

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The sequence represents Mycobacterium tuberculosis fusion protein, HTCC#1(1-149) TDH9-HTCC#1(161-392) and includes a His tag at the HTCC#1(1-149) TDH9-HTCC#1(161-392) and includes a His tag at least 2 N-terminus to aid purification. Compositions comprising at least 2 heterologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially humans) against infection by Mycobacteria. The compositions contain at least 2 heterologous antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease frequently affecting patients with acquired immunodeficiency disease,
                                        383
                                                                              248
                                                                                                                         443
                                                                                                                                                                                                      503
                                                                                                                                                                                                                                            368
LTYI PVVGHALSAAFQAPFCAGAMAVVGGALAYLVVKTLINATQLLKLLAKLAELVAAAI
                                                                          189 ADIISDVADIIKGTLGEVWEFITNAKLLNGLKELWDKLTGWVTGLFSRGWSNLESFFAGV
                                                                                                                                                           249 PGLTGATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQ
                                                                                                                                                                                                                               109 VHAASTRQALRERADGEVGAAAEQVGGQSQLVSAQGSQGMGGPVGMGGMHPSSGASKGTT
                                          ADIISDVADIIKGILGEVWEFITNA--LNGLKELWDKLTGWVTGLFSRGWSNLESFFAGV
                                                                                                                       PGLTGATSCLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQ
                                                                                                                                                                                                      444 VHAASTRQALRPRADGPVGAAAEQVGGQSQLVSAQGSQGMGGPVGMGGMHPSSGASKGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccinating against Mycobacteria infections in mammals using fusion proteins comprising combinations of heterologous antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tuberculosis;
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AIDS; acquired immunodeficiency disease; His Tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         region used
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                                                                                                                                                                                                                                                                                                              369 TKKYSEGAAAGTEDAERAPVEADAGGGGKVLVRNVV
                                                                                                                                                                                                                                                                                    504 TKKYSEGAAAGTEDAERAPVEADAGGGOKVLVRNVV
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/note= "In frame STOP codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        purification of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3..8
/label= Histidine_tag
/note= "Nickel chelating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                             AAU01903 standard; Protein; 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .0-OCT-2000; 2000WO-US28095
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99US-0158425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
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Binding-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence is Mycobacterium tuberculosis HTCC#1(TM-1) representing HTCC#1 (an M. tuberculosis antigen) lacking all the transmembrane domains and includes a His tag at the N-terminus to aid purification. Compositions comprising at least 2 heterologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially humans) against infection by Mycobacteria. The compositions contain at least 2 heterologous antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease frequently affecting patients with acquired immunodeficiency disease, AIDS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 DKYAGKNRNHVNFFQELADLDRQLISLIHDQANAVQTTRD--ILEGAKKGLEFVRPVAVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lodes ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaccinating against Mycobacteria infections in mammals using fusion proteins comprising combinations of heterologous antigens
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                                                                                                                                                                                                                                                                                                                                                                                      /note= "These residues are deleted to form the
HTCC#1(TM-2) protein sequence"
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                                                                                                                                                                                                                                                               Location/Qualifiers
1..8
/labl= Histidine_tag
/note= "Nickel chelating region used to aid
purification of the protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dillon DC,
                                                                                                                                                                 HTCC#1(TM-2); antigen; vaccine; tuberculosis; AIDS;
acquired immunodeficiency disease; His Tag.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= OTHER
/note= "In frame STOP codon"
                                                                                                                         M. tuberculosis antigen HTCC#1(TM-2)
      standard; Protein; 408 AA
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                                                                                   (first entry)
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Best Local Similarity 98.7
Matches 391; Conservative
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N-PSDB; AAS03778.
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Binding-site
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07-OCT-1999;
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301 STRÓGTRSQAGVSAELSTEQFGGQQEPVSAQGSQGMGGSQGMGGMTPASTKSKKDERKKK
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                                                                                                                DKYAGKNRNHVNFFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDLT
                                                                          148 MSRAFIIDPTISAIDGLYDLLGIGIPNQGGILYSSLEYFEKALEELAAAFPGDGWLGSAA
                                                                                             MSRAFIIDPTISAIDGLYDLLGIGIPNQGGILYSSLEYFEKALEELAAAFPGDGWLGSAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGPVGMGGMHPSSGASKGTTTKKYSEGAAAGTEDAERAPVEADAGGGQKVLVRNVV
                                                         384;
                                     Length 788;
                                                         Indels
                                                                                                                                                     YIPVVGHALSAAFQAFFCAGAMAVVGGALAYLV-----
                                     Score 1718; DB 22;
Pred. No. 2.2e-134;
2; Mismatches 6;
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                                     62.8%;
49.5%;
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                                                         Conservative
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                   Sequence
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61 DXYAGQNRKRVDIFQELAELDKELIELIHNQANSVQTTRGILDGAKKALLFVRPVAIDLN '120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to a novel method for identifying essential genes for survival or virulence of mycobacteria species. The method comprises aligning the genomic sequence of a first mycobacterium species on a genomic sequence of a second mycobacterium species and selecting a polymucleotide sequence that is highly conserved in both genomes with no conterparts in other bacterial genomic sequences and that corresponds to an essential gene for the survival or virulence of mycobacterium species. The method of the invention is useful for detecting M. Tuberculosis or M. leprae infection. The method reduces the number of potential new targets and protective antigens for new drugs and vaccine compositions to treat and prevent mycobacterial diseases, particularly tuberculosis and Mycobacterium tuberculosis and Mycobacterium ieprae infention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mycobacteria by a comparative genomic analysis of the sequences Mycobacterium tuberculosis and M. leprae -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying and selecting genes for survival or virulence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.1%; Score 1263; DB 23;
62.9%; Pred. No. 7.8e-97;
ive 55; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 17; Page 224-225; 874pp; English
                                                                                                                                                                                                                                                                                           22-FEB-2001; 2001US-270123P.
                                                                                                                                                                                                                            2002WO-IB01973
Mycobacterium tuberculosis.
Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                          (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-759885/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 248; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  394 AA;
                                                                                              WO200274903-A2
                                                                                                                                                                                                                            32-FEB-2002;
                                                                                                                                                             26-SEP-2002
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267

9

240

505 360

> KYSEGAAAGTDDAERAPIEVQSGGKRALAQHVV 394 KYSEGAAAGTEDAERAPVEADAGGGQKVLVRNVV

8

Mycobacterioses; survival; virulence; protective antigen; vaccine; mycobacterial disease; tuberculosis; leprosy.

M. tuberculosis and M. leprae marker protein #53

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The sequence represents Mycobacterium tuberculosis fusion protein, HTCC#1(184-392)-TDH9-HTCC#1(1-129) and includes a His tag at the N-terminus to aid purfication. Compositions comprising at least 2 heterologus antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially humans) against infection by Mycobacteria. The compositions contain at least 2 heterologus antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease frequently affecting patients with acquired immunodeficiency disease,
128′YIPVVGHALSAAFQAPFCAGAMAVVGGALAYLVVKTLINATQLLKLLAKLAELVAAAIAD 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVADIIKGILGEVWEFITNALNGLKELWDKLTGWVTGLFSRGWSNLESFFAGVPGLTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 DVADIIKGILGEVWEFITINALNGLKELWDKLTGWYTGLFSRGWSNLESFFAGVPGLTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lodes ML;
                                                                                                                                                                                                                                                                                                                                 tuberculosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fusion
                                                             328 IISDVADIIKGILGEVWEFIINALNGLKELWDKLTGWVTGLFSRGWSNLESF 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vaccinating against Mycobacteria infections in mammals using proteins comprising combinations of heterologous antigens -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3..8
/label= Histidine_tag
/note= "Nickel chelating region used to aid
purification of the protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dillon DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                             AIDS; acquired immunodeficiency disease; His Tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 38.7%; Score 1060; DB 22; Best Local Similarity 100.0%; Pred. No. 1.7e-79; Matches 209; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                          M. tuberculosis antigen HTCC#1 fusion protein #1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McNeill PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= OTHER
/note= "In frame STOP codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                        AAU01902 standard; Protein; 744 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Skeiky Y, Reed S, Houghton RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 14; Fig 10; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-OCT-2000; 2000WO-US28095.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0158338
                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
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Binding-site
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07-0CT-1999;
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                                                                                                                                                                                                                                                    29-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       331
                                                                                                                                                                                                             AAU01902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                      AAU01902
                                                                                                                                   RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 DKYAGKNRNHVNFFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDLT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 MSRAFIIDPTISAIDGLYDLLGIGIPNQGGILYSSLEYFEKALBELAAAFPGDGWLGSAA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 representing the first transmembrane domain of HTCC#1 (an M. tuberculosis antigen) and includes a His tag at the N-terminus to aid purification: Compositions comprisaling at least 2 heterologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially humans) against infection by Mycobacteria. The compositions contain at least 2 heterologous antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease frequently affecting patients with acquired immunodeficiency disease, AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 MSRAFIIDPTISAIDGLYDLLGIGIPNQGGILYSSLEYFEKALBELAAAFPGDGWLGSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208 DKYAGKNRNHVNFFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lodes ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaccinating against Mycobacteria infections in mammals using fusion proteins comprising combinations of heterologous antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
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                                                                                                                                                                                                                                                                                                                                                                      region used to aid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dillon DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence is Mycobacterium tuberculosis HTCC#1(1-223),
                                                                                                                                                                                                             HTCC#1(1-223); antigen; vaccine; tuberculosis; AIDS;
acquired immunodeficiency disease; His Tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McNeill PD,
                                                                                                                                                                                                                                                                                                                                                                                                                             /label= OTHER
/note= "In frame STOP codon"
                                                                                                                                                                                                                                                                                                                                               /label= Histidine tag
/note= "Nickel chelating rec
purification of the protein
240
                                                                                                                                                                        M. tuberculosis antigen HTCC#1(1-223).
                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                       AAU01883 standard; Protein; 242 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Fig 7a; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reed S, Houghton RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0158338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000WO-US28095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0158425
                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis.
                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 99.6 es 231; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAS03774.
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Binding-site
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                                                                                                                                   29-AUG-2001
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                                                                                              AAU01883;
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Best Local 2
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                  RESULT 13
                                       AAU01883
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The sequence represents Mycobacterium tuberculosis fusion protein, HTCC#1(184-392) TDH9-HTCC#1(1-200) and includes a His tag at the N-terminus to aid purification. Compositions comprising at least 2 heterologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially humans) against infection by Mycobacteria. The compositions contain at least 2 heterologous antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease frequently affecting patients with acquired immunodeficiency disease,
                                                     510
                                                                    450
                   SGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAASTR
SGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAASTR
                                                     QALRPRADGPVGAAAEQVGGQSQLVSAQGSQGMGGPVGMGCMHPSSGASKGTTTKKYSEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lodes ML
                                                                                                                                                                                                                                                                                                                        HTCC#1(184-392)-TbH9-HTCC#1(1-200); antigen; vaccine; tuberculosis; AIDS; acquired immunodeficiency disease; His Tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaccinating against Mycobacteria infections in mammals using fusion proteins comprising combinations of heterologous antigens
                                                                                                                                                                                                                                                                                                                                                                                                                          3..8
/labbl= Histidine tag
/note= "Nickel chelating region used to aid
purification of the protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dillon DC,
                                                                                                                                                                                                                                                                                           M. tuberculosis antigen HTCC#1 fusion protein #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McNeill PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= OTHER
/note= "In frame STOP codon"
                                                                                                             539
                                                                                                                                      189 AAAGTEDAERAPVEADAGGGOKVLVRNVV 217
                                                                                                           AAAGTEDAERAPVEADAGGGOKVLVRNVV
                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                           AAU01904 standard; Protein; 815 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Fig 12; 168pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Houghton RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-OCT-2000; 2000WO-US28095.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0158338.
99US-0158425.
                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-290576/30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  815 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                             Key
Binding-site
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07-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                             511
                                                                                                                                                                                                                                       AAU01904;
391
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Length 815;

38.7%; Score 1060; DB 22;

Query Match

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                                                                                                                           450
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                                                                                           68
                                                                                                                                                                                       451 QALRPRADGPVGAAAEQVGGQSQLVSAQGSQGMGGPVGMGGMHPSSGASKGTTTKKYSEG
                                                                                                                                                                                                        129 QALKPRADGPVGAAAEQVGGQQLVSAQGSQGWGGPVGMGGMHPSSGASKGTTTKKYSEG
                                                            331 DVADIIKGILGEVWEFITNALNGLKELWDKLTGWVTGLFSRGWSNLESFFAGVPGLTGAT
                                                                                  9 DVADIIKGILGEVWEFIINALNGLKELMDKLIGWVIGLFSRGWSNLESFFAGVPGLIGAT
                                                                                                                           391 SGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAASTR
                                                                                                                                               Gaps
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0
                                Indels
             Pred. No. 1.9e-79; Mismatches 0;
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                                                                                                                                                                                                                                                                                    189 AAAGTEDAERAPVEADAGGGGKVLVRNVV 217
                                                                                                                                                                                                                                                                                                                                  Search completed: November 21, 2003, 16:03:21 Job time : 33.6333 secs
100.0%; Pr
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             Best Local Similarity
Matches 209; Conser
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Sequence Sequence Sequence Sequence Sequence Sequence

Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence

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148 MSRAFIIDPTISAIDGLYDLLGIGIPNQGGILYSSLEYFEKALEELAAAFPGDGWLGSAA
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ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EMB PC Compatible
COMPUTER: EMB PC Compatible
COMPUTER: DEM PC Compatible
COMPUTER: DEM PC COMPA:
COMPUTER: DEM PC COMPA:
COMPUTER: DEM PC COMPA:
COMPUTER: DEM PC COMPA:
APPLICATION DATA:
APPLICATION NUMBER: US/9/973,009
FILING DATE: 05-MAY-1998
CLEASIFICATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.441C1
TELEFAM: 206-622-4900
TELEFAM: 206-622-4900
TELEFAM: 206-622-4900
TELEFAM: 392 amino acids
FWACTH: 392 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 138, Application US/09073009
Patent No. 6555653
GENERAL INFORMATION:
APPLICANT: Alderson, Mark
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF
TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF
CORRESPONDENCES: 144
CORRESPEED: SEED and BERRY
STREET: 6300 Coumbia Center, 701 Fifth Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1963; DB 4;
Pred. No. 4.5e-166;
0; Mismatches 1;
US-09-620-412C-325
US-09-598-419-325
US-09-508-419-325
US-09-606-421B-354
US-09-606-421B-354
US-09-620-412C-349
US-09-598-419-349
US-09-598-419-399
US-09-598-419-399
US-09-598-419-309
US-08-818-1112-79
US-08-818-1112-79
US-08-00-556-79
US-08-00-756-79
US-08-18-111-67
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US-08-818-111-67
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US-08-818-111-67
US-08-818-111-67
US-08-818-111-67
US-09-056-556-67
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(c) 1993 - 2003 Compugen Ltd.
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TITLE OF INVENTION: COMPOSITIONS AND METHODS F
TITLE OP INVENTION: DIAGNOSIS OF CHLAMYDIAL I
FILE REPERBNCE: 210121.46907
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING BATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FASTSEQ for Windows Version 3.0/4.0
                                                                                                 348 ALQQLAQPTQGTTPSSKLGGLWKTVSPHRSP---
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Patent No. 6448234
GENERAL INFORMATION:
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LENGTH: 585
TYPE: PRT
ORGANISM: Chlamydia trachomatis
US-09-620-412C-337
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APPLICANT: Skeiky, Yasir
APPLICANT: Alderson, Mark
APPLICANT: Campos Mark
APPLICANT: Campos Mark
APPLICANT: Campos Marco, Antonio
APPLICANT: Campos Marco, Antonio
TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: Mad The True of September 10408
CURRENT PELINON NUMBER: US/09/223,040
CURRENT FILING DATE: 1998-12-30
NUMBER OF SEQ. ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
LENGTH: 729
LENGTH: 729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 TKSGGTRTGNVTLAEGPPAEFLVPRGSM----SRAFIIDP---TISAIDGLYDLLGIGI 172
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                          DKYAGKNRNHVNFFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDLT
                                                                                               XIPVVGHALSAAFQAPFCAGAMAVVGGALAXLVVKTLINATQLLKLLAKLAELVAAAIAD
                                                                                                                                                  IISDVADIIKGILGEVWEFITNALNGLKELWDKLTGWVTGLFSRGWSNLESFFAGVPGLT
                                                                                                                                                                          181 IISDVADIIKGTLGEVWEFITNALNGLKELWDKLTGWVTGLFSRGWSNLESFFAGVPGLT
                                                                                                                                                                                                                                                         241 GATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 PNQGGILYSSLEYFEKALEELAAAFPGDGWLGSAADKYAGKONRNHVNFFQ-----ELAD
DKYAGKNRNHVNFFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDLT
                                                                      YI PVVGHALSAAFQAPFCAGAMAVVGGALAYLVVKTLINATQLLKLLAKLABLVAAAIAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.6%; Score 809; DB 4; Length 729; 40.0%; Pred. No. 3.5e-63;
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                                                                                                                                                                                                                                                                                                                                                                                                       361 SEGAAAGTEDAERAPVEADAGGGQKVLVRNVV 392
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ORGANISM: Artificial Sequence
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US-09-223-040-2
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Best Local S:
Matches 221
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  526
                                         464 ASAATSTPKS----APVSTALSTPSSSTVSSLTILLAASSQASPATSNKETQDPNAD 515
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471 QSQLVSAQGSQGMGGPVGMGGMHPSSGASKGTTTKKYSEGAAAGTEDAERAPVEAD
                                                                                                                               ISOUR 5
IS-00-620-412C-353
S-00-620-412C-353
Sequence 353, Application US/09620412C
Patent No. 6448234
GENERAL INFORMATION:
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REPERENCE: 210121.469C7
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
LENGTH: 583
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PRGANISM: Chlamydia trachomatis
3-620-412C-353
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SENERAL INFORMATION:
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US-09-598-419-333
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; Pred. No. 3.8e-56;
49; Mismatches 186; Indels 140;
                         Sequence 313, Application US/09598419
Fatent No. 6565656
GENERAL INFORMATION:
APPLICANT: Scholler, John
TITLE OF INVENTION:
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: 10121.46906
CURRENT APPLICATION NUMBER: US/09/598,419
CURRENT APPLICATION NUMBER: US/09/598,419
CURRENT APPLICATION NUMBER: US/09/598,419
CURRENT APPLICATION NUMBER: US/09/598,419
CURRENT APPLICATION NUMBER: US/09/598,419
CURRENT FILING DATE: 2000-06-20
NUMBER: OF SEQ ID NOS: 357
SOFTWARE: FREESEQ for Windows Version 3.0/4.0
                                                                                                                                                                                                                                                            TYPE: PRT , ORGANISM: Chlamydia trachomatis US-09-598-419-353
                                                                                                                                                                                                                                                                                                                            26.6%;
37.8%;
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Matches 228; Conservative
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             -09-598-419-353
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; Sequence 333, Application US/09620412C; Patent No. 6448234

RESULT 7 US-09-620-412C-333

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NNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -APVKKPTEPK 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 175;
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.46907
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: PastSEQ for Windows Version 3.0/4.0
SEQ ID NO 333
                                                                                                                                                                                                                                                                                                                                                                                                         Length 518;
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APPLICANT: Scholler, John
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C6
CURRENT APPLICATION NUMBER: US/09/598,419
NUMBER OF SEQ ID NOS: 357
                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 722.5; DB 4;
; Pred. No. 9.9e-56;
44; Mismatches 132;
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Best Local Similarity 37.3%;
Matches 209; Conservative 44
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Conservative
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ilarity 71.3%;
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Best Local Similarity
Matches 149; Conserv
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Matches 149; Conserv
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                                                                                                                                                          Indels 175;
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APPLICANT: Bhatia, Ajay
APPLICANT: Bhatia, Ajay
APPLICANT: Bhatia, Ajay
APPLICANT: Fling, Steve
APPLICANT: Fling, Steve
APPLICANT: Maisonneuve, Jeff
APPLICANT: Maisonneuve, Jeff
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REPERENCE: 210121.469CS
CURRENT APPLICATION NUMBER: US/09/556,877
CURRENT APPLICATION NUMBER: US/000-04-19
NUMBER OF SEQ ID MOS: 305
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 518,
                                                                                                                       26.4%; Score 722.5; DB 4; 37.3%; Pred. No. 9.9e-56; ive 44; Mismatches 132;
SOFTWARE: FastSEQ for Windows Version 3.0/4.0 SEQ ID NO 333 LENGTH: 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              315 GAIFGGSTISL-SGITKATFSCNSAEVP-
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Patent No. 6432916
GENERAL INFORMATION:
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                                                    TYPE: PRT ORGANISM: Chlymadia trachomatis
                                                                                                                                        Similarity 37.3
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ORGANISM: Chlamydia
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US-09-556-877-196
                                                                            ; OKGAN15M: UNS-09-598-419-333
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                                                                                                                       Query Match
Best Local S
Matches 209
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61 NNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQ 120
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                                                                                              1 MHHHHHHAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVD
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Length 525;
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Sequence 196, Application US/09598419

Sequence 196, Application US/09598419

Patent No. 665886

GRENEAL INFORMATION:
APPLICANT: Scholler, John
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C6
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                                                   Indels
     DB 4;
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Score 717.5; DB 4;
Pred. No. 2.8e-55;
6; Mismatches 13;
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Pred. No. 2.8e-55;
6; Mismatches 13
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Fatent No. 6448234
GENERAL INPORMATION:
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFF;
FILE REFERENCE: 210121.469C7
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FateseQ for Windows Version 3.0/4.0
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Query Match 25.9%; Score 709.5; DB 4; Best Local Similarity 37.5%; Pred. No. 2.3e-54; Matches 214; Conservative 53; Mismatches 187;
                                                                                                                                                                                                                                                                                            360 KRLSYHGYSSASKGYTVSSQASGAHGHKFLL 490
                                                                                                                                                                                                                                                                          SEGAAAGTEDAERA-PVEADAGG--GQKVLV 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Chlamydia trachomatis
US-09-598-419-321
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LENGTH: 715
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ORGANISM:
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                                                                                                                                                                                           41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 321, Application US/09620412C
Patent No. 6448234
GENERAL INFORMATION:
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
FILE REFERENCE: 210121,469C7
CURRENT APPLICATION NUMBER: US/09/620,412C
UNRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOPTWARE: FastSEQ for Windows Version 3.0/4.0
                                                                                                                                                             Length 525;
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                                                                                                                                                             DB 4;
                                                                                                                                                                                           13;
                                                                                                                                                           Score 717.5; DB 4.
Pred. No. 2.8e-55;
6; Mismatches 13.
CURRENT APPLICATION NUMBER: US/09/596,419
CURRENT FILING DATE: 2000-06-20
CUMBER OF SEQ ID NOS: 357
SOFTWARE: FASCSEQ for Windows Version 3.0/4.0
SEQ ID NO 196
LENGTH: 525
TYPE: PRT
ORGANISM: Chlamydia
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US-09-620-412C-321
                                                                                                                                                           26.2%;
71.3%;
                                                                                                                                                          Query Match
Best Local Similarity 71.3
Matches 149; Conservative
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Sequence 321, Application US/09598419
Sequence 321, Application US/09598419
Sequence 321, Application US/09598419
GENERAL INFORMATION
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Skelky, Yasir A.W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REPERENCE: 210121.46966
CURRENT APPLICATION NUMBER: US/09/598,419
CURRENT FILING DATE: 2000-06-20
SURRENT FILING DATE: 2000-06-20
SURMER OF SEQ ID NOS: 357
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
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397 TGLFGAAGLSASSGLAHADSLASSASLP---ALAGIGGGSGFGGLPSLAQVHAASTRQAL
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Patent No. 656586
GENERAL INFORMATION:
TOTALE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT APPLICANT: Scholler, John
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C6
CURRENT APPLICATION NUMBER: US/09/598,419
CURRENT FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 357
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
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APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C7
CURRENT APPLICATION NUMBER: US(9)/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
ENGTH: 715
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                                                                                                                                                                 508 SEGAAAGTEDAERA-PVEADAGG--GOKVLV 535
                                                                                                                                                                                                         460 KRLSYHGYSSASKGYTVSSQASGAHGHKFLL 490
                                                                                                                                                                                                                                                                                                                  Sequence 329, Application US/09620412C Patent No. 6448234
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ORGANISM: Chlamydia trachomatis
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; ORGANISM: Chlamydia trachomatis
US-09-598-419-329
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US-09-620-412C-329
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                                                                                                                                                                                                                                                                                             ---LVPRGSMSRAFIIDPTISAIDGLYDLL 168
                                                                                                                                         1 MHHHHHHTAASDNFQLSQGGGFAIPIGQAMAIAGQIK----LPTVHIGPTAFLGLGVVD 56
                                                                                             1 MHHHHHHAASDNFQLSQGGGGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVD
                                                 24;
Length 715;
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Score 708; DB 4;
Pred. No. 3.1e-54;
13; Mismatches 26
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ne : 12.3667 secs
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ilarity 70.7%;
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Sequence 29, Appl
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Sequence 2, Appli
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Sequence 55, Appl
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                                                                                                                                                November 21, 2003, 16:08:22 ; Search time 21.0222 Seconds (without alignments) 4680.740 Million cell updates/sec
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1 MHHHHHTAASDNFQLSQGG......RAPVEADAGGGQKVLVRNVV 539
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-793-366-138
US-10-080-170-A-29
US-10-080-170-610
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US-10-080-170-610
US-10-359-460-2
US-10-098-772A-16
US-10-098-772A-16
US-10-098-772A-18
US-09-841-132-333
US-10-359-460-28
US-10-359-460-28
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Listing first 45 summaries
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ALIGNMENTS

US-09-073-009-138

J Sequence 138, Application US/09073009

J Sequence 138, Application US/09073009

Sequence 138, Application US/09073009

Sequence 138, Application US/09073009

APPLICANT: Aderson, Mark

APPLICANT: Dillon, Davin C.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Campos-Netc, Antonio

TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF NUMBER OF SEQUENCES: 144

CORRESPONDENCES: 144

CORRESPONDENCES: 144

CORRESPONDENCES: 1600

STREET: 6300 Coumbia Center, 701 Fifth Ave.

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98104

COUNTRY: US

ZIP: 98104

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: 108/09/073,009

FILING BATE: 05-MAY-1998

CLASSIFICATION NUMBER: 210121.441C1

TELEPANE: 206-622-4900

TELEPANE: 206-622-4900

TELEPAN: 206-622-4910

TELEPAN: 206-622-4910

TELEPAN: 206-622-4910

TELEPAN: 206-622-4910

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Best Local Similarity 99.7
Matches 391; Conservative
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APPLICANT: John, Shyian
APPLICANT: Lodes, Michael
APPLICANT: Lodes, Michael
APPLICANT: Lodes, Michael
APPLICANT: Corrixa Corporation
ITILE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy
ITILE OF INVENTION: Of Tuberculosis
ITILE OF INVENTION: Of Tuberculosis
ITILE OF INVENTION WINBER: US, 60/185,037
CURRENT APPLICATION NUMBER: US, 60/185,037
PRIOR APPLICATION NUMBER: US, 60/185,037
PRIOR APPLICATION NUMBER: US, 60/223,828
PRIOR APPLICATION NUMBER: US, 60/223,828
PRIOR APPLICATION NUMBER: US, 60/223,828
PRIOR APPLICATION NUMBER: US, 60/223,828
NUMBER OF SEQ ID NOS: 164
SEQ ID NO 03: 164
SEQ ID NO 03: Lode
CENTRALE: PatentIN Ver. 2.1
SEQ ID NO 138
CENTRALE: PATENTION NUMBER: US, 60/223,828
COFTWARE: PATENTION NUMBER: US, 60/223,828
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99.7%; Pred. No. 4.9e-145;
iive 0; Mismatches 1;
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Similarity 99.7%; Pred. No. 4.9e-145;
91; Conservative 0; Mismatches 1;
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                           TOPOLOGY: linear

MOLECULE TYPE: protein

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        STRANDEDNESS:
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Best Local Simil
Matches 391; C
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Publication No. US20030175294A1

GENERAL INFORMATION:

APPLICANT: Skeiky, Yasir

APPLICANT: Generan Jeffrey

APPLICANT: Goderian Jeffrey

APPLICANT: Corrac Corporation

TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a

TITLE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION UNMERS: US/10/098,732A

CURRENT FILING DATE: 2003-04-29

PRIOR FILING DATE: 2003-04-29

PRIOR FILING DATE: 2003-04-29

PRIOR FILING DATE: 2003-04-39

PRIOR FILING DATE: 2003-04-39

SOFTWARE: PatentIn Ver. 2.1
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MSRAFIIDPTISAIDGLYDLLGIGIPNQGGILYSSLEYFEKALEELAAAFPGDGWLGSAA
                                                         DKYAGKNRNHVNFFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDLT
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US-10-098-732A-29
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TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYDAXIS OR TITLE OF INVENTION: TERATHENT OF MYCOBACTERIOSES
FILE REFERENCE: 03495,0218
CURRENT PEPLICATION NUMBER: US/10/080,170
CURRENT PILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/270,123
PRIOR FILING DATE: 2001-02-2
SOFTWARE: PALENTIN VEY: 2.1
SEQ ID NOS: 652
SOFTWARE: PALENTIN VEY: 2.1
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GATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAA 447
                               241 GATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLFSLAQVHAA 300
                                                                                                              STROALRPRADGPVGAAAEQVGGQSQLVSAQGSQGMGGPVGMGGMHPSSGASKGTTTKKY 360
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                                                                                                                                                     SEGAAAGTEDAERAPVEADAGGGQKVLVRNVV 539
                                                                                                                                                                            361 SEGAAAGTEDAERAPVEADAGGGOKVLVRNVV 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-080-170-610
                                                                                                                                                                                                                                                                                        , Sequence 610, Application US/10080170 ; Publication No. US20030129601A1 ; GENERAL INFORMATION:
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US-10-080-170-610
388
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Sequence 53, Application US/10080170 Publication No. US20030129601A1

RESULT 5 US-10-080-170-53

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APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Seelly, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
TITLE OF INVENTION: Fusion Prottiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: Posion Prottiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: 1999-04-07
FILE OF INVENTION NUMBER: US 09/2287,849
CURRENT FILING DATE: 1999-04-07
FRIOR APPLICATION NUMBER: US 08/912,578
FRIOR APPLICATION NUMBER: US 08/925,197
FRIOR FILING DATE: 1998-02-18
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APPLICANT: COLE, S.T.
TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
FILE REFERENCE: 03495,0218
CURRENT APPLICATION NUMBER: US,10/080,170
CURRENT FILING DATE: 2002-06-10
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 652
SOFTWARE: 2001-02-22
SOFTWARE: 2001-02-22
SOFTWARE: 2001-02-22
SOFTWARE: 2001-02-22
SOFTWARE: 304
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46.1%; Score 1263; DB 16;
Best Local Similarity 62.9%; Pred. No. 2.1e-90;
Matches 248; Conservative 55; Mismatches 89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Mycobacterium leprae
US-10-080-170-53
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US-09-287-849-2
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APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Carixa Corporation
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
FILE REFERENCE: 014058-009020US
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                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
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                                                                                                                                                                                                                                    29.6%; Score 809; DB 9; Length 729;
40.0%; Pred. No. 1.4e-54;
tive 69; Mismatches 170; Indels
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/223,040
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 729
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; Publication No. US20030147911A1
; GENERAL INFORMATION:
                                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 40.0
Matches 221; Conservative
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US-10-359-460-2
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276 ISAAFQAPFCAGAMAVVGGALAYLVVKTLINATQLLKLLAKLAELVAAAIAD-IISDVAD 334
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OTHER INFORMATION: Description of Artificial Sequence:tri-fusion US-10-359-460-2
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Best Local Similarity 40.0%; Pred. No. 1.4e-54;
Matches 221; Conservative 69; Mismatches 170;
CURRENT APPLICATION NUMBER: US/10/359,460
CURRENT FILING DATE: 2003-02-05
PRIOR FILING DATE: 1899-04-07
PRIOR FILING DATE: 1997-04-07
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-03-13
PRIOR PILING DATE: 1997-03-13
PRIOR PILING DATE: 1997-03-13
PRIOR PILING DATE: 1997-00-01
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
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US-10-008-732A-16
Gequence 16, Application US/10098732A
; Publication No. US20030175294A1
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ORGANISM: Artificial Sequence
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## APPLICANT: Brancon, Mark
### APPLICANT: Guderian, Jeffrey
### APPLICANT: Guderian, Jeffrey
### APPLICANT: Corixa Corporation
### TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
### TITLE OF INVENTION: Heishmania Antigen
### TITLE OF INVENTION: Leishmania Antigen
### CURRENT FILING DATE: 201201005
### CURRENT FILING DATE: 2003-04-29
### PRIOR APPLICATION NUMBER: US 60/275,837
### RICA FILING DATE: 2001-03-13
### NUMBER OF SEQ ID NOS: 80
### SSCTWARE: PatentIn Ver. 2.1
### SSCTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             348 ALQQLAQPTQGTTPSSKLGGLWKTVSPHRSP-----ISMMVSMANNHMSMTNSG 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V-SMINTLS--SMLKGFAPAARQAVQTAAQNGVRAMSSLGSSLGSSGLGGGGVAANLGRA 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGFGGLPSLAQVHAASTRQALRPRADG----PVGAAAEQVGGQSQLVSAQGSQGMGG-PV 487
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                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MHHHHHHHAASDNFQLSQGGGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVD
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                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                           Description of Artificial Sequence:tri-fusion protein MTB72F (Ral2-TbH9-Ra35 or MTB32-MTB39 fusion)
                                                                                                                                                                                                                                                                                                                                                                                                         92;
                                                                                                                                                                                                                                                                                                                                                                      29.6%; Score 809; DB 12; Length 729; llarity 40.0%; Pred. No. 1.4e-54; Conservative 69; Mismatches 170; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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OTHER INFORMATION: DO
OTHER INFORMATION: P
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US-10-098-732A-16
                                                                                                                                                                                                                                                                                                                                                                                                 221,
                                                                                                                                                                                                                EQ ID NO 16
LENGTH: 729
TYPE: PRT
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Best Local S
Matches 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  335 IIKGI-----LGEVWEFITNALNGLKELWDKLTGWVTGLFSRGWSNLESFFAG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----SNMVSMANN 388
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APPLICANT: Skelky, Yasir
APPLICANT: Brannon, Mark
APPLICANT: Brannon, Mark
APPLICANT: Grata Corporation
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
TITLE OF INVENTION: Heterologous Fusion Protein Constructs
TITLE OF INVENTION: Heterologous Fusion Protein Constructs
TITLE OF INVENTION: Leishmania Antigen
FILE REFERRNCE: 01408-01201003;
CURRENT FILING DATE: 2003-04-29
PRIOR PRING DATE: 2001-03-13
SOFTWARE: Patentin Ver. 2.1
SSOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 PNOGGILYSSLEYFEKALEELAAAFPGDGWLGSAADKYAGKNRNHVNFFQ-----ELAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence:WTB72FWutSA OTHER INFORMATION: (Ra12-TbH9-Ra35MutSA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227 LDRQLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDL--TYIPVVG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.6%; Score 809; DB 12;
39.5%; Pred. No. 1.4e-54;
iive 66; Mismatches 169;
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, Sequence 65, Application US/10098732A
; Publication No. US20030175294A1
; GENERAL INFORMATION:
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Best Local Similarity 39.5'
Matches 220; Conservative
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18;

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US-10-359-460-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNMVSMANN 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230 AQVRVAAAAYETAYGLTVPPPVI--AENRAELMILIATNLLGQNTPAIAVNEAEYGEMWA
                                                                                                                                                                                                                                                                                                                                                                                          CTHER INFORMATION: Description of Artificial Sequence:WTB72F-WAPS
CTHER INFORMATION: (195f) fusion construct, TB MTB72F (Ral2-TbH9-Ra35)
OTHER INFORMATION: linked to Leishmania thiol-specific antioxidant
CTHER INFORMATION: (TSA or MAPS)
US-10-098-7323-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                APPLICANT: Guderian, Jeffrey
APPLICANT: Guderian, Jeffrey
APPLICANT: Gorixa Corporation
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising
TITLE OF INVENTION: Letshmania Antigen
FILE REFERENCE: 014058-01201005
CURRENT APPLICATION WIMBER: US,10/098,732A
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: US 60/275,837
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 12: Length 930; Local Similarity 39.5%; Pred. No. 1.9e-54; Locservative 66; Mismatches 169; Indels 102;
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                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
Skeiky, Yasir
                                                                                                                                                                                                                                                                              SEQ ID NO 65
LENGTH: 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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US-09-287-849-28 ; Sequence 28, Application US/09287849 ; Patent No. US2002009459A1

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APPLICANT: SERIE, W. APPLICANT.
APPLICANT: Alexanon, Mark
APPLICANT. Alderson, Mark
APPLICANT. Alderson, Mark
APPLICANT. Alderson, Mark
APPLICANT. Alderson, Mark
APPLICANT. Campos-Neco, Antonio
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APPLICANT. Campos-Neco, Antonio
APPLICANT. Campos-Neco, Antonio
APPLICANT. Read, Steven G.
APPLICANT. National Dillon, Davin C. Antonio
APPLICANT. National Dillon, Davin C. Antonio
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                                                                            269 IPVVGHALSAAFQAPFCAGAMAVVGGALAYLVVKTLINATQLLKLLAKLAELVAAAIADI
                                                                                                                                                                                                                                                                                         364 LINNISEKHGGGAFVIKEISQIYTSDVETIPGIT-PVHGETVITGNKSTGGNGGGVCTKR
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                                                                                                                  TNITG-IIEIANNKATDVGGGAYVKGTL-----TCENSHR-LQFLKNSSDKQGG----
                                                                                                                                                               329 ISDVADIIKGILGEVWEFITNALNGLKELWDKLTGWVT--GLFSRG-----WSNLESF-
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Patent No. US20020061848A1
GENERAL INPORMATION:
APPLICANT: Bhatia.
APPLICANT: Bhatia.
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: Deter
FILE REFERENCE: 210121.469C8
CURRENT APPLICANT: 2001-04-23
NUMBER OF SEQ ID NOS: 599
SOFTWARE: EastSEQ for Windows Version 3.0/4.0
SEQ ID NO 353
LENGTH: 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.6%; Score 728; DB 9; Length 583; 37.8%; Pred. No. 2.1e-48; Live 49; Mismatches 186; Indels 140;
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US-09-841-132-353
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Best Local Similarity 37.8
Matches 228; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                           MHHHHHHHTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVD 61
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                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence:bi-fusion US-10-359-460-28
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                                                                                                                                                                                                                                                                                                         Length 231;
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                                                                                                                                                                                                                                                                                                  27.0%; Score 739; DB 12;
llarity 100.0%; Pred. No. 8.1e-50;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 337, Application US/09841132
| Sequence 337, Application US/09841132
| Patent No. US200200061848A1
| GENERAL INFORMATION:
| APPLICANT: Bhatia, Ajay
| APPLICANT: Skeiky, Yaair A.W.
| APPLICANT: Probst, Peter
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INF!
| FILE REPERENCE: 210121.469C8
| CURRENT APPLICATION NUMBER: US/09/841,132
| CURRENT FILING DATE: 2001-04-23
| NUMBER OF SEQ ID NOS: 599
| SEQ ID NO 337
| LENGTH: 585-
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR FILING DATE: 1998-04-07
PRIOR PLILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFUMARE: Patentin Ver: 2.1
LENGTH: 231
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Best Local Similarity
Matches 141; Conserva
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US-09-841-132-337
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Matches 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171 GIPNOGGILYSSLE----YFEKALEELAAAFPGDGWLG-----SAADKYAGKNRNHV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       219 NFFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDLTYIPVVGHALSA 278
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                                                                                                                     406 SASSGLAHADSLASSASL----PALAGIGGGSGFGGLPSLAQVHAASTRQALRPRADGP 460
                                                                                                                                                                                 461 VGAAAE----QVGGQSQLVSAQGSQGMGGPVGMGGMHPSSGASKGTTTKKYSEGAAAGTE 516
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                :: : | | | | :: : | | | 328 --KINRFFASTAEPAAPSLIEAESDQTDQTETSDTNSDIDVSIENILNVAINQNTSAKKG 385
                                                                                    -----GAIYGKKAKLSRINNLE-----LSGNSSQDVGGGLCLTESVEFDAIG- 427
                                                                                                                                                ---SLLSHYNSAAKEGGVIHSKTVILSNLKSTFTFADNTVKAIVESTPEAPBEIPPVEGE 484
                                                            354 LKELWDKLTGWVTGLFSR--GWSNLESFFAGVPGLTGATS-----GLSQVTGL-FGAAGL 405
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-- IIKGILGEVWEFITNALNG 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 175; Gaps
                                                                                                                                                                                                                                                                                                                                                  DB 9; Length 518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 26.4%; Score 722.5; DB 9;
Best Local Similarity 37.3%; Pred. No. 4.8e-48;
Matches 209; Conservative 44; Mismatches 132;
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 307 ATQLLKLLAKLAELVAAAIADIISDVAD---
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                                                                                                                                                                                                                                                  517 DAE 519
                                                                                                                                                                                                                                                                               545 SNE 547
                                                                                                                                                                                                                                                                                                                             RESULT 15
US-09-841-132-333
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ò	399LFGAAGLSASŞGLAHADSLASŞASLPALAGIGGGSGFGGLPSLAQVHASTRQALRPR 456
qq	315 GAIFGGSTISL-SGITKATFSCNSAEVPAPVKKFTEPK 351
ò	457 ADGPVGAAAEQVGGQSQLVSAQGSQGMGGPVGMGGMHPSSGASKGTTTKKXSEG 510
QQ	352 AQTASETSGSSSSSGNDSVSSPSSSRAEPAAANLQSHFICATAT 395
ò	511 AAAGTEDAERAFVEADAGGG 530
qq	396 PAAQIDIEISIPSHKPGSGG 415
Search Job ti	Search completed: November 21, 2003, 16:38:19 Job time : 22.0222 secs

us-09-688-672a-64.rpr

Н

OM protein - protein search, using sw model

November 21, 2003, 15:57:31 ; Search time 11.2444 Seconds (without alignments) 4609.825 Million cell updates/sec Run on:

US-09-688-672A-64 2737 1 MHHHHHHTAASDNFQLSQGG......RAPVEADAGGGQKVLVRNVV 539

Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	A	100	7281	7098	S47170	8724	7065	70	693	544	280	083	308	332	~	EART	S30971	EAMS	A75564	E70917	H70987	A70647	F84089	-	D70954	G70917				7081	
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149		148.5	148	147.5	147.5	147	147	147	146.5	146	146	'n.	145.5	'n	143.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT

A70957
hypothetical protein Rv3616c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence revision 17-Jul-1998 #text change 22-Oct-1999
C;Accession: A70957
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D., Gardon, e
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N. Holrow, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Smares
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Rarrell R.G.
A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome :
A; Reference number: A70500; MUID: 98295987; PMID: 9634230
A; Accession: A70957
A; Status: preliminary; nucleic acid sequence not shown: translation not shown
A; Molecule type: DNA
A;Residues: 1-392 <col/>
A; Cross-references: GB: Z95557; GB: AL123456; NID; a3242276; PIDN: CARDRAGO 1. DID. a316833.;
A, Experimental source: strain H37Rv
C; Genetics:

A; Gene: Rv3616c

0 447 207 267 120 327 180 387 240 241 GATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAA 300 507 301 STRQALRPRADGPVGAAAEQVGGGGQQLVSAQGSQGMGGPVGMGGMIPSSGASKGTTTKKY 360 9 328 IISDVADIIKGILGEVWEFITNALNGLKELWDKLTGWYTGLFSRGWSNLESFFAGVPGLT 148 MSRAFIIDPTISAIDGLYDLLGIGIPNQGGILYSSLEYFEKALEELAAAFPGDGWLGSAA 268 YIPVVGHALSAAFQAPFCAGAMAVVGGALAYLVVKTLINATQLLKLLAKLAELVAAAIAD 181 IISDVADIIKGTLGEVWEFITNALNGLKELMDKLTGWVTGLFSRGWSNLESFFAGVPGLT 388 GATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAA STRQALRPRADGPVGAAAEQVGGQSQLVSAQGSQGMGGPVGMGGMHPSGGASKGTTTKKY 208 DKYAGKNRNHVNFFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDLT . 0 Query Match
71.7%; Score 1963; DB 2; Length 392;
Best Local Similarity 99.7%; Pred. No. 2.4e-108;
Matches 391; Conservative 0; Mismatches 1; Indels 448 g $\stackrel{>}{\circ}$ Пр 8 Db QQ 8 Š Dp ò Db

SEGAAAGTEDAERAPVEADAGGGQKVLVRNVV 539

508

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126 342

282 99

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CiAccession: $47170
K.Cameron, R.M.; Stevenson, K.; Inglis, N.F.; Klausen, J.; Sharp, J.M.
Submitted to the EMBL Data Library, June 1993
A; Description: Isolation and characterisation of a 34KDa protein of Mycobacterium paratuk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.cross.references: EMBL:223092; NID:950550; PIDN:CAA80638.1; PID:9505551
C,Superfamily: Escherichia coli trypsin-like proteinase degs; GLGF domain homology; tryps
trypsin-like proteinase degS; GLGF domain homology; tryp$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Public secreted serine proteinase [imported] - Mycobacterium leprae probable secreted serine proteinase [imported] - Mycobacterium leprae [Species: Mycobacterium leprae [Species: Mycobacterium leprae [Species: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Dec-2002 [Species: Nature 20-Apr-2001 #sequence_revision 20-Apr-2001 #sequence_revision 20-Apr-2001 #sequence_revision 20-Apr-2001 #sequence_revision 20-Apr-2001 #sequence_revision 2001 #sequence_revision 2001 #sequence_revision 2001 #sequence_revision 2001 #sequence_revision 2001 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequence_revision 2002 #sequen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein 34K - Mycobacterium paratuberculosis
C;Species: Mycobacterium paratuberculosis
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Dec-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 VORVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290 VORVVNTGPAAAAGIAPGDVITGVDTVPINGATSMTEVLVPHHPGDTIAVHFRSVDGGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             231 TAATDSYKWS-GGGGFAIPIGRAMAVANQIRSGAGSNIVHIGPTAFLGLGVTDNNGNGAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGAR
                                                                                                                                                                                                                                      7 HTAASDNEQLSQGGQGFALPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGA
                                                                                                                                                                                                                                                                                            67 RVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                283 RVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.3%; Score 474.5; DB 2; Length 361; larity 69.7%; Pred. No. 7.6e-21; Conservative 17; Mismatches 22; Indels 1
                                                                                      2; Length 355;
                                                                                                                                                                    0; Indels
                                                                                      Score 676; DB 2;
Pred. No. 1e-32;
1; Mismatches
                                                                                          Query Match
Best Local Similarity 99.2%;
Matches 132; Conservative
                C; Superfamily: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 RIGNVILAEGPPA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         343 RTGNVTLAEGPPA 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | |:|||||||
350 TANITLAEGPPA 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-361 < CAM>
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A, Molecule type: DNA
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A;Gene: ML2659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S:
Matches 92
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Dec-2002
C;Accession: F70983
R;Cole, S. T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.: Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Atterence number: A70500; MUID:98295987; PMID:9634230
A;Accession: F70983
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: F70983
A;Redues: 1-355 <COL>
A;Accession: Efarences: GB:296071; GB:AL123456; NID:93242254; PIDN:CAB09453.1; PID:92181967
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: pepA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YIPVVGHALSAAFQAPFCAGAMAVVGGALAYLVVKTLINATQLLKLLAKLAELVAAAIAD 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STROGTRSOAGVSABLSTBOFGGOOEPVSAOGSOGMGGSOGMGGMTPASTKSKKDERKKK 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                         hypothetical protein B1620 C2_213 - Mycobacterium leprae C; Species: Mycobacterium leprae C; Species: Mycobacterium leprae C; Species: Mycobacterium leprae C; Species: Myar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001 C; Accession: S72814 R; Smith, D.R.; Robison, K. submitted to the BmBL Data Library, November 1993 A; Description: Mycobacterium leprae cosmid B1620. A; Reference number: S72584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 YIPLVGSVMSASIQAQACAAAMAAVSGGLAYLLVQTAIHTAKFVALLARLAHLLASAVAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKYAGKNRNHVNFFOELADLDROLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 MSRAFIIDPTISAIDGLYDLLGIGIPNQGGILYSSLEYFEKALEELAAAFPGDGWLGSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecule type: DNA
Residues: 1-394 <SMI>
Cross-references: EMBL:U00015, NID:g466931; PIDN:AAC43223.1; PID:g466935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

46.1%; Score 1263; DB 2; iength 394;
Best Local Similarity 62.9%; Pred. No. 3.6e-67;
Matches 248; Conservative 55; Mismatches 89; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KYSEGAAAGTEDAERAPVEADAGGGQKVLVRNVV 539
                                SEGAAAGTEDAERAPVEADAGGGQKVLVRNVV 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S72814
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Gaps

M.; Skelton, J.; Squares, R.; Squ

P.R.; Hor Holroyd,

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probable serine proteinase Rv0983 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Accesin: C70821
R;Cole S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Cole S.T.; Brosch, R.; Pevlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelten, S.; Hamlin, N.; Holroyd, S.; Nature 393, 537-544, 1998
A, Huthors: Squres, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A, Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome & A; Reference number: A70500; MUID:98295937; PMID:9634230
A, Reference number: A70500; MUID:98295937; PMID:9634230
A, Reference number: A70500; MUID:98295937; PMID:9634230
A, Reference number: A70500; MUID:98295937; PMID:9634230
A, Reference number: A70500; MUID:98295937; PMID:9634230
A, Reference number: A70500; MUID:98295937; PMID:963261538; PIDN:CAA17582.1; PID:e125391(A, R) Residues: 1444 cCOL>
A, Rose-references: GBARD021999; GB:AL123456; NID:g3261538; PIDN:CAA17582.1; PID:e125391(C, Genetics: Rv0983)
C; Superfamily: Escherichia coli trypsin-like proteinase degS; GLGF domain homology; tryps
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C.Species: Mycobacterium leprae
C.Species: Mycobacterium leprae
C.Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Dec-2002
C.Accession: #86330
R.Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho:
R.; Davies, R.M.; Devlin, K.M.
R.; Davies, R.M.; Robin, K.M.
Nature 409, 1007-1011, 2001
A.Authors: Rutter S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sqn
A.Attiels: Massive gene decay in the leprosy bacillus.
A.Accession: #86330
A.Accession: #86330
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A;Residues: 1-382 <STO>
A;Cross-references: GB:AL450380; NID:g13092536; PIDN:CAC29684.1; GSPDB:GN00147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     337 TLGADSADAQSGSIGLGFAIPVDQAKRIADELISTGKA-----SHASLGVQVTNDKDTL 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 GARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 AASDNFOLSOGGGFALPIGOAMAIAGOIRSGGGSPTVHIGPTAFLGLGVVDNNGN-GAR 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 TAASDNFQLSQG--GQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVV-DNNGN 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
6.9%; Score 188.5; DB 2; Length 382;
Best Local Similarity 39.8%; Pred. No. 0.00054;
Matches 51; Conservative 19; Mismatches 51; Indels 7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 7.3%; Score 199.5; DB 2; Length 464; Local Similarity 38.9%; Pred. No. 0.00015; es 51; Conservative 21; Mismatches 50; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 GTRTGNVTLAE 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     451 GSRIVOVILGK 461
525 ADAGGGQK 532
                                                                             388 AGTAASÓR 395
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C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: B7066
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 333, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: E70656
A;Accession: E70656
A;Accession: E70656
A;Accession: E70656
A;Accession: BNA
A;Residues: 1-402 <COL>
A;Accession: GB:Z83864; GB:AL123456; NID:g3261687; PIDN:CAB06237.1; PID:e301440; A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: RV3864
C, Superfamily: Escherichia coli trypsin-like proteinase degs; GLGF domain homology: tryg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 QQLRAQVMGBLDKLTGNMISNQAXYVSDTRDVLRAMKKMIDGVYKVCKGLEKIPLLGHLW 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165 RGILGRLIBMLTTLPKFPGLPSLPDIIDGLWPPKLPDIPIPGLPDIPGLPDFKWPPT 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     374 -----SNLESF-----FAGVPGLTGATSGLSQVTGLF-GAAGL------- 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               225 PGSPLFFDLPSFPGFPGFPEFPAIPGFP-ALPGLPSIPNLFPGLPGLGDLLPGVGDLGKL 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          284 PTWTELAALPDFLGGFAGLPSL-GFGNLLSFASLPTVGQVTATMGQLQQLVAAGGGPSQL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            465 AEQVGGQSQLVSAQGSQGMGGPVGMGGMHPSSGASKGTTTKKYSEGAAAGTEDAERAPVE 524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    337 KGILGEVWEFITN-----ALNGLKELWDKLTG-W--------VTGLFSRGW--- 373
                                                                                                                                                                                                                                                                          67 RVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                          282 RVARVVATGPAAMAGISVGDIITSVDGVPISEATAMTNVLVPHHPGETVAVNYRSAGGCD 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 14.1%; Score 385.5; DB 2; Length 402; Best Local Similarity 30.4%; Pred. No. 1.5e-15; Matches 130; Conservative 47; Mismatches 156; Indels 95; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         406 -SASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAASTRQALRPRADGPVGAA
                                                                                                                                                           1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein Rv3864 - Mycobacterium tuberculosis (strain H37RV)
                                                                         DB 2; Length 354;
                                                                     Query Match 16.8%; Score 460.5; DB 2; Length 3
Best Local Similarity 66.2%; Pred. No. 4.9e-20;
Matches 88; Conservative 18; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 RIGNVILAEGPPA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      342 LTANVTLAEGPPA 354
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Db 258 ADSGDAQSGSIGLGFAIPVDQAKRIADELISTGKATHASLGVQVATDKGTPGAK 311	Db 66 TEAARGVNIPVDVNVDKDTKGGFLSRLLGGKKGLSSLGDDAAKASSQVQHLGKSFLDLTR 125
OY 68 VQRVVGSAPAASLGISTGDVITAVDGAPINSATANADALNGHHPGDVISVTWQTK6GGTR 127	OY 51 TAFLGLGVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATA 101
Qy 128 TGNVTLAE 135 Db 372 TVQVTLGK 379	QY 102 MADALNGHHPGDVISVTWQTKSGGTRTGNVTLAEGPPAEFLV 143
TA5448 probable serine proteinase (EC 3.4.21) MLCB373.28 [similarity] - Mycobacterium leprae C;Species: Mycobacterium leprae C;Species: Mycobacterium leprae C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Dec-2002 C;Accession: T45448 R;James, K.D.; Parkhil, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, February 1998	PRGSMSRAFIIDPTISAIDGLYDLLGIGIPNOGGILYSSLEYFEKALEEL
A; Status: pre-indinary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Mesidues: 1-452 - 0.4MA A; Mesidues: 1-452 - 0.4MA A; Cross-references: EMBL; AL035500; PIDN: CAB36690.1 A; Experimental source: cosmid L373 C; Genetics: McB373.28 C; Superfamily: Escherichia coli trypsin-like proteinase degS; GLGF domain homology; tryp; C; Meywords hydrolase; serine proteinase degS; GLGF domain homology; tryp; F; 182, 224, 305/Active site: His, Asp. Ser #seatus predicted	. 266 266 417 296 472 473
Query Match 6.9%; Score 188.5; DB 2; Length 452; Best Local Similarity 39.8%; Pred. No. 0.00066; Matches 51; Conservative 19; Mismatches 51; Indels 7; Gaps 3; Qy 9 AASDNPQLSQGQGGAPTPIGQAMAIAQIRSGGGSPTVHIGPTAFLGLGVVDNNON-GAR 67 Db 328 ADSGDAQSGSIGLGFAIPVDQAKRIADELISTGKATHASLGVQVATDKGTPGAK 381	532 SIASPLIGGISRLVGVLADCVGAVAEWV-GSWSSGVQVSDFVGQLPGKIKSW 390TSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPS 191
QY 68 VQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTR 127 Db 382 VMDVVAGGAAANAAVPKGVVLTKVDDRLISSADALVAAVRSKAPGDKVSLTYQDQSGSSR 441 QY 128 TGNVTLAE 135 Db 442 TVQVTLGK 449	637 PSRVFAEIGQFTAEGFGNG-FEEGFQPVIEKAKALAAELSQAMESGVDP-SGILA 501 GTTKKYSEGAAAGTEDAERAPVEADA 527 690 GISTKELKQYSAALEQERKRIQVEKNA 716
RESULT 10 minor tail subunit protein - Mycobacterium phage D29 minor tail subunit protein - Mycobacterium phage D29 C;Species: Mycobacterium phage D29 C;Species: Mycobacterium phage D29 C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 20-Apr-2001 C;Date: 12-Nov-1999 C;Date: 12-Nov-1999 C;Date: 12-Nov-1999 C;Date: 12-Nov-1999 C;Date: 12-Nov-1999 C;Date: 12-Nov-1999 C;Date: 12-Nov-1999 C;Date: 12-Nov-1999 C;Date: 12-Nov-1999 C;Date: 12-Nov-1999 C;Date: 137-164, 1998 A;Reference number: A72800, MUID:98300335; PMID:9636706 A;Accession: H72802 A;Actuse: Prealiminary A;Molecule type: DNA A;Residues: 1-837 cFOR> A;Cross-references: GB:AF022214; NID:93172250; PIDN:AAC18467.1; PID:93172274 A;Genetics:	RESCULT 11 H70839 Hypothetical glycine-rich protein Rv0109 - Mycobacterium tuberculosis (strain H37RV) C.5pecides: Mycobacterium tuberculosis C.5pecides: Mycobacterium tuberculosis C.5pecides: Mycobacterium tuberculosis C.5pecides: Mycobacterium tuberculosis C.5pecides: Mycobacterium tuberculosis C.5pecides: Mycobacterium tuberculosis C.5pecides: Mycobacterium tuberculosis R.7conorx, R.7 Davish, R.7 Perkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connorx, R.; Davish, R.; Devilin, K.; Feltwell, T.; Gentles, S.; Harris, D.; Gordon, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seger, K.; Sklton, S.; Squares, S. Nature 393, 537-544, 1998 A.Athorors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A.Athorors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A.Accession: H70839 A.Ac
6.3%; Score 173; DB 2; Length 837; ty 19.8%; Pred. No. 0.011; ervative 94; Mismatches 245; Indels 212; Gaps 25; AlPIG	C,Genetics: A,Gene: Rv0109 C,Superfamily: Phaseolus glycine-rich cell wall protein 1.8 CJenery Match G,2%; Score 169; DB 2; Length 496; Best Local Similarity 25.5%; Pred. No. 0.01; Indels 110; Gaps 14; Matches 83; Conservative 26; Mismatches 107; Indels 110; Gaps 14;

Db 1037 ALGG		QY 51 TAFLGLGVVDNNGRGARVQRVVGSAPAASLGISTGDVITAV 91 Db 229 TTFIGLEDSAKTAVSKTEALVKANQAFGGTGENLKGVVQAGGGASAG	QY 137 PPABFLVPRGSMSRAFIIDPTISAIDGLYDLLGIGIPNQGGILYSSLEY 185 339 SSSATKTIRDTWSGFNEDLSQALIPTLEALTPVINALIDEWDWGKGAGKAIENVVKY 396 QY 186 FEKALEELAAAFPG-DGWLGSAADKYAGKNRNHV 218	397 FQDLFKQLQQNGAITQFSAIWDNLKSAFGSVIGIIGNLIKSFAGVDESTSKNSTSVENVA 219 NFFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDLT	Oy 268 YIPVVGHALSAAFOAPFCAGAMAVVGGALAYLVVKTLINATOLLKLLAKLABLVA 322 Db \$17 YNKIVEAGTIIQGAFNALMAVNPFVLLGIALAAVVAGLVYFFTQTTCKKAWASFVDFLK 576 Qy 323 AAIADIISDVADIISTGILGEVWEFI 347
HALSAAFQAPFCAGAMAVVG	A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br Joulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, of Pseudomonas aeruginosa PA01, an opportunistic patho 9437337; PMID:10984043 8:AE004091; NID:G9950769; PIDN:AAG07929.1; GSPDB:GN001	A;Gene: PA4541 Query Match Query Match Best Local Similarity 22.1%; Pred; No. 0.042; Matches 139; Conservative 77; Mismatches 206; Indels 206; Gaps 31; Oy 19 GQQGFAIPIGQAMAIAG	Db 782 GGNSSFLSIGNASAFGGTFDGLGNTIDNLAVYGTGAYSGLFSVNRGTLRNLNLERISADG 841 Qy 42 GSPTVHIGPTAFLGLGVVDN-NGNGARVQRVVGSAPAASLGISTGDVITAVDGAPIN 97 Db 842 AQATHYNVQVGSLAAVNLGRIDNVNASDIRIAAASKLNSLGGLVALNLGSID 893	VTWOTKSGGTRIGNVTLAEGPPABELVP	, H & S

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A, Accession: A30878
A, Status: preliminary
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Residues: 781-864 * CBA>
A, Cross-references: GB: U04035; NID: 9207442; PIDN: AAA42268.1; PID: 9207443
B; Franzblau, C.; Pratt, C.A.; Faris, B.; Colannino, N.M.; Offner, G.D.; Mogayzel Jr., P.C.
B; Franzblau, C., Pratt, C.A.; Frais, B.; Colannino, N.M.; Offner, G.D.; Mogayzel Jr., P.C.
A, Title: Role of tropoelastin fragmentation in elastogenesis in rat smooth muscle cells.
A, Reference number: A36523; MUID: 89359327; PMID: 2768256
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C;Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F;1-21/Domain: signal sequence #status predicted <SIG>
F:22-864/Product: elastin #status predicted <MAT>
F;854-859/Disulfide bonds: #status predicted
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A;Resdidus: 1.864 GB:MO647; GB:WO5292; NID:G207444; PIDN:AAA42269.1; PID:G207445
A;Cross-references GB:M60647; GB:WO5292; NID:G207444; PIDN:AAA42269.1; PID:G207445
R;Deak, S.B.; Pierce, R.A.; Belsky, S.A.; Riley, D.J.; Boyd, C.D.
J. Biol. Chem. 263, 13504, 13507, 1988
J. Biol. Chem. 263, 13504, 13507, 1988
A;Ritle: Rat tropolastin is synthesized from a 3.5-kilobase mRNA.
A;Reference number: A30878; MUID:88330868; PMID:2971041
                                                                      668 IENAHSNVHVAAQSTERNSLGGVGGLVGLNAKGMIRASGSQGKVET--YRPGLNVGGLVG 725
                                                                                                                                                                                                                                                                                                                                                                                                                   CiSpecies: Rattus norvegicus (Norway rat)
CiDacesian.1991 #seques (Norway rat)
CiDacesion: Asian.1991 #seques ervision 16-Aug-1996 #text_change 22-Jun-1999
CiDacesion: Asia0106, A300919, A360813, S02173, IS4172, I68505
R;Pierce, R.A.; Deak, S.B.; Stolle, C.A.; Boyd, C.D.
Biochmeistry 29, 9677-9683, 1990
A;Title: Heterogeneity of rat tropoclastin mRNA revealed by cDNA cloning.
A;Reference number: A36106, MUID:91104868; PMID:1702999
            --VSAQGSQ-----GMGGPVGMG--GMHPSSGASKGTTTKKYSEGAAAG----
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A;Molecule type: DNA
A;Resdidues: 264-533 <RES>
A;Cross.references: GB:M86372; NID:g207455; PIDN:AAA42271.1; PID:g554527
A;Accession: 168505
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Cross-references: GB:M86376; NID:g207459; PIDN:AAA42272.1; PID:g207462
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A; Title: Elements of the rat tropoelastin gene associated A; Reference number: 154172; MUID:92241859; PMID:1572637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 22-31 <FRA>
R; Rich, C.B.; FOSter, J.A.
Arch. Biochem. Biochys. J. 268, 551-558, 1989
A; Title: Characterization of rat heart tropoelastin.
A; Reference number: S02173; MUID:89117149; PMID:2913947
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                                                                                                                                          -----TEDAERAPVEADAGGGKVLV 535
                                                                                                                                                                                                    726 YNMFGHVSDSSASGQVEAGGAGNTGGLV 753
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                                                                                                                                                                                                                                                                                                                                                                                         N;Alternate names: tropoelastin
                                                                                                                                                                                                                                                                                                                                                               elastin precursor - rat
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C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: H83135
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Jorure 406, 959-964, 200
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAOI, an opportunistic pathon A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: H83135
A;Accession: H83135
A;Accession: Basinary
A;Molecule type: DNA
A;Residues: 1-1018 <SIO>
A;Cross-references: GB:AE004824; GB:AE004091; NID:g9950277; PIDN:AAG07469.1; GSPDB:GN001
A;Experimental source: strain PAOI
C;Genetics:
A;Gene: PA4082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28;
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                                      637 WITVIGGIQSVWGGVTGFFSGIFDAVSSVVSTVFSAIGGFASSAMNVLVSVWSAVAGFFG 696
                                                                                                                    436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        446 KIVLGGAGSALAMDAGEGHRVNGTASVSLAGANATYVSGGYYYTVVONLAQLQAINKNLD 505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASLPALAG-----IGGGSGFGGLPSLAQVHAASTRQALRPRADGPVGAAAEQVGGQSQL 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       618 NALGGLVGRNISGQIANASVSGGVTG----YAAST----AVGGLVGENFTTAWGPEAV 667
SRGWSNLESFFAGVPGLTG 388
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                                                                                                                                                                    697 GIFNAVSGV--VSSVFSAIGSFASSAMGVVQSIWSAVSGFFSGIFNSVSSVVSGVFSALG 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                       -SGFG
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   - TNALNGLKELWDKLTGWVTGLF.
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Best Local Simi
Matches 149;
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Search completed: November 21, 2003, 16:09:59 Job time : 13.2444 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

November 21, 2003, 15:51:11; Search time 6.35556 Seconds

(without alignments)

3988.226 Million cell updates/sec

Perfect score: 2737
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 127863 segs, 47026705 residues

1 MHHHHHHTAASDNFQLSQGG.....RAPVBADAGGGQKVLVRNVV

Sequence:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000

MAXIMUM DE Seq length: 2000000000
POSt-processing: Minimum Match 0%
MAXIMUM Match 100%
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SwissProt_41:*

Database :

Q9wx62 acetobacter	P27393 ascaris suu	P15921 rickettsia	P05790 bombyx mori	P19837 nephila cla	007322 daucus caro	Q01149 mus musculu	P37894 caulobacter	P08392 herpes simp			
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                                                                                ----TIGTALTTALQAIQPMLPTLVDSFKQLSETLVTSLGPYLPQIGEAFGQIVGAVIQ 470
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                                                                                                                                                                                                                                                                    Genomics 12:651-658(1992).
-!- FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND
NUCRAL LICAMBUT, WHICH WUST EXPAND RAPIDLY AND RECOVER COMPLETELY.
-!- SUBUNIT: THE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED TOGETHER
                                                                                                                       || :: :|| | || LAPTIISSLIPAFQTLIPAIAQLAPSLVQIVQAFTKLMPVIVPVVQIVINLAAAVVQAGA
                                                                                                                                                                                                                                                     441 LAQVHAASTRQALRPRADGPVGAAAEQVGGQSQLVSAQGSQGMGGPVGMGGMHPSSGASK
           ---ILEGAKKGLEFVRPVAVD
                                   356 MPALTSVSSLLGNVLGTLGTQLAPITTALTPAFTTLADTLGTMLTGALQALGPVLTVVAE
                                                          ---PFCAGAMAVVGGA---
                                                                                                         -----TQLLKLLAKLAELV---AAAIADIIS
                                                                                                                                                         331 DVADIIKGILGEVWEFITNALNGLKELWDKLTGWVTGLFSRGWSNLESFFAGVPGLTGA-
                                                                                                                                                                             531 SIASFLIGGISRLVGVLADCVGAVAĖ------WV-GSWSGVQQVSDFVGQLPGKIKSW
                                                                                                                                                                                                       -----TSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPS
                                                                                                                                                                                                                            583 FDDAGSWLIEACKNVVQCLINGIGSMISSAVSKAKELASSVK-----NAVTGFLGIHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91104868; Pubmed=1702999; Pierce R.A., Deak S.B., Stolle C.A., Boyd C.D.; Heterogeneity of rat tropoelastin mRNA revealed by cDNA cloning."; Biochemistry 29:9677-9683(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                558-864 FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 264-533 AND 558-864 FROM N.A., AND ALTERNATIVE SPLICING MEDIINE=92241659; PubMed=1572637; Boyd C.D.; Blerce R.A., Alatawi A., Deak S.B., Boyd C.D.; Elerce R.A., Alatawi A., Deak S.B., Boyd Seciated with alternative splicing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTO AN EXTENSIBLE 3D NETWORK.
SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX OF ELASTIC FIBERS.
ALTERNATIVE PRODUCTS:
Bvent=Alternative splicing; Named isoforms=8;
Comment=Experimental confirmation may be lacking for some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 781-864 FROM N.A.
MEDDIINE=88330868; PubMed=2971041;
Deak S.B., Pierce R.A., Belsky S.A., Riley D.J., Boyd C.D.;
"Rat tropoelastin is synthesized from a 3.5-kilobase mRNA.";
J. Biol. Chem. 263:13504-13507(1988).
              LDROLISLIHDOANAVOTTRD-
                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-SEP-2003 (Rel. 42, Last annotation update)
Elastin precursor (Tropoelastin) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                        864 AA.
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                                                                                                            LAYLVVKTLINA-----
                                                             266 LTYIPVVGHALSAAFQA-
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IsoId=Q99372-1; Sequence=Displayed;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---SAADKYAGKNRNHVNFFQELADLDRQL 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 APAAS-LGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTCNVTL
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                                                                                                                                                                                                                                                   VSP_004245, VSP_004246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210; Indels 172;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interPro, IPR003979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
Structural protein; Connective tissue; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              456894BB09E79FD4 CRC64;
                                                                                                                                 IsoId=Q99372-5; Sequence=VSP_004244, VSP_004245;
                                                                                                                                                                      IsoId=099372-6; Sequence=VSP_004245, VSP_004246;
                                                                                                                                                                                                              IsoId=Q99372-7; Sequence=VSP_004244, VSP_004246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5,
                                                                                                                                                                                                                                                   ISOId=099372-8; Sequence=VSP 004244, VSP 0042
PTM: THE CROSSLINKS ARE MADE OF DEAMINATED LYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Missing (in isoform 2, and isoform 8).
/FIId=VSP 004244.
Missing (in isoform 3, e and isoform 9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VSP_004245.
Missing (in isoform 7 and isoform 8).
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ELASTIN.
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Name=2;
IsoId=Q99372-2; Sequence=VSP_004244;
                                                      IsoId=Q99372-3; Sequence=VSP_004245;
                                                                                             IsoId=Q99372-4; Sequence=VSP_004246;
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AAA42271.1; JOINED.
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EMBL; J04035; AAA42268.1; -.
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AAA42271.1;
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M86366; 7
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                                                                                                                                                                      431 PMLPSLMQSFQQISDVLVTSLAPHIPALATALGQVAGAVLQLAPTIISTLVPA--FVQLV 488
                                                                                                                                                                                                                   -TGATSGLSQVT 397
                                                                                                                                                                                                                                                                                                                              549 SNVIK-----KVSEWVSS-FSGAQQIAAKAAELPGMIQSALANLMAIGLQAGKDLVQ 600
                                                                                               --LAD
                                      ---GPLSTFINGFGDLFVSLMPALTSVSGLIGNVLGT
                                                                                                                                                 -PFCAGAMAVVGGA---LAYLVVKTLINATQLLKLL
                                                                                                                                                                                                                                                                                                                                                               398 GLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAASTRQALRPRA
                                                                                                                                                                                                                                                                                                                                                                                                   GLINGIGGMVSAAVNKAKELASSVA-----GAVKGFLGIESPSKLFTEYGQFTAEGFG
                                                                                                                                                                                                                                                                                                                                                                                                                                       DGPVGAAAEQVGGQSQLVSAQGSQGMGGPVGMGGMHPSSGASKGTTTKKYSEGAAAGTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -chromosome 7.";

Genomics 23:125-131(1994).

-! FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND

-! FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND

NUCHAL LIGAMENT, WHICH MUST EXPAND RAPIDLY AND RECOVER COMPLETELY.

-!- SUBUNIT: THE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED TOGETHER

-!- SUBCELLULAR LOCATION: SYTRACELULAR MATRIX OF ELASTIC FIBERS.

-!- SUBCELLULAR LOCATION: ANTRACELULAR MATRIX OF ELASTIC FIBERS.
                                                                                                                                                                                                                                                        489 PKVAELVPIIVNLVQSFANLMPVVLPLAQALVSVAGAVIQVGVSIGGALIGALANLTEII
                                                                      LDRQLISLIHDQANAVQTTRDILEGAKKG-LEFVRPVAVDLTYI-PVVGHALSAAFQA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TYSTAIN=BALB/C; TISSUB=Lung;
MPDLINE=91130060; PubMed=7829060;
Wydner K.S., Sechler J.L., Boyd C.D., Passmore H.C.;
"Use of an intron polymorphism to localize the tropoelastin gene t mouse chromosome 5 in a region of linkage conservation with human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                            TNALNGLKELWDKLTGWVTGLFSRGWSNLESFFAGVPGL----
     FEKALEELAAAFPGDGWLGSAADKYAGKNRNHVNFFQE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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01-0CT-1996 (Rel. 34, Last sequ
15-SEP-2003 (Rel. 42, Last anno
                                    FNRLMESGLOAM---GOLG--
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MGI:95317; Eln.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              518 AERAPVE 524
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                                    291
                                                                                                                                             --SOAAAAAA---AKAAKYGAGGAGTLGGLVPGAV 499
                                                                                                                                                                           NGLKELWDKLIGWVTGLFSRGWSNLESFFAGVPG-LIGATSGLSQVTGLFGAAGLSASSG 410
                                                                                                                                                                                                                PG-----ALPGAVPGALP-----GAVPGALPGAVPGVPGTGGVPGAGTPAAAA 543
                                                                                                                                                                                                                                                  LAHADSLASSASL---PALAGIGGGSGFGGLP---SLAQVHAAST--RQALRPRADGPVG 462
                                                                                                                                                                                                                                                                                          ---GDIG 600
                                                                                                                                                                                                                                                                                                                          AAAEQVGGQSQLVSAQGSQ-----GMGGP-VGMGGMHPSSGA----SKGTTTKKYSE 509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265 TQA-FLTLSNAGANSFGTLLAPLQEFTNGFNDMVNRVTSNGVFEGAMOGLSQTLGSVLNL 323
                                                                    ----GARGGVG------IPTYG--VGAGGFPGYGVGAGAG 464
                                                                                                     VGGALAYLVVKTLINATQLLKLLAKLAELVAAAIADIISDVADIIKGILGEVWEFITNAL 351
                                                                                                                                                                                                                                                                                                                                                           GAGTPAAAKSAAKAAAKAQYRAAGLGAGVPGLGVGAGVPGFGAGAGGFGAGAGVPGFGA 660
                                ISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDLTYIPVVGHALSAAFQAPFCAGAMAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206 GPMLTAITPNLONVASGLVNWAGSITDVIT-QAPGLQQIQNILTKTGEFFTGLGPVLATG
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Mycobacteriophage L5.
Mycobacteriophage L5.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
L5-like viruses.
NCBI_TaxID=31757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of mycobacteriophage
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22.5%; Pred. No. 0.034;
.ive 75; Mismatches 203; Indels 146;
                                                                                                                                                                                                                                                                                      544 AAAAKAAAKAGQYGLGPGVGGVPGGVGVGGLPGGVGPGGVTGIGTGPGTGLVP
PGIGGPGIVGGPGAVSPAAAAKAAKAAKY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        836 AA; 86258 MW; 52E3040AA42BAD28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 28, Created)
(Rel. 28, Last sequence update)
(Rel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "DNA sequence, structure and gene expression a phage system for mycobacterial genetics."; Mol. Microbiol. 7:395-405(1993).
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Hatfull G.F., Sarkis G.J.;
"DNA sequence, structure and gene
                                                                                                                                                                                                                                                                                                                                                                                                                                  GAVPGSLAASKAAKYGAAGG 680
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PIR; S30971; S30971.
INIT MET 0 0
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Minor tail protein GP26.
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Best Local Similarity
Matches 123; Conserv
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01-FEB-1994
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316
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                                                                                                                                                                                                                                                                                                                                                                                     EGPPAEFLVPRGSMSR---AFIIDPTISAIDGLYDLLGIGIPNOGGILYSSLEYFEKALE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGSGFGGLPSLAQVHAASTRQALRPRADGPVGAAAEQVGGQSQLVSAQGSQGMG-GPVG
                                                                                                                                                                                                                              GGQGFAIPIGQAMAIAGQIRSGGGSPTVHIG--PTAFLGLGVVDN--NGNGARVQRVVGS
                                                                                                                                                                                                                                                                                                          APAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNVTLA
                                                                                                                                                                                                                                                                                                                                              317 AKAKYGAGGAGVLPGVGGGGIPGGAGAIPGIGG-----IAGAGTPAAAAAAAAAAAA
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MEDLINE=87289668; PubMed=3039501;
Indix Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
Rosenbloom J.C., Peltonen L., Rosenbloom J., Peltonen L., Rosenbloom J., Alternative splicing of human elastin mRNA indicated by sequence analysis of cloned genomic and complementary DNA.";
Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                           186; Indels 165;
                                                                                                                                                       DB 1; Length 860;
                                                                                                                                                                                                                                                                                                                                                                                                                          KYGAAGGLVPGGPGVRLPGAGI--PGVGGIPGVGGIPGVGGPGIGG-
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                                                                                             BY SIMILARITY.
0COBESAAE1EDD7F1 CRC64;
                                    Connective tissue.
                                                                                                                                                                       .063;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---PGIVGGPGAVSPAAAAAAAKAAKY-----
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                                                                                                                                                                                           38; Mismatches
                                                                                                                                                     5.8%; Score 159.5;
23.3%; Pred. No. 0.0
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InterPro; IPRU03373, PROISOO; TROPOELASTIN.
Structural protein; Repeat; Signal; Constructural protein; Repeat, Signal, 27
                                                                           ELASTIN
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TISSUE=Skin fibroblast;
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855 BY
71955 MW;
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Conservative 3
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                                                                         28 8
850 8
860 AA;
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Matches 118; Conserv
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                                                                                             DISULFID
SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Fazio M.J., Olsen D.R., Kauh E.A., Baldwin C.T., Indik Z., Ornstein-Goldstein N., Yauh E.A., Baldwin C.T., Indik Z., Crnstein-Goldstein N., Yauh E.A., Bosenbloom J., Uitto J., "Cloning of full-length elastin cDNAs from a human skin fibroblast recombinant cDNA library: further elucidation of alternative splicing utilizing exon-specific oligonucleotides.";
J. Invest. Dermatol. 91:458-464(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FINCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND NUCHAL LIGAMENT, WHICH MUST EXPAND RAPIDLY AND RECOVER COMPLETELY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TSOID=P15502-2; Sequence=VSP 004243; PTM: THE CROSSLINKS ARE WADE OF DEAMINATED LYS. DISEASE: Haploinsufficiency of ELM may be the cause of certain cardiovascular and musculo-skeletal abnormalities observed in williams.Beuren syndrome (WBS), a rare developmental disorder. is a contiguous gene deletion syndrome involving genes from chromosome band 7411.23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Hippocampus, and Placenta,
MEDLINE-96291399; PubMed-8689688;
MEDLINE-96291399; PubMed-8689688;
Bertrand J., Ewalt B.F., Morris C.A., Mervis C.B.,
Green E.D., Proeschel C., Gutowski N.J., Noble M., Atkinson D.L.,
Geblerg S.J., Keating M.T.;
LIM-kinasel hemizygosity implicated in impaired visuospatial
constructive cognition.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTO AN EXTENSIBLE 3D NETWORK.
-!- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX OF ELASTIC FIBERS.
-!- ALTERNATIVE PRODUCTS:
Event-Allernative splicing; Named isoforms=2;
Comment-Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                        MEDLINE=88156138; PubMed=2831431; Fazio M.J., Davidson J.M., Fazio M.J., Olsen D.R., Kuivaniemi H., Chu M.L., Davidson J.M., Rosenbloom J., Uitto J., Uitto J., Illian and Lose and characterization of human elastin cDNAs, and age-associated variation in elastin gene expression in cultured skin
                                                                                                                                                                                                                                                                   SEQUENCE OF 164-724 FROM N.A. (ISOFORM B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=P15502-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'fibroblasts.";
Lab. Invest. 58:270-277(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 603-730 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M17282; AAC98394.1; EMBL; M16983; AAC98394.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell 86:59-69(1996)
                                                                                                                                                                                                                                                                                                     TISSUE=Placenta;
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M36860;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 --GPQPG-----VPLGY-PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAAGKAGYP 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GWVTGLFSRGWSNLESFFAGVPGLTGATSGLSQVTGLFGAAGLSASSGLAHADSLASSAS 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 GVPGVGGLGVSAGAVVPQ-PGAGVKPGKVPGVGLPGVYPGGVLP-----GARFPGVG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 LEGAKKGLEFVRPVAVDLTYIPVVGHALSAAFQAPFCAGAMAV-----VGGALAYLVVK 302
                                                                                                                                                                                                                                       M. M. 194000; -. (Coxtracellular matrix, TAS. RG) GO:0005578; C:extracellular space; TAS. RG) GO:0005515; C:extracellular space; TAS. RG) GO:0005201; F:extracellular matrix structural constituent; TAS. RG) GO:0008203; P:call proliferation; TAS. RG) GO:0008203; P:call proliferation; TAS. RG) GO:00007397; P:histogenesis and organogenesis, TAS. RG) GO:0007397; P:histogenesis and organogenesis, TAS. RO; GO:0007397; P:histogenesis and organogenesis, TAS. RINGEPPO; IRR00399; tropoelastin.

R Interpro.; IRR00399; tropoelastin.

R Structural protein; Connective tissue; Repeat; Signal; W Williams-Beuren syndrome; Alternative splicing.

T CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      376 AAKAAKYGARPGVGVGGIPTYGVGAGGFPGFGVGVGGIPGVAGVPSVGGVPGVPGVPGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNG--NGARVQRVVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match
Local Similarity 20.4%; Pred. No. 0.13;
les 117; Conservative 46; Mismatches 182; Indels 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           720 725 BY SIMILARITY.
472 477 Missing (in isoform 2).
FITIG=VSP 004243.
730 AA; 63260 MW, AB06D15BA567AR46 CRC64;
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EMBL; M24782; AAA53190.1; --
EMBL; U62292; AAB1754.1; --
EMBL; X15603; CAA33627.1; --
PIR; A32707; EAHU.
HSSP; P50099; 1ZFU.
Genew; HGNC:3327; ELN.
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VARSPLIC
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RESULT 6 WA22_MYCTU

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"Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Pleterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.
                                                                                                                                                                                                                                                                                                                                                                                                    Harris
                                                                                                                                                                                                                                                                                                                                                             MEDLINE 9029597; PubMed=9634230;

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglameier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Horsby T., Jagels K., Kroph A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Bulston J.E., Taylor K., Mitchead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
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                                                                                                                                     Mycobacterium Lobacrollosis.

Mycobacterium Actinobacteria; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.

NCBI_TaxID=1773;
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(Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 40, Last annotation update)
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larity 24.5%; Pred. No. 0.17;
Conservative 40; Mismatches 2
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SIGNAL 3 POTENTIAL.
CHAIN 31 914 WAG22 ANTIGEN.
                                                                                           WAG22 antigen precursor.
WAG22 OR RV1759C OR MT1807 OR MTCY28.25C.
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EMBL; AE007040; -; NOT_ANNOTATED_CDS
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InterPro, IPR000084; PE_region.
Pfam; PF00934; PE, 1.
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TIGR; MT1807; -.
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Best Local Similarity
Matches 133; Conserv
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30-MAY-2000 (
16-OCT-2001 (
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Best Local
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           AEGPPAEFLVPRGSMSRAFIIDPTISAIDGLYDLLGIGIPNQGGILYSSLEYFEKALEEL 193
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Fleischmann N.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                           | : | | : | | : | | : | | : | AGKSGFGGLLGADGY----NAPESTSPWHNLQQDILSFINEPTEAL-TGRPLIGN
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                                                             A--AAFPGDGWLGSAADKYAGKNRNHVNFFQELADLDRQLISLIHDQANAVQTTRDIL--
                                                                                                            ------EGAKKGLEFVRFVAVDLTYIPVVGHALSAAFQAPFCAGAMAVVGGALAYL
                                                                                                                                    ------GNGGNGGAGAGTNGSAGGAGGIL
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Gas S., Bary C.E. III. Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Comnor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd E. Hensby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Seeger K., Skelton S., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., Complete genome sequence:

"Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence:"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                   --NAV----LIGNG--GEGGI
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30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical PE-PGRS family protein Rv0747 precursor.
RV0747 OR MI0772.5 OR MIV041.21
                                                                                                                                                                                                                                                                                                                                                                                                                                                    801 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 DIIKGILGEVWEFITNALNGLKELWDKLTGWVTGLFSRGWSNLESFFAGVPGLTGATSGL 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----GAGGLFGSGG-----AGGASTDVAGGAGGAGGAGG--NAGMLFGAAGVGGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RPRADGPVGAAAEQVGGQSQLVSAQGSQGMGGPVGMGGMHPSSGASKGTTTKKYSEGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          394 SQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAASTRQAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            275 ALSAAFQAPFCAGAMAVVGGALAYLVVKTLINATQLLKLLAKL-AELVAAAIADIISDVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 NGAPG-----GAPGAGG-----PGGWLIGNGGAGGS-----GAPGAGGNG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal; Complete proteome.
POTENTIAL.
HYPOTHETICAL PE-PGRS FAMILY PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50;
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01-JUL-1993 (Rel. 26, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update).
28-FBB-2003 (Rel. 41, Last annotation update).
Discs large-1 tumor suppressor protein.
Discs large-1 tumor suppressor protein.
Discs large-1 tumor suppressor protein.
Discs large-1 tumor suppressor protein.
Discsphila.
Discsphila.
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
[1]
PGRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : Pred. No. 0.2;
23; Mismatches 111; Indels
SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EA54C9BF45A00F41
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A -> P (IN REF. 2
T -> A (IN REF. 2
MISSING (IN REF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 150;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                           TIGR; MT0772.5; -...
TubercuList; Rv0747; -..
InterPro; IPR000084; PE_region.
Pfan; PF00934; PE; 1.
Hypothetical protein; Repeat; Sig SIGNAL
                                                                                                                                                                                                                                                                                   EMBL; AL021958; CAA17514.1; -. EMBL; AE006968; AAK45011.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          595
                                                                                                                                                                                                                                                                                                                                           PIR; F70824; F70824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          580
801 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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2225
2227
2227
2295
3300
3338
577
                           SUBFAMILY
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297
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                                                                                                                   SEQUENCE
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                                                            DOMAIN
                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
YI40_MYCTU
         STTTTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SMISS-PROT entry is copyright. It is produced through a collaboration the burpean the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                     Woods D.F., Bryant P.J.;

The discs-large tumor suppressor gene of Drosophila encodes a woods D.F., Bryant P.J.;

Type discs-large tumor suppressor gene of Drosophila encodes a gramplate kinase homolog localized at septate junctions.";

Cell 66:451-464(1991).

Cell 66:451-464(1991).

General folial problem of the presence of a gramplate kinase domain suggests involvement in cellular adhesion as well as signal transduction to control cellular proliferation.

Required for maintenance of cell polarity.

CHOPLASMIC FACE OF THE MEMBRANE IN THE CELLULAR BLASTODERM AND BENGES ASSOCIATED WITH SEPTATE JUNCTIONS WHICH BEGIN TO FORM BEYMEN EPITHELIAL CELLS THE SPEATE DURCTIONS WHICH BEGIN TO FORM BEYMEN EPITHELIAL CELLS THE TIME OF DORSAL CLOSURE. IN ADULT FILES, LOCATED AT THE APICAL-LATERAL MEMBRANE BOUNDARY OF EPITHELIAL CELLS.

CELLS.

COMMENTATIVE PRODUCTS:

COMMENTATIVE PRODUCTS:

COMMENTATIVE SPORTATE AT THE TIME OF DORSAL CLOSURE.

COMMENTATIVE PRODUCTS:

COMMENTATIVE PRODUCTS:

COMMENTATIVE AND SPORTATE AT THE APICAL-LATERAL MEMBRANE BOUNDARY OF COMMENTATIVE PRODUCTS:

COMMENTATIVE AND SPORTATE AT THE APICAL-LATERAL MEMBRANE BOUNDARY OF COMMENTATIVE PRODUCTS:

EVENT ALTERNATIVE PRODUCTS:

COMMENTATIVE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPORTATE AND SPOR
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Isold=P31007-1; Sequence-Displayed;
TISSUE SPECIFICITY: In embryos, expression is seen in epithelial
cells and some nervous tissue. In larvae, expression is seen as a
belt around salivary glands and imaginal disks, also in
proventriculus and parts of the brain. Expressed in adult
proventriculus and parts of the brain. Expressed in adult
throughout tissues.
DBVELOPMENTAL STAGE: Expressed both maternally and zygotically
throughout development.
SIMILARITY: EBLONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
SIMILARITY: Contains 3 PDZ/DHR domains.
SIMILARITY: Contains 1 SH3 domain.
SIMILARITY: Contains 1 guanylate kinase-like domain.
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polarit...; I
polarit...; N
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R FIRE J. M. 19229; AAA268 11; -..

R FYBASE; P31016; 1BFE.

R GO; GO:0045179; C:spical cortex; IDA.

GO; GO:004519; C:spical protein localization; IMP.

GO; GO:004519; P:setablishment and/or maintenance of pola GO; GO:004519; P:setablishment and/or maintenance of pola GO; GO:000391; P:dorsal closure; NAS.

GO; GO:004519; P:setablishment and/or maintenance of pola GO; GO:000393; P:setablishment and/or maintenance of pola GO; GO:000393; P:setablishment and/or maintenance of pola GO; GO:000393; P:setablishment and/or maintenance of pola GO; GO:000393; P:setablishment and/or maintenance of pola GO; GO:000393; P:setablishment and/or maintenance of pola GO; GO:0004519; P:setablishment and/or maintenance of pola GO; GO:0004519; P:setablishment and/or maintenance of pola GO; GO:0004519; P:setablishment and/or maintenance of pola GO; GO:0004519; P:setablishment and/or maintenance of pola GO; GO:0004519; P:setablishment and/or maintenance of pola GO; GO:0004519; P:setablishment and/or maintenance of pola GO; GO:0004519; P:setablishment and/or maintenance of pola GO; GO:0004519; P:setablishment and/or maintenance of pola GO; GO:0004519; P:setablishment and/or maintenance of pola GO; GO:0004519; P:setablishment and/or maintenance of pola GO; GO:0004519; P:setablishment and/or maintenance of pola GO; GO:0004519; P:setablishment and/or maintenance of pola GO; GO:0004519; P:setablishment and/or maintenance of pola GO; GO:0004519; P:setablishment and/or maintenance of pola GO; GO:0004519; P:setablishment and/or maintenance of pola GO; GO:0004519; P:setablishment and/or maintenance of pola GO; GO:0004519; P:setablishment and/or maintenance of pola GO; GO:0004519; P:setablishment and/or maintenance of pola GO; GO:0004519; P:setablishment and/or maintenance of pola GO; GO:0004519; P:setablishment and/or maintenance of pola GO; GO:0004519; P:setablishment and/or maintenance of pola GO; GO:0004519; P:setablishment and/or maintenance of pola GO; GO:0004519; P:setablishment and/or maintenance of p
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PROSITE; PS50052; GUANVLATE KINASE 2; 1.
PROSITE; PS50106; PD2; 3.
PROSITE; PS50002; SH3; 1.
Transducer; SH3 domain; Alternative splicing; Repeat.
DOMAIN 40 126 PDZ 1.
                           TISSUE=Embryo;
MEDLINE=91330294; PubMed=1651169;
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122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 SGGAAAADGRLSINDIIVSVNDVSVVDVPHASAVDALK--KAGNVVKLHVKRKRGTATTP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 SGGTRTGNV--TLAEGPPA-EFLVPRGSMSRAFIIDPTISAIDGLYDLLGIG---IPNQG 176
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                                                                                                                                                                                                                                                                                                                                   EDIQLERGNSGLGFSI-----TKLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 AAGSAAGDARDSAASGPKVIEIDLVKGGKGLGF-----SIAG-----GIGNQHIPGDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --AGKNRNHVNFPQELADLDRQLI----SLIHDQANAVQTTRDILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354 NDSSKLPPSLGANSSISISNSNSNSNS-----SNNINNINSI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             390 --NNNNSSSSSTTATVAAATPTAA-----SAAAAAASS--PPANSFYNNASMPALP
                                                                                                                                                                                                                                                                                                DNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRV
                                                                                                                                                                                                                                                                                                                                                                                                                     VGSAPAASLGISTGDVITAVDGAPINSA--TAMADALNGHHPGDVISV-----TWQTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GILYSSL--------BYFEKALEELAAAFPGDGWLGSAADK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 GIYVTKLTDGGRAQVDGRLSIGDKLIAVRTNGSEKNLENVTHELAVA-----TLKSITDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237 VILIIGKTQHLTTSASGGGGGGLSSGQQLSQSQSQLATSQSQSQVHQQQHATPMVNSQST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAKKGLEFVRPVAVDLTYIPVVGHALSAAFQAPFCAGAMA----VVGGALAYLVVKTLINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GA---LINSMGQTVVDSPSIPQAAAAAAAAAAAAASASASVIASNNTISNTTVTTVTATATAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   308 TQLLKLLAKLAELVAAAIADIISDVADIIKGILGEVWEFITNALNGLKELWDKLTGWVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       368 LFSRGWSNLESFFAGVPGLTGATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           428 GIGG------GSGFGGLPSLAQV-----HAASTRQALR-PRA----DGPVGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 437 VESNQTNNRSQSPQPRQPGSRYASTNVLAAVPPGTPRAVSTEDITREPRITIQKGPQGL
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris
Gordon S.V., Biglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock B. Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                            Length 960;
                                                                                                                                                                            5.4%; Score 147; DB 1; Length 96
21.4%; Pred. No. 0.36;
tive 60; Mismatches 207; Indels
244 PDZ 2.
566 PDZ 3.
670 SH3
960 GUANYLATE KINASE.
102468 MW, BFB7A4262F1B6AD5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                464 AAEQVGGQSQLVSAQGSQGM-----GGPVGMG 490
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
19-othetical PE-PGRS family protein Rv1840c.
RV1840C OR MI1888 OR MICYIAII.04 OR MICY359.33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ā
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                                                                                                                                                                                                                                           Conservative
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154
486
600
768
960 AA;
                                                                                                                                                                                                        Best Local Similarity
Matches 123; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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NCBI_TaxID=1773;
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                                                                                        333 NG 334
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                                            529 GG
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P56877;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    321 VAAAIADIISDVADIIKGILGEVW-----EFITNALNGLKELWDKLTGWVTGLFSRGWS 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        414 ADSLASSASLPALAGI --GGGSGFGGLPSLAQVHAASTRQALRPRADGPVGAAAEQV--G 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 278 GDGGSVGAAPTGIGNGGNGGWLYGDGGSGGSTLQGFSDGGTGG----NAGMFGDGG 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----GNGGNGGNGGIGOPGGAGGDAGLIGNGGNG-------GIGGPGAT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 GLAGGAGGVGGLLFGDGONGCAGGLGTGPVGATGGIGGPGGAAVGLFGHGGAGGAGGLGK 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 AGKNRN----HVNFFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 SAAVADLFGAHAQAYQALS----AQAALFHEQFVHAMTAG---AGAYAGAE----AADA
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                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Pleischmann R.D., Alland D., Eisen J.A., Kaft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                  "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                     laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Ruter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.B., Taylor K., Whitchead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE007047; ARK46159.1; -.
PIR; H70663; H70663.
TIGR; MT1888; -.
Tuberculist; Rv1840c; -.
InterPro; IPR000084; PE_region.
Bycan: PF0034; PE; 1.
Hypor, PF0034; PE; 1.
PYDANSMEM 1 2.
POTENTAL.
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POTENTIAL.
2 2 E D C 8 B C C C C 6 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z83859; CAB06114.1; -.
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Conservative 3
                                                                                                                    complete genome sequence
Nature 393:537-544(1998)
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185
219
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                                                                                                                                                                                                                                                                                                                              Bishai W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Holroyd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDINE=98285987; PubMed=9634230;

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr Gordon S.V., Basbam D., Barry C.E. III, Tekala F., Badcock K., Basbam D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroy Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quali R., Rajandream M.J., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Whole genome comparison of Mycobacterium tuberculosis clinical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS
                                                                                                                                                                                                                                                                      Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL PE-PGRS FAMILY
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MISSING (IN REF. 2).
R -> G (IN REF. 2).
71EBABD4177BA47C CRC64;
                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical PB-PGRS family protein Rv0278c precursor.
                                                                                                                                                                                                                                                                                                  Corynebacterineae; Mycobacteriaceae; Mycobacterium
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EMBL, AE006936; AAK4511.1; ALT_INIT.
PIR, D70835; D70835.
TIGR, MT0291; -
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                                                                                                                                                                                                                               Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D.
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30
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163
807
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158
807
957 AA;
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DB 1; Length 957;

Score 146;

5.3%;

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15;
                                                                                                                                                                                                                                                                                         404 GLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAASTR----QALRPRADG 459
                                                         257 EFVRPVAVDLTYIPVVGHALSAAFQAP-----FCAG-----AMAVVGGA--LAYLVV 301
                                                                                                                                   302 KTLINA--TQLLKLLAKLAELVAAAIADIISDVADIIKGILGEVWEF------ITNA 350
                                                                                                                                                                        66 SAQAQAFHAQFVQALTSGGGAYAAAEAAAVSPLLDPIN------EFFLANTGRPLIGNG 118
                                                                                                                                                                                                               LNGLKELWDKLT-----GWVTGLFSRGWSNLESFFAGVPGLTGATSGLSQVTGLFGAA 403
                                                                                                                                                                                                                                                    119 ANGAPG-----TGANGGDGGWLIGNGGAGGS-----GAAGVNGGAGGNGGAGGNGGAG 166
                                                                                                                                                                                                                                                                                                                                GLIGNGGAGGAGGVASS-----GIGGSGGAGGNAMLFGAGGAGGAGGAGGVVALTGGAGG 219
                                                                                                                                                                                                                                                                                                                                                                     460 PVGA-----AAEQVGGQ----SQLVSAQGSQGMGGPVGMGGMHPSSGASKGTTTK 505
                                                                                                                                                                                                                                                                                                                                                                                                            220 AGGAGGNAGLLFGAAGVGGAGGFTNGSALGGAGGAGGAGGLFATGGVGGSGGAG---- 273
                                                                                Biol. Chem. 268:17377-17383(1993).

FUNCTION: THIS PROTEGGLYCAN IS A MAJOR COMPONENT OF EXTRACELLULAR
MATRIX OF CARTILAGENOUS TISSUES. A MAJOR FUNCTION OF THIS PROTEIN
IS TO RESIST COMPRESSION IN CARTILAGE. IT BINDS AVIDLY TO
HYALURONIC ACID VIA AN AMINO-TERMINAL GLOBULAR REGION. MAY PLAY A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. Glant T.T., Adams M.E., Kwok S.X.F., Huang D., Fueloep C.; "Complete coding sequence and deduced amino acid sequence of aggrecan of canine cartilage."; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   028343; 028310;
01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Aggrecan core protein precursor (Cartilage-specific proteoglycan core protein) (CSPCP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUB=Cartilage;
PURDILINE=23552525;
PURDILINE=23552525;
FUELOED C., Walcz E., Valyon M., Glant T.T.;
Fueloep C., Walcz E., Valyon M., Glant T.T.;
"Expression of alternatively spliced epidermal growth factor-like domains in aggrecans of different species. Evidence for a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canis familiaris (Dog).
Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
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88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barry F.P., Neame P.J., Sasse J., Pearson D., Intength variation in the keratan sulfate domain of mammalian
                    17; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1830-2333 FROM N.A.
Adams M.E., Kowk S.X.F., Huang D., Glant T.T., Fullop C.
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
  Pred. No. 0.41;
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MEDLINE=95128522; PubMed=7827755;
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                    89; Conservative
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Best Local Similarity
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1. SUDCILLULAR ROCATION: SECRETCH CARGING BESTON THE CARTILAGE.

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PRT; 2124 AA
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01-FEB-1991 (Rel. 17, Last seq
15-SEP-2003 (Rel. 42, Last ann
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                                          1080 VGDLSRL-
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REVISION TO 698
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Pred. No. 1.5
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Matches 127; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                  435 FGGLPSLAQVHAASTRQALRPRADGP-VGAAAEQ-----VGGQSQLVSAQGSQGMGG-PV 487
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SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
SIMILARITY: Contains 1 C-type lectin family domain.
SIMILARITY: Contains 1 C-type lectin family similarity: Contains 1 Sushi (SCR) domain.
SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
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DOMAIN: TWO GLOBULAR DOMAINS, G1 AND G2, COMPRISE THE AMINO TERMINUS OF THE PROTEOGLYCAN, WHILE ANOTHER GLOBULAR REGION, G3, MAKES UP THE COOH TERMINUS. G1 CONTAINS LINK DOMAINS AND THUS CONSISTS OF THREE DISULFIDE-BONDED LOOP STRUCTURES DESIGNATED AS THRE A, B, B' MOTIFS. G2 IS SIMILAR TO G1. THE KERATAN SULPATE (KS) AND THE CHONDROITIN SULFATE (CS) ATTACHMENT DOMAINS LIE BETWEEN G3 AND G3.
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MEDLINE-86250699; Pubmed-2424993;

Partial CDNA sequence encoding a globular domain at the C terminus of the rat cartilage proteoglycan...

1 Biol. Chem. 261:8108-8111(1986)...

1 FUNCTION: THIS PROTEOGLYCAN IS A MAJOR COMPONENT OF EXTRACELLULAR MATRIX OF CARTILAGENOUS TISGUES. A MAJOR FUNCTION OF THIS PROTEOR NOT STORESTOR TO REALTH AND THE PROTEOR PROFESSION IN CARTILAGE. IT BINDS AVIDLY TO HYALURONIC ACID VIA AN AMINO-TERMINAL GLOBULAR REGION. MAY PLAY A REGULAROR FOLE. IN THE MATRIX ASSEMBLY OF THE CARTILAGE.

1 SUBURDILATIOR FOLE IN THE MATRIX ASSEMBLY OF THE CARTILAGE.

2 SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1991 (Rel. 17, Last sequence update)
15-EEP-2003 (Rel. 42, Last annotation update)
Aggrecan core protein precursor (Cartilage-specific proteoglycan core
protein) (CSPCP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBL_TaxID=10116;
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=88087070; PubMed=3693370;
Boege K., Sasaki M., Horigan E., Hassell J.R., Yamada Y.;
"Complete primary structure of the rat cartilage proteoglycan profein deduced from cDNA clones."
J. Biol. Chem. 262:17757-17767(1987).
                                                                                                                                                                                   ---VEADAGG
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J. Biol. Chem. 263:10040-10040(1988).
                                                                                                                                                                                   488 GMGGMHPSS---GASKGTTTKKYSEGAAAGTEDAERAP-
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Similarity
  Best Local
Matches 12
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PROSITE; PS0041; C_TYPE_LECTIN_2; 1.
PROSITE; PS50041; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
PROSITE; PS01241; LINK; 4.
Glycoprotein; Cartilage; Proteoglycan; Lectin; Signal; Sushi; Repeat; Immunoglobulin domain.
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HSSP; P98066; ITSG.
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Length 2124;

DB 1;

Score 142.5;

5.2%;

Query Match

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1021 EDVÍQLPTERGGL-ETSÁSGIEDÍTVLPTGRENLETSASGVEDVSGLPSGKEG----LE 1074
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SEQUENCE FROM N.A.

STARIN-H97RV;

WEDLINE-98295987;

PubMed-9634230;

A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

A Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

A Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

A Hornsby T., Jagels K., Krogh A., Mclean J., Moule S., Murphy L.,

A Oliver S., Seeger K., Skelton S., Squares S., Squares T.,

Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

T "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                  24 AIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            441 LAQVHAASTRQALRPRADGPVGAAAEQVG----GQSQLV-SAQGSQGMG----GPVGMGG
                                                                                                                                                                                                                                                                                                                                     880 PTVDRLPSGGES----LEGSASA-SGTGDL--SGLPSGGEITETS----ASGTEEISG--
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                     ----845 SGDLDSSGLGPTVSSGLPVESGSASGDG----EIPWSS---
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1D Y034 MYCTU

1D Y034 MYCTU

AC P71933;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last, sequence update)
DT 01-NOV-1997 (Rel. 35, Last, sequence update)
DT H5-OCT-2001 (Rel. 40, Last annotation update)
DE HYDOTherical PE-PORS Family protein RV2634C.
GN RV2634C OR MT2712 OR MTCY441.04C.
OS MYCOBacterium theoreticals.
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21.9%; Preq. nc.
                                     126; Conservative
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                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license also remember (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D Gordon S.V., Biglmeier K., Gas S., Barry C.B. III, Tekaia F., Badcock K., Basham D., Erown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.
                                                                                                                                           "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.", Babacterium tuberculosis clinical and Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
STRAIN=CDC 1551 / Oshkosh;
STRAIN=CDC 1551 / Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg (
Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula in the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the cont
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Corynebacterineae, Mycobacteriaceae, Mycobacterium.
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30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical PE-PGRS family protein Rv3508 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 422 SLPALAGIGGGSGFGGLPSLAQVHAASTRQALRPRAD--
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PIR; F70963; F70963.
TIGR; MT2712; -.
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053553;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 GGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFL----GLGVV-----DNNGNGARVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGGWLFGVGGAGGVGG----AGGGTGGAG-GPGGLIWGGGGAGGVGGAGGGTGGAGGRAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 RVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGH--------HPGDVISVTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----TDGGP--GATG---GTGGHGGVGGDGGWLAPGGAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            382 VGVGGTGGQGGAGGA----------GAAGADAPASTGLTGGTGF
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                                                                                                                                                               NATURE 393:537-544 (1998).
-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS SUBFAMILY.
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J Cutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from complete genome sequence.";
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1.5;
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POTENTIAL.

HYPOTHETICAL PE-PGRS FAMILY
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Pred. No. 1
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PIR; F70806; F70806.
Tuberculist; Rv3508; -.
InterPro; IPR00084; PE_region.
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ProDom, PD001223, PE_region; 1.
Hypothetical protein, Repeat, S
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                                                                           PGCA_MOUSE STANDARD; PRT; 2132 AA.

G61282 to 646421.

G1-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
AGGTOR AGC.

Mus musculus (Mouse).

Eukaryota; Motazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TAXID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
SIMILARITY: Contains 4 link domains.
SIMILARITY: Contains 1 EGF-like domain.
SIMILARITY: Contains 1 C-type lectin family domain.
SIMILARITY: Contains 1 C-type lectin family domain.
SIMILARITY: Contains 1 Sushi (SCR) domain.
SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTECGLYCAN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=129/Sv;
MEDLINE=95004579; PubMed=7920633;
Watanabe H., Kimata K., Line S., Strong D., Gao L.-Y., Kozak C.A.,
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=95104847; bubmed=780622;

Walcz B., Deak F., Erhardt P., Coulter S.N., Fueloep C., Horvath Doege K.J., Glant T.T.;

"Complete coding sequence, deduced primary structure, chromosomal localization, and structural analysis of murine aggrecan.";
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SEQUENCE OF 211-326 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the aggrecan gene.";
Nat. Genet. 7:154-157(1994).
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PubMed=10400671;
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STRAIN=H97RV.

CRAIN=H97RV.

STRAIN=H97RV.

MEDLINE=9829599; PubMed=9634230;

A Gordon S.V. Biglmeier K., Gas S., Barry C.B. III, Tekaia F.,

Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

A Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

A Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J.,

A Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

T Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.";

Nature 393:537-544(1998).
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STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann T.D., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corymebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Rv3616G.
RV3616C OR MT3718 OR MTCYO7H7B.06.
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Q93J30
Q93J30
Q9NPK0
Q8NPK0
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Q92KQ8
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Q9ESZ9
Q8C9L8
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Q8P942
Q8XRM8
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080116 bacteriopha
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1 MHHHHHHTAASDNFQLSQGG......RAPVEADAGGGQKVLVRNVV 539
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(c) 1993 - 2003 Compugen Ltd.
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SEQUENCE OF 231-394 FROM N.A.
Oliver K., Harris D., Parkhill J., Barrell B.G., Rajandr
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                  MEDLINE-93189700; Pubmed-8446027;
MEDLINE-93189700; Pubmed-8446027;
Eiglmeier K., Honore N., Woods S.A., Caluse of an ordered cosmid library to defor Mycobacterium leprae...;
MOI. Microbiol. 7:197-206(1993).
EMBL; AL583918; CAC29913.1;
EMBL; CAC37179; CAB09940.1;
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Smith D.R., Robison K.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                  TIGR; MT3718; -.
Tuberculist; Rv3616c; -.
Hypothetical protein; Complete proteome.
CONFLICT 192 192 T -> I (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
Hyporhetical protein ML0405.
ML0405 OR B1620_C2_213 OR MLCL383.01.
Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Actinobacteria, Actinobacteridae, Actinor
Corynebacterineae, Mycobacteriaceae, Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Massive gene decay in the leprosy bacillus."; Nature 409:1007-1011(2001).
                                                                                                                                                                                                                                                                                                                                                                                                         361 SEGAAAGTEDAERAPVEADAGGGQKVLVRNVV 392
                                                                                                                                                                                                                                                                                                                                                                                             SEGAAAGTEDAERAPVEADAGGGOKVLVRNVV 539
                                                                            71.7%; Scor. No. 2...
99.7%; Pred. No. 2...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        394 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
EMBL; Z95557; CAB08950.1; -. EMBL; AE007171; AAK48077.1;
                                                                                              Local Similarity 99.7
nes 391; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1769;
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                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09
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D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKYAGKNRNHVNFFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YIPVVGHALSAAFQAPFCAGAMAVVGGALAYLVVKTLINATQLLKLLAKLAELVAAAIAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IISDVADIIKGILGEVWEFITNALNGLKELWDKLTGWVTGLFSRGWSNLESFFAGVPGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 GATSGLSQVTGLFGVPGLAGSSGLLSGESLLSTENLPSLAGVGAGLGLGSLPQLAQLHAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRQALRPRADGPVGAAAEQVGGQSQLVSAQGSQGMGGPVGMGGMHPSSGASK--GTTTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MSRAFIIDPTISAIDGLYDLLGIGIPNQGGILYSSLEYFEKALEELAAAFPGDGWLGSAA
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                                                                                                                                                                                                                                                                                                                                       Gaps
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris
Cole S.T., Explaneier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd (
                                                                                                                                                                                                                                                                                                                                             ..
                                                                                                                                                                                                                                    394;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              007175 PRELIMINARY, PRT; 355 AA.
007175;
01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
PRPA OR RV0125 OR MTCH418B.07 OR MTCH418B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07 OR MTCH318B.07
                                                                                                                                                                                                                        3; DB 16; Length
4e-63;
thes 89; Indels
Hypothetical protein, Transmembrane, Complete proteome.
TRANSMEM 279 299 POTENTIAL.
SEQUENCE 394 AA, 40754 MW, DOB455C74ED7A10C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               506 KYSEGAAAGTEDAERAPVEADAGGGQKVLVRNVV
                                                                                                                                                                                                                        46.1%; Score 1263; D 62.9%; Pred. No. 4e-6
                                                                                                                                                                                                                  Query Match
Best Local Similarity 62.9
Matches 248; Conservative
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Mycobacterium leprae.
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Barrell B.G.;
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Q9CCY9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99
                                                                                         SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Haft D., Hickey E.,
Feterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       283 RVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 HTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                            "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.
EMBL; 296071; CAB09453.1; --
EMBL; AE006925; AAK44357.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=JD88/107;
WEDINES-256054449; PubMed=7921248;
Cameron R.M., Stevenson K., Inglis N.F., Klausen J., Sharp J.M.;
"Identification and characterisation of a putative serine protease
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Csborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34XDa protein precursor.
Mycobacterium paratubarculosis.
Bacteria, Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50106; PDZ; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Hydrolase; Hypothetical protein; Serine protease; Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       355 AA; 34926 MW; 16CE9E21A97BF192 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.7%; Score 676; DB 16; 99.2%; Pred. No. 2.8e-30; ive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 AA
                                                                                                                                                                                                                                                                      TIGR, MT0133; -.

Tuberculist, Rv0125; -.

Tuberculist, Rv0125; -.

Tuberculist, Rv0125; -.

InterPro; IPR001478; PDZ.

InterPro; IPR001264; Ser_protease_Try.

InterPro; IPR001264; Ser_protease_Try.

Ffam; PF00585; PDZ; 1.

Pfam; PF00589; trypsin; 1.

Pfam; PR0089; trypsin; 1.

Pfam; PR0089; trypsin; 1.

Pfam; PR0089; trypsin; 1.

Pfam; PR0089; trypsin; 1.

Pfam; SR00839; V8PRTEASESC.

SMART; SM00228; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 RIGNVILAEGPPA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIGNVILAEGPPA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 132; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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SEQUENCE 355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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290 VQRVVNTGPAAAAGIAPGDVITGVDTVPINGATSMTEVLVPHHPGDTIAVHFRSVDGGER
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Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honcer N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Errown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Woule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rucherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 VQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
expressed in vivo by Mycobacterium avium subsp paratuberculosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 361;
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Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   361 AA; 35709 MW; 30FEF78FD6F3C411 CRC64;
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Nature 409:1007-1011(2001).
-!- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.3%; Score 474.5; DB 2;
69.7%; Pred. No. 5.6e-19;
iive 17; Mismatches 22;
                                                                                                                                                                                                                                                                                                               SMART; SM00228; rud, 1.
PROSITE; PS50106; PDZ; 1.
Hydrolase; Protease; Serine protease; Signal.
38 POTENTIAL.
                       Microbiology 140:1977-1982(1994).
-!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
EMBL, Z23092, CAA80638.1,
INGETPO, IPRO01478; PDZ.
INGETPO, IPRO01249, Protease2C.
INGETPO, IPRO01254, Ser_protease_Try.
Pfam; PF00595; PDZ; 1.
Pfam; PF0089; trypsin; 1.
PRINTS; PR00834; PROTEASES2C.
SMANT; SM00228; PDZ; 1.
PROSITE; PS50106; PDZ; 1.
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InterPro; IPR001940; Protease2C.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR00126; Ser_proteas_V8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probable secreted serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam, PF00595; PDZ; 1.
Pfam, PF00689; trypsin; 1.
PRINTS; PR00834; PROTEASES2C.
SMART; SM00228; PDZ; 1.
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Best Local Similarity 69.75
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 TGNVTLAEGPPA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        350 TANITLAEGPPA 361
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217 HVNFFQELADLDRQLISLIHDQANAVQTTRDILEGAKKGLEFVRPVAVDLTYIPVVGHAL 276
                                                                                                           71 QQLRAQVMGDLDKLTGNMISNQAKYVSDTRDVLRAMKKMIDGVYKVCKGLEKIFLLGHLW 130
                                                                                                                                                                SAAFQAPFCAGAMAVVGGALAYLVVKTLINATQLLKLLAKLABLVAAAIADIISDVADII 336
     11 TSNFIWGQLLLLGEGIPDPGDIFNTGSSLFKQISDKMGLAIPGTNWIGQAAEAYLNQNIA 70
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                                                                                                                                                                                                                                                                 223 NTAATDNYKM-LGGQGFAIPIGQAMEVVGAIRSGAGSNTVHIGPTAFFGLGVLDNNGNGA
                                                                                                                                                                                                                                                                                                                   RVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGT
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Perwon D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Sulston J.E., Taylor K., Whitehead S., Squares R.,
"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                             Gaps
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STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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                                                                                                         Query Match
16.8%; Score 460.5; DB 16; Length 354;
Best Local Similarity 66.2%; Pred. No. 3.3e-18;
Matches 88; Conservative 18; Mismatches 26; Indels 1;
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14.1%; Score 385.5; DB 16; Length 402;
Best Local Similarity 30.4%; Pred. No. 6.3e-14;
Matches 130; Conservative 47; Mismatches 156; Indels 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                               .3e-18;
es 26; Indels
PROSITE, PS50106, PDZ, 1.
Hydrolase, Protease, Serine protease, Complete proteome.
SEQUENCE 354 AA, 35265 MW, 612F23261BC9EA4A CRC64,
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Submitted (APR-2001) to the BMBL/GenBank/DDBJ databases.
EMBL; Z83864; CAB06237.1; -.
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Hypothetical protein; Complete proteome.
SEQUENCE 402 AA; 42068 MW; B400E0E22D482765 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
1-MAR-2004 (TremBland)
1-MAR-2004 (TremBland)
1-MAR-2004 (TremBland)
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                                                                                                                                                                                                                                                                                                                                                                                                                         127 RTGNVTLAEGPPA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                342 LTANVTLAEGPPA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W.;
                                          AEQVGGQSQLVSAQGSQGMGGPVGMGGMHPSSGASKGTTTKKYSEGAAAGTEDAERAPVE
337 KGILGEVWEFITN-----ALNGLKELWDKLTG-W-------VTGLFSRGW---
                                                                                                                                                                                225 PGSPLFPDLPSFPGFPGFPEFPAIPGFP-ALPGLPSIPNLFPGLPGLGDLLPGVGDLGKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corynebacterineae, Mycobacteriaceae, Mycobacterium.
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Sibmitted (APR-201) to the EMBL/GenBank/DDBJ databases.
EMBL; AE006985; AAK45259.1; -
TIGR; MT1011; -
TIGR; MT1011; -
TIGR; MT0011; -
TIGR; MT0011; -
TIGR; MT0011; -
TIGR; MT0011; -
TIGR; MT001264; Ser_Drotease_Try.
InterPro; IPR001254; Ser_Drotease_Try.
Pfam; PF00099; trypsin; 1.
PRINTS; PR00814; PR0TEASES2C.
SNART; SM00228; PDZ; 1.
PROSITE; PS50106; PDZ; 1.
SEQUENCE 446 AA; 44484 MW; 54170CBEA8FE872B CRC64;
                                                                                                                     374 ----SNLESF-----FAGVPGLTGATSGLSQVTGLF-GAAGL-
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Last annotation update)
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01-MAR-2002 (TEMBLrel. 20, Create
01-MAR-2002 (TEMBLrel. 20, Last s
01-UUN-2002 (TEMBLrel. 21, Last a
Heat shock protein HtrA, putative.
MT1011.
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157 TISAIDGLYDLLGIGIPNQGGILYSSLEYFEKALEELAAAFPGDGWLGSAADKYAGKNRN 216

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Putative serine protease.
MLCB373.28.
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nes 51; Conservative
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                                                                                                            FROM N.A.
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                                                                                                            SEQUENCE
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                                319 TLGADSADAQSGSIGLGFAIPVDQAKRIADELISTGKA-----SHASLGVQVTNDKDTP 372
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                                                                                                                                                                                                                                                               MEDLINE=9825987; PubMed=9634230; Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Peltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Kroph A., McLean J., Moule S., Murphy L., Oliver S., Oborne J., Quail M.A., Rajandream M.A., Rogers J., Stelton S., Stelton S., Squares R., Stelton S., Statell B.G., State S., State S., State S., State S., State S., State S., State S., State S., State S., Barrell B.G., Deciphering the biology of Mycobacterium tuberculosis from the
                    GARVORVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                      Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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Hydrolase; Protease; Serine protease; Complete proteome.
SEQUENCE 464 AA; 46452 MW; AE93BFCC53E1EC8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                     Created)
                                                                                                                                  PRT;
                                                                                                                                                   01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-MAR-2003 (TrEMBLrel. 23, Putative serine protease. RV0983 OR MTV044.11.
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Best Local Similarity 38...
Best Local Similarity 38...
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                                                           125 GTRIGNVTLAE 135
                                                                               433 GSRÍVQVÍLGK 443
                                                                                                                                  PRELIMINARY;
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382 AA

PRT;

PRELIMINARY;

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258 ADSGDAQSGSIGLGFAIPVDQAKRIADELISTG--KATH----ASLGVQVATDKGTPGAK 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               312 VMDVVAGGAAANAAVPKGVVLTKVDDRLISSADALVAAVRSKAPGDKVSLTYQDQSGSSR 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 AASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGN-GAR
                                                                                                                                                                                                                                                                                                                     MEDLIRE=21128732; PubMed=11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honroson N. Garnier T., Churcher C., Harris D.R., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Machen J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford M., Stutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
                                                                                                                                   Mycobacterium leprae.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NC31_TaxID=1769;
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Harris D., Taylor K.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase; Protease; Serine protease; Complete proteome.
SEQUENCE 382 AA; 37084 MW; 3DDBDDDBAE32A80D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Squares S., Stevens K., Taylor K., Whitehead S., Woo Barrell B.G.;
"Massive gene decay in the leprosy bacillus.";
Nature 409:1107-1011(2001).
-i- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY:
EMBL, ALS83917; CAC29684.1;
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Last sequence update)
Last annotation update)
01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.9%; Score 188.5; DB 16;
39.8%; Pred. No. 0.0065;
tive 19; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       452 AA
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Interpro; IPR001478; PDZ.
InterPro; IPR001264; Ser_protease_Try.
Pfam; PF00089; PDZ; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00834; PROTEASES2C.
SMART; SM00228; PDZ; 1.
                                                                                      Possible secreted serine protease.
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 AASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGN-GAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                        Caudron B., Cole S.T.; deduce the genomic organization
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24.7%; Pred. No. 0.014;
tive 60; Mismatches 200; Indels 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Ralstoniaceae; Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 188.5; DB 2; Length 452;
; Pred. No. 0.0081;
19; Mismatches 51; Indels 7
                   James K.D., Parkhill J., Barrell B.G., Rajandream M.A., Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                     protease.
V; 6CA675EB0911F983 CRC64;
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459 AA; 41117 MW; FE06C4144483ACC9 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 22, Last annotation update)
Putative hemagglutinin-related transmembrane protein.
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Ralstonia solanacearum (Pseudomonas solanacearum).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  459 AA
                                                                                                                                                                                                                                EMBL; ALG35500; CALCOLL TERRORY BY PDZ.
InterPro; IPR001940; Protease2C.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; Frygsin, 1.
PALMY; PR00089; Frygsin, 1.
PALMY; PR000894; PROTEASES2C.
SMART; SM00228; PDZ; 1.
                                                                                                                MEDLINE=93188700; PubMed=8446027; Eiglmeier K., Honore N., Woods S.A., "Use of an ordered cosmid library to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=GMI1000;
MEDLINE=21681879; PubMed=11823852;
                                                                                                                                                                               of Mycobatterium leprae.";
Mol. Microbiol. 7:197-206(1993).
EMBL; AL035500; CAB36690.1; -.
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Best Local Similarity
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                                                                                            SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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SEQUENCE
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87

32 AIAGQIRSGG----GSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGISTGDV

Matches 133; Conservative

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22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    384 PGLTGATSGLSQVTGLFGAAGLSASS--GLAHADSLASSASL-PALAGIGGGSGFGGLPS 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        266 LTYIPVVGHALSAAFQAPFCAGAMAVVGGAL--AYLVVKTLINATQLLKLLAKLAELVAA 323
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---GMGGMHPSSGASKGTTTKKYSEGAAAGTEDA------ERAPVEADAGG 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   390 VISALGSVGGTTGG--GTLAPVASITAPVGTVVÄTVGSTLISTGATTPLAPVTGSAGG 445
                                                                                                                                                                                                                                                88 ITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSG-GTRTGNVTLAEGPPAEFLVPRG
                                                                                                                                                                                                             147 SMSRAFIIDPTISAIDGLYDLLGIGIPNQGGILYSSLEYFEKALEELAAAFPGDGWLGSA
                                                                                                                                                                                                                                                                                                                                                                                         ----IGSNPNPIG--TTVASTG----NVVTGVGNTVTSAGTLVGGLGTGQLSPLAPVTTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             324 AIADIISDVADIIKGILGEVWEFITNALNGLKELWDKLTGWYTGLFSRGWSNLESFFAGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Posterior silk gland;
Zurovec M., Kodrik D., Yang C., Sehnal F.;
Luchain fibroin of Galleria mellonella L.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF095239; AAG10393.1;
NOW TER
SEQÜENCE 1468 AA; 122705 MW; 2DAS9E1181BB3DDF CRC64;
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Last annotation update)
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(TrEMBLrel. 16, Last seq
(TrEMBLrel. 22, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heavy-chain fibroin (Fragment)
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01-MAR-2001 (
01-OCT-2002 (
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Bishai W.;
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Q8VKR5;
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GSGAAGSSAASAASGAAGPAPVIVIEDGSSAAS----AAAAAGSGASGLGLGLGAMGTL 640
                                                                                                                                                                                                GLKELWDKLTGWVTGLFSRGWSNLESFFAGVPGL-TGATSGLSQVTGLFGAAG-----L 405
                                                                                                                                                                                                                                                  406 SASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAASTRQALRPRADGPVGAAA 465
                                                                                                                                                                                                                                                                           DDRSSAASAAAGSGASGPGGLGLGVWGPLGGIGPIGASSASASASGAGL----GGVGAAG 852
                                                                                                                                                                                                                                                                                                      EQ----VGGQSQLVSAQGSQGMG-GPVGMGGMHPSSGASKGTTTKKYSEGAAAGTEDAER 520
                                       GGILYSSLEYFEKALEELAAAFPGDGWLGSAADKYAGKNRNHVNFFQELADLDRQLISLI 235
                                                                                                                  ---LASAASGAAGAAPVI-----VIEDGSSAASAAAAGSGASGVGGLG 714
                                                                                                                                           294 -GALAYLVVKTLINATQLLKLLAKLAELVAAAJADIISDVADIIKGILGEVWEFITNALN 352
                                                                                                                                                                     ---------GGIGPIGASSAGASGAGLGGVGAAGTSGLG 751
                                                                                                                                                                                                                                                                                                                             853 TSGLGGLGGAG--ASAAGSAGAGLGGIGASGSSGSSVASAASGTS--GAGEVIVIDDRSS 908
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XX MEDLINE-98295987; PubMed=9634230;
XX MEDLINE-98295987; PubMed=9634230;
XA Cole S.T., Brosch R., Parkhill J., Barry C.E. III, Tekaia F.,
A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Hornsby T., Jagels K., Kragh A., McLean J., Moule S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Kragh A., McLean J., Moule S., Murphy L.,
RA Hornsby T., Skelton S., Squares R.,
Rutter S., Seeger K., Skelton S., Squares R.,
Rutter S., Seeger K., Whitehead S., Barrell B.G.;
RY Complete ganome sequence.;
RT Complete ganome sequence.;
RT Nature 393:337-544(1998).
REL, ALO21926, CAA17303.1; -.
DR Tuberculist, Rv0109; -.
DR Tuberculist, Rv0109; -.
DR TuterPro, IPR00084; PE_region.
                                                                                         HDQANAVQTTRDILEGAKKGLEFVRPVAVDLTYIPVVGHALSAAFQAPFCAGAMAVVG--
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Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1773;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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25.5%; Pred. No. 0.11;
ative 26; Mismatches 107;
                                                             641 GGIGPNGVS--SASATGSAAGSIGSGLCGSGA---AGSS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                    496 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis.
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RV0109 OR MTV031.03C.
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                                                                                                                              ---- OALQTVQQNVLTVVNAP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                       -KGILGEVWEFITNALNGLKELWDKLTGWVTG----LFSRGWSNLESFFAGVPGLTGATS 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94
                           68
GALAYLVVKTLINATQLLKLLAKLABLVAAAIADIISDVADII---
                                                                                                                                                                                                                                                                                      392 GLSQVTGLFGAAGL--SASSGLAHADSLASSASLPA----LAGIGGGSGFGGLPSLAQV
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                                                                                                                                                                                                                                                                                                                                                                                           445 HAASTRQALRPRADGPVGAAAEQVGGQSQLVSAQGSQGMGGPVGMGGMHPSSGASKGTTT
                                                                                                                                                                                                                                                                                                                                  156 GVDQAGGNGGAAGLIGNGGSGGVGGPGIAGSAGGAGGAGGLLFGNGGPGGAGGIGTTGD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ABC06923; AAK44341.1; ---
IIGR; MT0118; ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAINGED, SISEN J.A., Carpenter L., White O., Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.2%; Score 169; DB 16; Length 533;
26.2%; Pred. No. 0.13;
cive 25; Mismatches 134; Indels 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
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                                                                                                                                                                                                                                 116 TQALLGR--PIİGNGANGLPN----TGQDGGPGGLLFGNGGN----
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Last annotation update)
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                                                                                                                              69 ALAFHDQFVQALNMGAVCYAAAET-ANATPL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               505 KKYSEGAAAGTEDAERAPVEADAGGG 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258 GLFGHGGAGGAGGIGSADGGLGGGGG 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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ProDom; PD001223; PE_region; 1.
SEQUENCE 533 AA; 46785 MW;
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InterPro; IPR000084; PE_region.
Pfam; PF00934; PE; 1.
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Best Local Similarity 26.27
Matches 89, Conservative
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378 SFFAGVPGLTGATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIG 430 189GGSGGVDQAGGNGGAAGLIGNGGSGGVGGPGIAGSAGGAGGGLFCGNG 238 431 GGSGFGGLPSLAQVHAASTRQALRPRADGPVGAAABQVGGQSQLVSAQGSQGNGGPVGMG 450	RESULT 15 Q9HVN6 D Q9HVN6 D Q9HVN6 D Q9HVN6 D G1-MAR-2001 (TrEMBLrel. 16, Last sequence update) D 10-MAR-2001 (TrEMBLrel. 16, Last sequence update) D 10-MAR-2001 (TrEMBLrel. 15, Last annotation update) D 10-MAR-2001 (TrEMBLrel. 15, Last annotation update) D 10-MAR-2001 (TrEMBLrel. 15, Last annotation update) D 10-MAR-2001 (TrEMBLrel. 16, Last sequence update) D 10-MAR-2001 (TrEMBLrel. 16, Last sequence update) D 10-MAR-2001 (TrEMBLrel. 16, Last sequence update) D 10-MAR-2001 (TrEMBLrel. 13, Last annotation update) D 10-MAR-2001 (TrEMBLrel. 13, Last annotation update) D 20-MAR-2001 (TrEMBLrel. 13, Last annotation update) D 20-MAR-2001 (TrEMBLrel. 16, Last sequence update) D 20-MAR-2001 (TrEMBLrel. 16, Last sequence annotation annotation update) D 20-MAR-2001 (TrEMBLrel. 16, Last sequence of Pseudomonas aeruginosa PAOI, annotation	Match
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